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(71) Applicant: ZYMOGENETICS, INC. [US/US]; 1201
Eastlake Avenue East, Seattle, WA 98102 (US).

(72) Inventors: CONKLIN, Darrell, C.; 117 East Louisa
Street, #421, Seattle, WA 98102 (US). YEE, David, P.;
116 Henry Street, Cambridge, MA 02139 (US).

(74) Agent: PARKER, Gary, E.; ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102 (US).

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(54) Title: NOVEL PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract: The present invention provides polynucleotides and secreted proteins encoded by the polynucleotides. The proteins include a variety of fusion proteins, including fusions comprising a signal peptide selected from the group consisting of signal peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide. The invention further provides therapeutic and diagnostic methods utilizing the polynucleotides, polypeptides, and antagonists of the polypeptides.

Description

5 NOVEL PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

BACKGROUND OF THE INVENTION

Within the field of genetic engineering, polynucleotides encoding proteins of interest have been identified and cloned by methods that require a detailed
10 knowledge of the structure and/or function of the polynucleotide or the encoded protein. These methods include hybridization screening, polymerase chain reaction (PCR), and expression cloning.

With the more recent advent of large DNA sequence databases and the accompanying data analysis tools, identification of genes of interest is possible through
15 the analysis of raw sequence data. Databases can be "mined" to locate sequences that resemble (are "homologous to") sequences of known function. Alignment of similar sequences can be used to place novel sequences within families of structurally similar sequences. These analytical tools can be combined with structural information obtained from, for example, X-ray crystallography to predict the higher order structure
20 of a novel polypeptide. These analyses also facilitate prediction of polypeptide function. These recent technological advances have greatly increased the pace of gene discovery.

Genetic engineering has made available a number of genes and proteins of pharmaceutical or other economic importance. Such proteins include, for example,
25 tissue plasminogen activator (t-PA) (U.S. Patent No. 4,766,075), coagulation factor VII (U.S. Patent No. 4,784,950), erythropoietin (U.S. Patent No. 4,703,008), platelet derived growth factor (U.S. Patent No. 4,889,919), and various industrial enzymes (e.g., U.S. Patents Nos. 5,965,384; 5,942,431; and 5,922,586).

Although estimates vary as to the amount of the human genome that has
30 been identified to date, there remains a need in the art for further characterization of the human genome and the proteins encoded thereby. Previously unknown genes and proteins will be useful in the treatment and/or prevention of many human diseases, included diseases that have heretofore been refractory to treatment.

35 SUMMARY OF THE INVENTION

Within one aspect of the invention there is provided an isolated polypeptide comprising fifteen contiguous amino acid residues of a polypeptide as

shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422. Within one embodiment, the isolated polypeptide is from 15 to 2235 amino acid residues in length. Within another embodiment, the at least fifteen contiguous amino acid residues of SEQ ID NO:M are operably linked via a peptide bond or polypeptide linker to a second

5 polypeptide selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag, and a peptide as shown in SEQ ID NO:423. Within another embodiment, the polypeptide comprises at least 30 contiguous residues of SEQ ID NO:M. Within a further embodiment, the polypeptide comprises at least 47 contiguous residues of SEQ ID NO:M. Within additional embodiments, the

10 polypeptide is selected from the group consisting of polypeptides of SEQ ID NOS: 4, 6, 8, 10, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 82, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 136, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 186, 202, 204, 206, 208, 210, 224, 230, 232, 234, 236, 240, 242, 250, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 310, 312, 314, 316, 322,

15 324, 328, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, and 420; the group consisting of polypeptides of SEQ ID NOS: 4, 6, 8, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270,

20 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, and 420; the group consisting of polypeptides of SEQ ID NOS: 4, 6, 8, 12, 16, 18, 24, 28, 42, 48, 54, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234,

25 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, and 416; or the group consisting of polypeptides of SEQ ID NOS: 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240,

30 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, and 416.

Within a second aspect of the invention there is provided an isolated, mature protein encoded by a polynucleotide sequence selected from the group

35 consisting of SEQ ID NO:N, wherein N is an odd integer from 1 to 421. Within certain embodiments, N is 3, 5, 7, 9, 11, 15, 17, 23, 27, 41, 47, 53, 61, 65, 67, 69, 71, 81, 89, 91, 93, 95, 97, 101, 105, 107, 109, 111, 121, 123, 129, 133, 135, 137, 139, 155,

157, 161, 163, 165, 167, 173, 177, 179, 185, 201, 203, 205, 207, 209, 223, 229, 231, 233, 235, 239, 241, 249, 251, 253, 257, 261, 269, 271, 283, 285, 287, 293, 299, 301, 305, 309, 311, 313, 315, 321, 323, 327, 325, 335, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 405, 407, 411, 415, or 419; N is 3, 5, 7, 11, 15, 17, 23, 27, 41, 47, 53, 61, 65, 67, 69, 71, 89, 91, 93, 95, 97, 101, 105, 107, 109, 111, 121, 123, 129, 133, 137, 139, 155, 157, 161, 163, 165, 167, 173, 177, 179, 201, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 261, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 321, 323, 325, 335, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 405, 407, 411, 415, or 419; N is 3, 5, 7, 11, 15, 17, 23, 27, 41, 47, 53, 65, 67, 69, 71, 89, 91, 93, 95, 97, 101, 105, 107, 109, 111, 121, 123, 129, 133, 137, 139, 155, 157, 161, 163, 165, 167, 173, 177, 179, 201, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 261, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 321, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 405, 407, 411, or 415; or N is 5, 7, 11, 17, 23, 41, 47, 53, 65, 67, 69, 71, 89, 91, 95, 97, 101, 105, 109, 121, 133, 137, 139, 155, 157, 161, 163, 167, 173, 177, 179, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 407, 411, or 415.

A third aspect of the invention provides isolated polynucleotides encoding the polypeptides disclosed above. Within certain embodiments of the invention the polynucleotides comprise a sequence of nucleotides as shown in SEQ ID NO:N, wherein N is an odd integer as defined above

Within a fourth aspect of the invention there is provided an expression vector comprising the following operably linked elements: a transcription promoter; a DNA segment encoding a polypeptide as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422; and a transcription terminator. Within certain embodiments, M is 4, 6, 8, 10, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 82, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 136, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 186, 202, 204, 206, 208, 210, 224, 230, 232, 234, 236, 240, 242, 250, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 310, 312, 314, 316, 322, 324, 328, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, or 420; M is 4, 6, 8, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, or 420; M is 4, 6, 8, 12, 16, 18, 24, 28, 42,

48, 54, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, or 416; or M is 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, or 416.

10 A fifth aspect of the invention provides a cultured cell comprising the expression vector disclosed above. The cultured cell can be used, *inter alia*, within a method of producing a polypeptide, the method comprising (a) culturing the cell under conditions whereby the sequence of nucleotides is expressed, and (b) recovering the polypeptide. The invention also provides a polypeptide produced by this method.

15 Within a sixth aspect of the invention there is provided an isolated polynucleotide encoding a fusion protein, wherein the fusion protein comprises a secretory peptide selected from the group consisting of secretory peptides shown in SEQ ID NO:M, wherein M is an even integer as defined above, operably linked to a second polypeptide.

20 Within a seventh aspect of the invention there is provided an expression vector comprising the following operably linked elements: a transcription promoter; a DNA segment encoding a fusion protein as disclosed above; and a transcription terminator. The invention further provides a cultured cell comprising this expression vector, wherein the cell expresses the DNA segment and produces the encoded fusion protein. Also provided is a method of producing a protein comprising culturing the cell under conditions whereby the DNA segment is expressed, and recovering the second polypeptide. Within one embodiment the recovered second polypeptide is joined to a portion of a protein of SEQ ID NO: M, wherein M is an even integer as defined above.

30 Within a further aspect of the invention there is provided a computer-readable medium encoded with a data structure comprising SEQ ID NO:X, wherein X is an integer from 1 to 422.

 Within an additional aspect of the invention there is provided an antibody that specifically binds to a protein selected from of the group consisting of SEQ ID NO:M, wherein M is an even integer as defined above.

35 These and other aspects of the invention will become evident upon reference to the following detailed description of the invention.

DETAILED DESCRIPTION OF THE INVENTION

Prior to setting forth the invention in detail, it may be helpful to the understanding thereof to define the following terms:

The term "affinity tag" is used herein to denote a polypeptide segment that can be attached to a second polypeptide to provide for purification of the second polypeptide or provide sites for attachment of the second polypeptide to a substrate. In principal, any peptide or protein for which an antibody or other specific binding agent is available can be used as an affinity tag. Affinity tags include a poly-histidine tract, protein A (Nilsson et al., *EMBO J.* 4:1075, 1985; Nilsson et al., *Methods Enzymol.* 198:3, 1991), glutathione S transferase (Smith and Johnson, *Gene* 67:31, 1988), Glu-Glu affinity tag (Grussenmeyer et al., *Proc. Natl. Acad. Sci. USA* 82:7952-7954, 1985; see SEQ ID NO:423), substance P, Flag™ peptide (Hopp et al., *Biotechnology* 6:1204-1210, 1988), maltose binding protein (Kellerman and Ferenci, *Methods Enzymol.* 90:459-463, 1982; Guan et al., *Gene* 67:21-30, 1987), streptavidin binding peptide, thioredoxin, ubiquitin, cellulose binding protein, T7 polymerase, immunoglobulin constant domain, or other antigenic epitope or binding domain. See, in general, Ford et al., *Protein Expression and Purification* 2: 95-107, 1991. Affinity tags can be used individually or in combination. DNAs encoding affinity tags and otehr reagents are available from commercial suppliers (e.g., Pharmacia Biotech, Piscataway, NJ; Eastman Kodak, New Haven, CT; New England Biolabs, Beverly, MA).

The term "allelic variant" is used herein to denote any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in phenotypic polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequence. The term allelic variant is also used herein to denote a protein encoded by an allelic variant of a gene.

The terms "amino-terminal" and "carboxyl-terminal" are used herein to denote positions within polypeptides. Where the context allows, these terms are used with reference to a particular sequence or portion of a polypeptide to denote proximity or relative position. For example, a certain sequence positioned carboxyl-terminal to a reference sequence within a polypeptide is located proximal to the carboxyl terminus of the reference sequence, but is not necessarily at the carboxyl terminus of the complete polypeptide.

A "complement" of a polynucleotide molecule is a polynucleotide molecule having a complementary base sequence and reverse orientation as compared to a reference sequence. For example, the sequence 5' ATGCACGGG 3' is complementary to 5' CCCGTGCAT 3'.

"Corresponding to", when used in reference to a nucleotide or amino acid sequence, indicates the position in a second sequence that aligns with the reference position when two sequences are optimally aligned.

The term "degenerate nucleotide sequence" denotes a sequence of
5 nucleotides that includes one or more degenerate codons (as compared to a reference polynucleotide molecule that encodes a polypeptide). Degenerate codons encompass different triplets of nucleotides, but encode the same amino acid residue (i.e., GAU and GAC triplets each encode Asp).

The term "expression vector" is used to denote a DNA molecule, linear
10 or circular, that comprises a segment encoding a polypeptide of interest operably linked to additional segments that provide for its transcription, wherein said segments are arranged in a way that does not exist naturally. Such additional segments include promoter and terminator sequences, and may also include one or more origins of replication, one or more selectable markers, an enhancer, a polyadenylation signal, etc.
15 Expression vectors are generally derived from plasmid or viral DNA, or may contain elements of both.

The term "isolated", when applied to a polynucleotide, denotes that the polynucleotide has been removed from its natural genetic milieu and is thus free of other extraneous or unwanted coding sequences, and is in a form suitable for use within
20 genetically engineered protein production systems. Such isolated molecules are those that are separated from their natural environment and include cDNA and genomic clones. Isolated DNA molecules of the present invention are free of other genes with which they are ordinarily associated, but may include naturally occurring 5' and 3' untranslated regions such as promoters and terminators. The identification of
25 associated regions will be evident to one of ordinary skill in the art (see for example, Dynan and Tijan, *Nature* 316:774-78, 1985).

An "isolated" polypeptide or protein is a polypeptide or protein that is found in a condition other than its native environment, such as apart from blood and animal tissue. In a preferred form, the isolated polypeptide or protein is substantially
30 free of other polypeptides or proteins, particularly other polypeptides or proteins of animal origin. It is preferred to provide the polypeptides or proteins in a highly purified form, i.e. greater than 95% pure, more preferably greater than 99% pure. When used in this context, the term "isolated" does not exclude the presence of the same polypeptide or protein in alternative physical forms, such as dimers or alternatively glycosylated or
35 derivatized forms.

A "mature protein" is a protein that is produced by cellular processing of a primary translation product of a DNA sequence. Such processing may include

removal of a secretory signal peptide, sometimes in combination with a propeptide. Mature sequences can be predicted from full-length sequences using methods known in the art for predicting cleavage sites. See, for example, von Heijne (*Nuc. Acids Res.* 14:4683, 1986). The sequence of a mature protein can be determined experimentally
5 by expressing a DNA sequence of interest in a eukaryotic host cell and determining the amino acid sequence of the final product. For proteins lacking secretory peptides, the primary translation product will be the mature protein.

"Operably linked", when referring to DNA segments, indicates that the segments are arranged so that they function in concert for their intended purposes, e.g.,
10 transcription initiates in the promoter and proceeds through the coding segment to the terminator. When referring to polypeptides, "operably linked" includes both covalently (e.g., by disulfide bonding) and non-covalently (e.g., by hydrogen bonding, hydrophobic interactions, or salt-bridge interactions) linked sequences, wherein the desired function(s) of the sequences are retained.

15 The term "ortholog" denotes a polypeptide or protein obtained from one species that is the functional counterpart of a polypeptide or protein from a different species. Sequence differences among orthologs are the result of speciation.

"Paralogs" are distinct but structurally related proteins made by an organism. Paralogs are believed to arise through gene duplication. For example, α -
20 globin, β -globin, and myoglobin are paralogs of each other.

A "polynucleotide" is a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. Polynucleotides include RNA and DNA, and may be isolated from natural sources, synthesized *in vitro*, or prepared from a combination of natural and synthetic
25 molecules. Sizes of polynucleotides are expressed as base pairs (abbreviated "bp"), nucleotides ("nt"), or kilobases ("kb"). Where the context allows, the latter two terms may describe polynucleotides that are single-stranded or double-stranded. When the term is applied to double-stranded molecules it is used to denote overall length and will be understood to be equivalent to the term "base pairs". It will be recognized by those
30 skilled in the art that the two strands of a double-stranded polynucleotide may differ slightly in length and that the ends thereof may be staggered as a result of enzymatic cleavage; thus all nucleotides within a double-stranded polynucleotide molecule may not be paired. Such unpaired ends will in general not exceed 20 nt in length.

A "polypeptide" is a polymer of amino acid residues joined by peptide
35 bonds, whether produced naturally or synthetically. Polypeptides of less than about 10 amino acid residues are commonly referred to as "peptides".

The term "promoter" is used herein for its art-recognized meaning to denote a portion of a gene containing DNA sequences that provide for the binding of RNA polymerase and initiation of transcription. Promoter sequences are commonly, but not always, found in the 5' non-coding regions of genes.

5 A "protein" is a macromolecule comprising one or more polypeptide chains. A protein may also comprise non-peptidic components, such as carbohydrate groups. Carbohydrates and other non-peptidic substituents may be added to a protein by the cell in which the protein is produced, and will vary with the type of cell. Proteins are defined herein in terms of their amino acid backbone structures;
10 substituents such as carbohydrate groups are generally not specified, but may be present nonetheless.

 A "secretory signal sequence" is a DNA sequence that encodes a polypeptide (a "secretory peptide") that, as a component of a larger polypeptide, directs the larger polypeptide through a secretory pathway of a cell in which it is synthesized.
15 The larger polypeptide is commonly cleaved to remove the secretory peptide during transit through the secretory pathway.

 The present invention is based in part upon the discovery of a group of novel, protein-encoding DNA molecules. These DNA molecules and the amino acid sequences that they encode are shown in SEQ ID NO:1 through SEQ ID NO:436.
20 Sequence analysis predicts that each of the encoded proteins includes an amino-terminal secretory peptide. These secretory peptides are shown below in Table 1, wherein residue numbers are in reference to the indicated SEQ ID NO. As will be understood by those skilled in the art, the cleavage sites predicted by conventional models of secretory peptide cleavage (e.g., von Heijne, *Nuc. Acids Res.* 14:4683, 1986)
25 are not always exact and may vary by as much as ± 5 residues. In addition, cleavage may occur at multiple sites within 5 residues of the indicated position. The mature form of any given protein may thus consist of a plurality of species differing at their amino termini.

Table 1

<u>Protein</u>	<u>SEQ ID NO:</u>	<u>Residues 1-</u>
AFP210015	2	14
AFP170681	4	26
AFP413680	6	28
AFP483037	8	14
AFP230872	10	27
AFP178828	12	14
AFP200134	14	23
AFP195796	16	22
AFP477303	18	18
AFP354334	20	25
AFP250287	22	17
AFP177000	24	26
AFP278176	26	21
AFP202885	28	18
AFP221312	30	23
AFP239757	32	22
AFP226311	34	20
AFP305901	36	20
AFP325549	38	20
AFP81988	40	14
AFP199200	42	20
AFP290395	44	23
AFP212675	46	20
AFP326051	48	17
AFP512441	50	18
AFP55098	52	15
AFP169796	54	21
AFP280706	56	25
AFP383165	58	23
AFP195467	60	26
AFP134225	62	22
AFP261193	64	28
AFP324422	66	28
AFP374312	68	28
AFP258118	70	24
AFP74517	72	25
AFP254653	74	18
AFP108666	76	21
AFP8766	78	15
AFP397185	80	20
AFP195042	82	21
AFP310695	84	26
AFP70022	86	19
AFP121670	88	22
AFP345861	90	15

AFP395942	92	16
AFP170291	94	21
AFP297548	96	22
AFP188135	98	28
AFP302388	100	19
AFP263430	102	17
AFP201273	104	18
AFP98983	106	25
AFP581958	108	20
AFP404202	110	19
AFP207203	112	15
AFP220790	114	19
AFP536326	116	23
AFP257473	118	22
AFP248380	120	16
AFP276202	122	20
AFP227568	124	23
AFP229039	126	20
AFP176297	128	17
AFP356885	130	17
AFP226938	132	16
AFP138504	134	29
AFP359196	136	24
AFP501809	138	27
AFP152733	140	15
AFP541394	142	23
AFP243183	144	20
AFP80739	146	18
AFP361806	148	26
AFP483930	150	21
AFP257336	152	25
AFP195800	154	23
AFP179530	156	19
AFP279267	158	14
AFP299766	160	29
AFP244615	162	16
AFP325761	164	22
AFP226024	166	22
AFP257094	168	27
AFP197103	170	27
AFP271855	172	17
AFP324816	174	29
AFP407963	176	25
AFP369635	178	17
AFP93743	180	28
AFP243230	182	15
AFP169316	184	21
AFP130852	186	15

AFP194191	188	22
AFP213472	190	21
AFP360430	192	22
AFP491309	194	21
AFP193428	196	23
AFP366534	198	22
AFP22706	200	27
AFP389012	202	14
AFP137186	204	24
AFP127023	206	21
AFP389687	208	16
AFP293220	210	25
AFP425535	212	25
AFP301494	214	25
AFP345421	216	19
AFP216667	218	26
AFP247951	220	29
AFP4464	222	22
AFP561930	224	28
AFP192851	226	22
AFP252759	228	20
AFP199044	230	20
AFP357958	232	28
AFP117501	234	15
AFP194554	236	23
AFP371069	238	23
AFP313600	240	19
AFP262739	242	18
AFP180730	244	27
AFP287227	246	28
AFP75785	248	26
AFP174843	250	15
AFP250422	252	15
AFP198645	254	17
AFP238111	256	16
AFP460626	258	24
AFP271081	260	14
AFP277752	262	16
AFP291338	264	15
AFP551038	266	22
AFP301579	268	20
AFP266188	270	16
AFP275580	272	28
AFP298054	274	21
AFP348226	276	23
AFP349106	278	23
AFP288248	280	15
AFP436476	282	19

AFP352125	284	14
AFP62060	286	25
AFP236718	288	21
AFP75775	290	25
AFP407487	292	23
AFP280451	294	27
AFP11675	296	29
AFP348656	298	16
AFP277451	300	19
AFP287436	302	14
AFP116043	304	28
AFP138740	306	26
AFP15192	308	17
AFP169968	310	27
AFP173341	312	23
AFP17588	314	23
AFP176427	316	20
AFP192633	318	14
AFP193013	320	15
AFP193881	322	16
AFP195562	324	16
AFP199922	326	18
AFP204736	328	17
AFP206179	330	27
AFP221877	332	23
AFP222758	334	26
AFP227032	336	24
AFP229269	338	27
AFP232213	340	25
AFP237679	342	21
AFP249599	344	28
AFP275215	346	21
AFP290397	348	26
AFP306591	350	18
AFP310297	352	20
AFP314720	354	19
AFP318671	356	29
AFP323575	358	21
AFP327160	360	20
AFP329002	362	29
AFP345415	364	24
AFP347179	366	24
AFP359138	368	23
AFP365372	370	17
AFP367284	372	23
AFP372822	374	26
AFP374595	376	29
AFP375952	378	25

AFP382913	380	17
AFP389184	382	23
AFP404208	384	20
AFP404279	386	29
AFP409112	388	26
AFP413111	390	19
AFP415635	392	15
AFP421092	394	17
AFP436666	396	25
AFP448623	398	19
AFP454192	400	20
AFP49026	402	28
AFP51688	404	28
AFP525341	406	16
AFP545268	408	15
AFP592620	410	22
AFP62197	412	23
AFP68229	414	25
AFP71288	416	15
AFP77851	418	27
AFP81957	420	15
AFP85168	422	27

A secretory peptide of a protein of the present invention can be used to direct the secretion of other proteins of interest from a host cell. Thus, the present invention provides, *inter alia*, fusions comprising such a secretory peptide of a protein disclosed herein operably linked to another protein of interest. The secretory peptide can be used to direct the secretion of other proteins of interest by joining a polynucleotide sequence encoding it, in the correct reading frame, to the 5' end of a sequence encoding the other protein of interest. Those skilled in the art will recognize that the resulting fused sequence may encode additional residues of a protein of the present invention at the amino terminus of the protein to be secreted. In the extreme case, the fusion may comprise an entire protein of the present invention fused to the amino terminus of a second protein, whereby secretion of the fusion protein is directed by the secretory peptide of the protein of the present invention. It will often be desirable to include a proteolytic cleavage site between the protein of the present invention (or portion thereof) and the other protein of interest. The joined polynucleotide sequences are then introduced into a host cell, which is cultured according to conventional methods. The protein of interest is then recovered from the culture media. Methods for introducing DNA into host cells, culturing the cells, and isolating recombinant proteins are known in the art. Representative methods are summarized below.

Within certain embodiments of the invention, the protein is selected from those listed in Table 2. Within related embodiments of the invention, the polynucleotide is selected from polynucleotides encoding the proteins listed in Table 2, i.e., for a protein of SEQ ID NO:M, the polynucleotide is SEQ ID NO:M-1.

5

Table 2

SEQ ID NO:	Protein	SEQ ID NO:	Protein
6	AFP413680	234	AFP117501
12	AFP178828	236	AFP194554
18	AFP477303	240	AFP313600
24	AFP177000	242	AFP262739
42	AFP199200	252	AFP250422
48	AFP326051	254	AFP198645
66	AFP324422	258	AFP460626
68	AFP374312	270	AFP266188
72	AFP74517	272	AFP275580
90	AFP345861	288	AFP236718
92	AFP395942	294	AFP280451
96	AFP297548	300	AFP277451
98	AFP188135	306	AFP138740
110	AFP404202	324	AFP195562
134	AFP138504	338	AFP229269
138	AFP501809	342	AFP237679
156	AFP179530	344	AFP249599
158	AFP279267	348	AFP290397
162	AFP244615	350	AFP306591
164	AFP325761	366	AFP347179
174	AFP324816	374	AFP372822
180	AFP93743	378	AFP375952
204	AFP137186	386	AFP404279
206	AFP127023	396	AFP436666
210	AFP293220	398	AFP448623
224	AFP561930	408	AFP545268
230	AFP199044	416	AFP71288

Higher order structures of the proteins of the present invention can be
10 predicted by computer analysis using available software (e.g., the Insight II® viewer and homology modeling tools available from MSI, San Diego, CA; and King and Sternberg, *Protein Sci.* 5:2298-310, 1996). In addition, analytical algorithms permit the identification of homologies between newly discovered proteins and known proteins. Such homologies are indicative of related biological functions.

AFP254653 is 49% identical in sequence to human lysozyme C. Lysozyme C is a secreted bacteriolytic enzyme with similarity to the alpha-lactalbumins. Both are small alpha + beta proteins with six conserved cysteines forming a disulfide core comprising three disulfide bonds. AFP254653 may also
5 exhibit bacteriolytic or other antimicrobial activity.

AFP581958 is 43% identical to wheat aluminum-induced protein, a member of the Bowman-Birk proteinase inhibitor family. All serine proteinases possess an exposed inhibitor loop that is stabilized by intermolecular interactions (usually disulfide bonds) between residues flanking the binding loop and the protein
10 core. Interaction between inhibitor and enzyme produces a stable complex that disassociates very slowly, producing either an unaffected or a modified inhibitor that is cleaved at the scissile bond of the binding loop. AFP581958 may be a secreted serine proteinase.

AFP220790 is 42% identical to chicken lysozyme G, a bacteriolytic
15 glycosyl hydrolase that hydrolizes peptidoglycan homopolymers of the prokaryote cell walls. AFP220790 may thus be a secreted bacteriolytic enzyme, and may exhibit other antimicrobial activity.

AFP271855 is 37% identical to bovine granulocyte peptide A precursor (antimicrobial BGP-A). Bovine and murine granulocyte peptide A precursor (also
20 called antimicrobial BGP-A) are disclosed in WIPO publication WO 97/29765. Bovine GP-A was isolated from a bone marrow library (WO 97/29765). GP-A exhibits activity against Gram-positive and Gram-negative bacteria, fungi and viruses. AFP271855 may exhibit antimicrobial (including one or more of anti-bacterial, anti-fungal, and anti-viral) activity.

AFP298054 is 24% identical to human T1/ST2 ligand. The T1 gene is also known as ST2, DER4, and Fit-1. It encodes a member of the interleukin-1 (IL-1) receptor family. It is transcribed in two forms, a soluble form and a membrane-bound form. The classical IL-1 ligands (IL-1 α , IL-1 β , and IL-1ra) do not bind T1. A putative ligand for T1 was disclosed in 1996 (Gayle et al., *J. Biol. Chem.* 271:5784-5789, 1996).
25 This protein binds T1 but is unable to initiate signal transduction by the membrane-bound form. The ligand is apparently a type I membrane protein. It has a predicted molecular weight (excluding the signal sequence and transmembrane domain) of about 22 kD, and has no sequence or hydrophobicity profile similarity to the beta-trefoil cytokines IL-1 or the FGFs. AFP298054 may be an antagonist that binds the receptor
30 and regulates the activity of an as yet undiscovered IL-1 homolog.
35

Table 3 lists homologies between AFP sequences and sequences contained in the GenBank database, Derwent protein (PSP) or polynucleotide (PSN) databases, or Protein Identification Resource (PIR).

5

Table 3

Locus	Accession Number & Description
AFP130852	AE003823 (fly genomic)
AFP169968	AE003515 (fly genomic)
AFP174843	AF283518 (<i>Mus musculus</i> elongation factor sec)
AFP176427	AE003808 (fly genomic)
AFP178828	PSN_V61483
AFP179530	AE003708 (fly genomic)
AFP188135	AE003677 (fly genomic)
AFP195042	PIR_T41241 (yeast oxysterol-binding protein family)
AFP198645	AE003718 (fly genomic)
AFP199200	AF113691 (human clone FLB4739 PRO1238 mRNA)
AFP204736	AC069237 (human chromosome 3 clone RP11-175M9)
AFP229269	AF247177 (<i>Mus musculus</i> sphingosine-1-phosphate phosphohydrolase)
AFP230872	AF150741 (<i>Rattus norvegicus</i> prolactin-like protein J mRNA)
AFP279267	AE003559 (fly genomic)
AFP347179	AE003499 (fly genomic) Z1041035F6P
AFP357958	AF283518 (<i>Mus musculus</i> elongation factor sec mRNA)
AFP359196	AE003530 (fly genomic)
AFP374312	AE003538 (fly genomic)
AFP389687	AE003831 (fly genomic)
AFP395942	AB041564 (mouse brain cDNA; clone MNCb-0914)
AFP404202	AL137255 (human mRNA; cDNA DKFZp434B1813)
AFP413680	X14971 (mouse mRNA for alpha-adaptin, MMADAPA1)
AFP477303	AE003778 (fly genomic)
AFP62060	PSP_Y94938 (Human secreted protein clone ye78_1)
AFP71288	AL161655 (human chromosome 20 clone RP11-116E13)
AFP74517	PIR_T16263 (<i>C. elegans</i> hypothetical protein F35D11.3)

Table 4 lists AFP proteins for which regions of identity have been found in the GenBank database.

Table 4

Locus	Accession Number & Description
AFP127023	SK000740 (human cDNA FLJ20733; clone HEP08550; by homology: molybdopterin cofactor sulfurase)
AFP134225	AB020970 (human mRNA; partial cds and 3'UTR; up-regulated by BCG-CWS)
AFP195562	AK000382 (human cDNA FLJ20375; clone HUV00942)

AFP199044	HSU80813 (human nucleoside diphosphate kinase homolog DR-nm23)
AFP227032	AK001848 (human cDNA FLJ10986; clone PLACE1001869; weakly similar to L-RIBULOKINASE; EC 2.7.1.16)
AFP237679	AB000465 (human mRNA; exon 1; 2; 3; 4; clone:RES4-24B; in genomic region of Huntington's disease locus)
AFP262739	AK000135 (human cDNA FLJ20128; clone COL06181)
AFP369635	PSN_Z24827 (Human secreted protein gene 17 clone HNF1Y77)
AFP81957	AF267730 (human 26S proteasome-associated UCH interacting protein 1; UIP1)
AFP93743	AK000066 (human cDNA FLJ20059; clone COL01349)

Table 5 lists AFP proteins for which longer regions of identity have been found in proteins contained in GenBank and other databases.

Table 5

Locus	Accession Number & Description
AFP117501	AK000505 (human cDNA FLJ20498; clone KAT08960)
AFP138740	HSM802370 (human mRNA; cDNA DKFZp434M1511)
AFP170291	AK000494 (human cDNA FLJ20487; clone KAT08245)
AFP170681	AK001698 (human cDNA FLJ10836; clone NT2RP4001228 close paralogue of human Kelch-like 1 protein (KLHL1) mRNA: AF252283)
AFP177000	AK000524 (human cDNA FLJ20517; clone KAT10235)
AFP193881	AK000382 (human cDNA FLJ20375; clone HUV00942)
AFP195796	AF251041 (human SGC32445 protein (SGC32445) mRNA; homology to PSP_W35393 Human TB2 gene product)
AFP202885	AB037808 (human mRNA for KIAA1387 protein)
AFP207203	AF250924 (human PNGase mRNA: peptide N-glycanase)
AFP226024	AK001952 (human cDNA FLJ11090; clone PLACE1005308)
AFP227568	AB019038 (human HMT-1 mRNA for beta-1,4 mannosyltransferase)
AFP244615	AK001009 (human cDNA FLJ10147; clone HEMBA1003369; weak homology: CENE_HUMAN CENTROMERIC PROTEIN E)
AFP250422	AF208849 (human BM-007 mRNA)
AFP266188	AK000272 (human cDNA FLJ20265; clone COLF9334; homology to major facilitator protein homolog, fission yeast: PIR_S62432)
AFP277451	AK001373 (human cDNA FLJ10511; clone NT2RP2000656)
AFP277752	AK000453 (human cDNA FLJ20446; clone KAT05231; weak homology to dinitrogenase reductase activating glycohydrolase (draG) <i>Archaeoglobus fulgidus</i> : PIR_C69465)
AFP280451	AL133355 (Human DNA sequence from clone RP11-541N10 on chromosome 10. Contains a novel gene and the 5' end of the gene for a novel protein; ortholog of mouse FISH protein)
AFP293220	AK001441 (human cDNA FLJ10579; clone NT2RP2003446)
AFP297548	AK000494 (human cDNA FLJ20487; clone KAT08245)
AFP306591	AL359700 (human chromosome 6 clone RP11-802L12)
AFP324816	AB032966 (human mRNA for KIAA1140 protein weak homology: Human O-linked GlcNAc transferase mRNA)

AFP356885	AK001544 (human cDNA FLJ10682; clone NT2RP3000072)
AFP389012	AK000428 (human cDNA FLJ20421; clone KAT02467; homologous to human bisphosphate 3'-nucleotidase mRNA: AF125042)
AFP436666	AK001608 (human cDNA FLJ10746; clone NT2RP3001679; likely human orthologue of <i>Rattus norvegicus</i> small rec (srec) mRNA: AF228917)
AFP501809	AK001963 (human cDNA FLJ11101; clone PLACE1005623)
AFP525341	AF189692 (human non-kinase Cdc42 effector protein SPEC2 mRNA)

A protein of the present invention can be prepared as a fusion protein by joining it to a second polypeptide or a plurality of additional polypeptides. Suitable second polypeptides include amino- or carboxyl-terminal extensions, such as linker peptides of up to about 20-25 residues and extensions that facilitate purification (affinity tags) as disclosed above. A protein of interest can be prepared as a fusion to a dimerizing protein as disclosed in U.S. Patents Nos. 5,155,027 and 5,567,584. Preferred dimerizing proteins in this regard include immunoglobulin constant region domains. Immunoglobulin-polypeptide fusions can be expressed in genetically engineered cells to produce a variety of multimeric analogs of a protein of interest. Fusion proteins can also comprise auxiliary domains that target the protein of interest to specific cells, tissues, or macromolecules (e.g., collagen). For example, a protein of interest can be targeted to a predetermined cell type by fusing it to a ligand that specifically binds to a receptor on the surface of a target cell. In this way, proteins can be targeted for therapeutic or diagnostic purposes. A protein can be fused to two or more moieties, such as an affinity tag for purification and a targeting domain. Protein fusions can also comprise one or more cleavage sites, particularly between domains. See, Tuan et al., *Connective Tissue Research* 34:1-9, 1996. Proteins of the present invention can also be used as targetting moieties within fusion proteins comprising, for example, cytokines, cytotoxins, or other biologically active polypeptide moieties.

Protein fusions of the present invention will usually contain not more than about 1,200 amino acid residues joined to the AFP protein. For example, an AFP protein can be fused to *E. coli* β -galactosidase (1,021 residues; see Casadaban et al., *J. Bacteriol.* 143:971-980, 1980), a 10-residue spacer, and a 4-residue factor Xa cleavage site. Such a protein comprising, for example, AFP345421 (SEQ ID NO:216), contains 2235 amino acid residues. In a second example, an AFP protein can be fused to maltose binding protein (approximately 370 residues), a 4-residue cleavage site, and a 6-residue polyhistidine tag.

As disclosed above, the proteins of the present invention or portions thereof can also be used to direct the secretion of a second protein. When such fusions

are designed so that the secreted protein retains a portion of the protein of the present invention, the fusion protein can be purified by means that exploit the properties of the protein of the present invention. Typical of such methods is immunoaffinity chromatography using an antibody directed against a protein of the present invention.

- 5 When such a fusion is engineered to contain a cleavage site at the fusion point, the fusion can be cleaved and the protein of interest recovered free of extraneous sequence.

The present invention also provides polynucleotide molecules, including DNA and RNA molecules, that encode the proteins disclosed above. Those skilled in the art will readily recognize that, in view of the degeneracy of the genetic code, 10 considerable sequence variation is possible among these polynucleotide molecules. The amino acid sequence information provided herein can be used by one of ordinary skill in the art to generate degenerate sequences comprising all nucleotide sequences encoding a particular polypeptide. Table 6 sets forth the one-letter codes used to denote degenerate nucleotide positions. "Resolutions" are the nucleotides denoted by a 15 code letter. "Complement" indicates the code for the complementary nucleotide(s). For example, the code Y denotes either C or T, and its complement R denotes A or G, A being complementary to T, and G being complementary to C.

TABLE 6

20

Nucleotide	Resolutions	Complement	Resolutions
A	A	T	T
C	C	G	G
G	G	C	C
T	T	A	A
R	A G	Y	C T
Y	C T	R	A G
M	A C	K	G T
K	G T	M	A C
S	C G	S	C G
W	A T	W	A T
H	A C T	D	A G T
B	C G T	V	A C G
V	A C G	B	C G T
D	A G T	H	A C T
N	A C G T	N	A C G T

Degenerate codons encompassing all possible codons for a given amino acid are set forth in Table 7, below.

TABLE 7

Amino Acid	One-Letter Code	Codons	Degenerate Codon
Cys	C	TGC TGT	TGY
Ser	S	AGC AGT TCA TCC TCG TCT	WSN
Thr	T	ACA ACC ACG ACT	CAN
Pro	P	CCA CCC CCG CCT	CCN
Ala	A	GCA GCC GCG GCT	GCN
Gly	G	GGA GGC GGG GGT	GGN
Asn	N	AAC AAT	AA Y
Asp	D	GAC GAT	GAY
Glu	E	GAA GAG	GAR
Gln	Q	CAA CAG	CAR
His	H	CAC CAT	CAY
Arg	R	AGA AGG CGA CGC CGG CGT	MGN
Lys	K	AAA AAG	AAR
Met	M	ATG	ATG
Ile	I	ATA ATC ATT	ATH
Leu	L	CTA CTC CTG CTT TTA TTG	YTN
Val	V	GTA GTC GTG GTT	GTN
Phe	F	TTC TTT	TTY
Tyr	Y	TAC TAT	TAY
Trp	W	TGG	TGG
Ter	.	TAA TAG TGA	TRR
Asn Asp	B		RAY
Glu Gln	Z		SAR
Any	X		NNN
Gap	-	---	

5

One of ordinary skill in the art will appreciate that some ambiguity is introduced in determining a degenerate codon, representative of all possible codons encoding each amino acid. For example, the degenerate codon for serine (WSN) can, in some circumstances, encode arginine (AGR), and the degenerate codon for arginine (MGN) can, in some circumstances, encode serine (AGY). A similar relationship

10

exists between codons encoding phenylalanine and leucine. Thus, some polynucleotides encompassed by the degenerate sequences may encode variant amino acid sequences, but one of ordinary skill in the art can easily identify such variant sequences by reference to the amino acid sequences disclosed in the accompanying

5 Sequence Listing.

Methods for preparing DNA and RNA are well known in the art. Complementary DNA (cDNA) clones are prepared from RNA that is isolated from a tissue or cell that produces large amounts of the cognate mRNA. Such tissues and cells are identified by methods commonly known in the art, such as Northern blotting

10 (Thomas, *Proc. Natl. Acad. Sci. USA* 77:5201, 1980). Databases of expressed sequence tags (ESTs) can be analyzed to produce an "electronic Northern" wherein sequences are assigned to specific cell or tissue sources on the basis of their abundance within libraries. Table 8, below, shows the results of such an analysis when, as the minimum significant abundance, it was required that at least 10% of all sequences for a given

15 protein were from a single source and at least five individual clones had been identified from that source. Sequences shown in the accompanying Sequence Listing but not listed in Table 8 were widely distributed among various tissues or were represented by few clones.

Table 8

AFP152733	K562 cells
AFP169796	T-cells
AFP173341	testis
AFP17588	fetal liver or spleen
AFP194554	fetal liver or spleen
AFP199922	testis
AFP229269	placenta
AFP237679	fetal liver or spleen
AFP257094	adult brain
AFP258118	epidermal breast keratinocytes
AFP263430	breast
AFP276202	infant brain
AFP287436	testis
AFP290397	testis
AFP306591	fetal heart
AFP325761	K562 cells
AFP352125	testis
AFP359138	infant brain
AFP369635	germinal center B-cells
AFP409112	kidney
AFP483037	neonatal keratinocytes
AFP49026	peripheral blood eosinophils of asthma patients
AFP545268	K562 cells
AFP561930	fetal liver or spleen
AFP62060	testis
AFP62197	pregnant uterus
AFP93743	germinal center B-cells
AFP98983	fetal heart

A panel of cDNAs from human tissues was screened for AFP expression using PCR. The panel was made from first strand cDNAs obtained from Clontech laboratories, Inc., Palo Alto, CA and contained 20 first-strand cDNA samples from the human tissues shown in Table 9. The panel was set up in a 96-well format that further included a human genomic DNA (obtained from Clontech Laboratories, Inc.) positive control sample and a water-only well as a negative control sample. Each well contained approximately 0.2-100 pg/ μ l of cDNA, diluted with water to 17.5 μ l. The

PCR reactions were set up by adding oligonucleotide primers, DNA polymerase (Ex Taq™; TAKARA Shuzo Co. Ltd. Biomedicals Group, Japan or Advantage™ 2 cDNA polymerase mix; Clontech Laboratories, Inc.) with the appropriate supplied buffer, dNTP mix (TAKARA Shuzo Co. Ltd.), and a density increasing agent and tracking dye
5 (RediLoad; Research Genetics, Inc., Huntsville, AL) to each sample on the panel. The amplification was carried out as follows: incubation at 94°C for 2 minutes; 35 cycles of 94°C for 30 seconds, 60°C for 20 seconds, and 72°C for 30 seconds; followed by incubation at 72°C for 5 minutes. About 10 µl of the PCR reaction product was subjected to standard agarose gel electrophoresis using a 4% agarose gel.

Table 9

Protein	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
AFP117501	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP127023	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	n	y	y	n	y	n	n
AFP137186	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP138504	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP138740	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP177000	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP178828	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP179530	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	y	y	n	y
AFP188135	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP194554	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP195562	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP198645	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n
AFP199044	n	n	n	y	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n
AFP199200	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP229269	y	y	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	n	y
AFP236718	n	y	y	y	y	y	y	n	n	y	n	n	n	y	n	n	n	y	y	y	n	y
AFP237679	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP244615	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP249599	n	y	y	n	n	y	y	y	n	n	n	n	n	n	y	y	n	n	n	n	n	y
AFP250422	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP262739	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP266188	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP275580	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP277451	y	y	y	y	y	y	y	y	y	nd	nd	y	y	y	y	y	y	y	y	y	n	n
AFP279267	y	y	y	y	y	y	y	y	n	y	y	y	n	y	y	y	y	y	y	y	n	n
AFP280451	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP290397	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP293220	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP297548	y	y	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	n	y
AFP306591	y	y	y	y	y	y	y	y	y	y	n	y	y	nd	y	nd	y	y	y	y	n	y
AFP313600	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP324422	n	n	y	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	y	n	n	y

Table 9, continued

Protein	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
AFP324816	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP325761	y	y	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	n	n
AFP326051	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP345861	y	y	y	y	y	y	y	nd	nd	y	nd	y	nd	y	y	y	y	y	y	y	n	n
AFP347179	y	y	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	n	y
AFP372822	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP374312	n	n	y	y	n	n	n	n	n	n	n	n	n	n	n	n	y	y	n	n	n	y
AFP375952	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	y
AFP395942	y	y	y	y	y	y	y	y	n	n	y	y	n	y	n	y	y	y	y	y	n	y
AFP404202	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP404279	y	y	y	y	n	y	y	n	y	y	y	y	y	y	y	y	n	y	y	y	n	y
AFP413680	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	nd	y	y	y	n	y
AFP436666	y	y	y	y	y	y	y	y	n	y	y	y	n	y	y	y	y	y	y	y	n	n
AFP448623	y	n	y	n	n	y	n	n	n	n	n	n	n	n	y	n	n	y	y	n	n	y
AFP460626	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	nd	y	y	y	n	y
AFP477303	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP501809	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP545268	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP561930	y	y	y	y	y	y	y	nd	y	y	n	y	y	nd	y	y	y	y	nd	y	n	y
AFP71288	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	y
AFP74517	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP93743	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y

Tissues screened were: 1, brain; 2, heart; 3, kidney; 4, liver; 5, lung; 6, pancreas; 7, placenta; 8, skeletal muscle; 9, colon; 10, ovary; 11, peripheral blood leukocytes; 12, prostate; 13, small intestine; 14, spleen; 15, testis; 16, thymus; 17, bone marrow; 18, fetal liver; 19, lymph node; 20, tonsil; 21, H₂O; 22, genomic DNA. Y=yes; n=no; nd=not determined.

Total RNA can be prepared using guanidine HCl extraction followed by isolation by centrifugation in a CsCl gradient (Chirgwin et al., *Biochemistry* 18:52-94, 1979). Poly (A)⁺ RNA is prepared from total RNA using the method of Aviv and Leder (*Proc. Natl. Acad. Sci. USA* 69:1408-1412, 1972). Complementary DNA (cDNA) is prepared from poly(A)⁺ RNA using known methods. In the alternative, genomic DNA can be isolated. For some applications (e.g., expression in transgenic animals) it may be preferable to use a genomic clone, or to modify a cDNA clone to include at least one genomic intron. Methods for identifying and isolating cDNA and genomic clones are well known and within the level of ordinary skill in the art, and include the use of the sequences disclosed herein, sequences complementary thereto, or parts thereof, for probing or priming a library. Such methods include, for example, hybridization or polymerase chain reaction ("PCR", Mullis, U.S. Patent 4,683,202). Expression libraries can be probed with antibodies to a protein of interest, receptor fragments, or other specific binding partners.

The polynucleotides of the present invention can also be prepared by automated synthesis. Synthesis of polynucleotides is within the level of ordinary skill in the art, and suitable equipment and reagents are available from commercial suppliers. See, in general, Glick and Pasternak, Molecular Biotechnology, Principles & Applications of Recombinant DNA, ASM Press, Washington, D.C., 1994; Itakura et al., *Ann. Rev. Biochem.* 53: 323-56, 1984; and Climie et al., *Proc. Natl. Acad. Sci. USA* 87:633-7, 1990.

The present invention further provides antisense polynucleotides that are complementary to a segment of a polynucleotide as set forth in one of SEQ ID NO:N, wherein N is an odd integer from 1 to 435. Such antisense polynucleotides are designed to bind to the corresponding mRNA and inhibit its translation. Antisense polynucleotides are used to inhibit gene expression in cell culture or in a patient, and can be used as probes or primers for research or diagnostic purposes.

Probes and primers of the present invention comprise a suitable fragment, and may comprise up to the complete sequence, of a polynucleotide as shown in SEQ ID NO:N or the complement thereof, wherein N is an odd integer from 1 to 421. Probes will generally be at least 20 nucleotides in length, although somewhat shorter probes (14-17 nucleotides) can be used. PCR primers are at least 5 nucleotides in length, preferably 15 or more nt, more preferably 20-30 nt. Shorter polynucleotide probes and primers are referred to in the art as "oligonucleotides," and can be DNA or RNA. Probes will generally comprise an oligonucleotide linked to a label, such as a radionuclide.

Probes and primers as disclosed herein can be used for cloning allelic, orthologous, and paralogous sequences. Allelic variants of the disclosed sequences can be cloned by probing cDNA or genomic libraries from different individuals according to standard procedures. Orthologous sequences can be cloned using information and compositions provided by the present invention in combination with conventional cloning techniques. For example, a cDNA can be cloned using mRNA obtained from a tissue or cell type that expresses the protein. Suitable sources of mRNA can be identified by probing Northern blots with probes designed from the sequences disclosed herein. A library is then prepared from mRNA of a positive tissue or cell line. A cDNA can then be isolated by a variety of methods, such as by probing with a complete or partial human cDNA or with one or more sets of degenerate probes based on the disclosed sequences. A cDNA can also be cloned by PCR using primers designed from the sequences disclosed herein. Within an additional method, the cDNA library can be used to transform or transfect host cells, and expression of the cDNA of interest can be detected with an antibody to the encoded protein. Similar techniques can also be applied to the isolation of genomic clones. Orthologous and paralogous sequences can be identified from libraries by probing blots at low stringency and washing the blots at successively higher stringency until background is suitably reduced.

Probes and primers disclosed herein can be used to clone 5' non-coding regions of a corresponding gene. In view of the tissue-specific expression observed for certain proteins of the invention (Tables 8 and 9), promoters of these genes are expected to provide tissue-specific expression. Such promoter elements can thus be used to direct the tissue-specific expression of heterologous genes in, for example, transgenic animals or patients treated with gene therapy. Cloning of 5' flanking sequences also facilitates production of a protein of interest by "gene activation" as disclosed in U.S. Patent No. 5,641,670. Briefly, expression of an endogenous gene in a cell is altered by introducing into its locus a DNA construct comprising at least a targeting sequence, a regulatory sequence, an exon, and an unpaired splice donor site. The targeting sequence is a 5' non-coding sequence that permits homologous recombination of the construct with the endogenous locus, whereby the sequences within the construct become operably linked with the endogenous coding sequence. In this way, an endogenous promoter can be replaced or supplemented with other regulatory sequences to provide enhanced, tissue-specific, or otherwise regulated expression.

The polynucleotides of the present invention further include polynucleotides encoding the fusion proteins, including signal peptide fusions, disclosed above.

The present invention further provides a computer-readable medium
5 encoded with a data structure that provides at least one of SEQ ID NO:1 through SEQ ID NO:436. Suitable forms of computer-readable media include magnetic media and optically-readable media. Examples of magnetic media include a hard or fixed drive, a random access memory (RAM) chip, a floppy disk, digital linear tape (DLT), a disk cache, and a ZIP® disk. Optically readable media are exemplified by compact discs
10 (e.g., CD-read only memory (ROM), CD-rewritable (RW), and CD-recordable), digital versatile/video discs (DVD) (e.g., DVD-ROM, DVD-RAM, and DVD+RW), and carrier waves.

The polypeptides of the present invention, including full-length proteins, biologically active fragments, immunogenic fragments, and fusion proteins,
15 can be produced in genetically engineered host cells according to conventional techniques. Suitable host cells are those cell types that can be transformed or transfected with exogenous DNA and grown in culture, and include bacteria, fungal cells, and cultured higher eukaryotic cells. Eukaryotic cells, particularly cultured cells of multicellular organisms, are generally preferred for the production of proteins
20 having higher eukaryotic-type post-translational modifications (e.g., γ -carboxylation) and for making proteins, especially secretory proteins, for pharmaceutical use in humans. Techniques for manipulating cloned DNA molecules and introducing exogenous DNA into a variety of host cells are disclosed by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory
25 Press, Cold Spring Harbor, NY, 1989, and Ausubel et al., eds., *Current Protocols in Molecular Biology*, Green and Wiley and Sons, NY, 1993.

In general, a DNA sequence encoding a polypeptide of interest is operably linked to other genetic elements required for its expression, generally including a transcription promoter and terminator, within an expression vector. The
30 vector will also commonly contain one or more selectable markers and one or more origins of replication, although those skilled in the art will recognize that within certain systems selectable markers can be provided on separate vectors, and replication of the exogenous DNA can be achieved through integration into the host cell genome. Selection of promoters, terminators, selectable markers, vectors and other elements is a
35 matter of routine design within the level of ordinary skill in the art. Many such elements are described in the literature and are available through commercial suppliers.

To direct a polypeptide into the secretory pathway of a host cell, a secretory signal sequence (also known as a leader sequence, prepro sequence or pre sequence) is provided in the expression vector. The secretory signal sequence may be that of the protein of interest, or may be derived from another secreted protein (e.g., t-PA; see U.S. Patent No. 5,641,655) or synthesized *de novo*. The secretory signal sequence is operably linked to the DNA sequence encoding the protein of interest, i.e., the two sequences are joined in the correct reading frame and positioned to direct the newly synthesized protein into the secretory pathway of the host cell. Secretory signal sequences are commonly positioned 5' to the DNA sequence encoding the protein of interest, although certain secretory signal sequences may be positioned elsewhere in the DNA sequence of interest (see, e.g., Welch et al., U.S. Patent No. 5,037,743; Holland et al., U.S. Patent No. 5,143,830).

Cultured mammalian cells are suitable hosts for use within the present invention. Methods for introducing exogenous DNA into mammalian host cells include calcium phosphate-mediated transfection (Wigler et al., *Cell* 14:725, 1978; Corsaro and Pearson, *Somatic Cell Genetics* 7:603, 1981; Graham and Van der Eb, *Virology* 52:456, 1973), electroporation (Neumann et al., *EMBO J.* 1:841-845, 1982), DEAE-dextran mediated transfection (Ausubel et al., *ibid.*), and liposome-mediated transfection (Hawley-Nelson et al., *Focus* 15:73, 1993; Ciccarone et al., *Focus* 15:80, 1993). The production of recombinant polypeptides in cultured mammalian cells is disclosed by, for example, Levinson et al., U.S. Patent No. 4,713,339; Hagen et al., U.S. Patent No. 4,784,950; Palmiter et al., U.S. Patent No. 4,579,821; and Ringold, U.S. Patent No. 4,656,134. Suitable cultured mammalian cells include the COS-1 (ATCC No. CRL 1650), COS-7 (ATCC No. CRL 1651), BHK (ATCC No. CRL 1632), BHK 570 (ATCC No. CRL 10314), 293 (ATCC No. CRL 1573; Graham et al., *J. Gen. Virol.* 36:59-72, 1977) and Chinese hamster ovary (e.g. CHO-K1; ATCC No. CCL 61) cell lines. Additional suitable cell lines are known in the art and available from public depositories such as the American Type Culture Collection, Rockville, Maryland. In general, strong transcription promoters are preferred, such as promoters from SV-40 or cytomegalovirus. See, e.g., U.S. Patent No. 4,956,288. Other suitable promoters include those from metallothionein genes (U.S. Patent Nos. 4,579,821 and 4,601,978) and the adenovirus major late promoter. Within an alternative embodiment, adenovirus vectors can be employed. See, for example, Garnier et al., *Cytotechnol.* 15:145-55, 1994.

Drug selection is generally used to select for cultured mammalian cells into which foreign DNA has been inserted. Such cells are commonly referred to as "transfectants". Cells that have been cultured in the presence of the selective agent and

are able to pass the gene of interest to their progeny are referred to as "stable transfectants." An exemplary selectable marker is a gene encoding resistance to the antibiotic neomycin. Selection is carried out in the presence of a neomycin-type drug, such as G-418 or the like. Selection systems can also be used to increase the expression level of the gene of interest, a process referred to as "amplification." Amplification is carried out by culturing transfectants in the presence of a low level of the selective agent and then increasing the amount of selective agent to select for cells that produce high levels of the products of the introduced genes. An exemplary amplifiable selectable marker is dihydrofolate reductase, which confers resistance to methotrexate. Other drug resistance genes (e.g. hygromycin resistance, multi-drug resistance, puromycin acetyltransferase) can also be used.

Insect cells can be infected with recombinant baculovirus, commonly derived from *Autographa californica* nuclear polyhedrosis virus (AcNPV). See, King and Possee, The Baculovirus Expression System: A Laboratory Guide, London, Chapman & Hall; O'Reilly et al., Baculovirus Expression Vectors: A Laboratory Manual, New York, Oxford University Press., 1994; and Richardson, Ed., Baculovirus Expression Protocols. Methods in Molecular Biology, Humana Press, Totowa, NJ, 1995. Recombinant baculovirus can also be produced through the use of a transposon-based system described by Luckow et al. (*J. Virol.* 67:4566-4579, 1993). This system, which utilizes transfer vectors, is commercially available in kit form (Bac-to-Bac™ kit; Life Technologies, Rockville, MD). See also, Hill-Perkins and Possee, *J. Gen. Virol.* 71:971-976, 1990; Bonning et al., *J. Gen. Virol.* 75:1551-1556, 1994; and Chazenbalk and Rapoport, *J. Biol. Chem.* 270:1543-1549, 1995.

For protein production, the recombinant virus is used to infect host cells, typically a cell line derived from the fall armyworm, *Spodoptera frugiperda* (e.g., Sf9 or Sf21 cells) or *Trichoplusia ni* (e.g., High Five™ cells; Invitrogen, Carlsbad, CA). See, in general, Glick and Pasternak, Molecular Biotechnology: Principles and Applications of Recombinant DNA, ASM Press, Washington, D.C., 1994. See also, U.S. Patent No. 5,300,435. Serum-free media are used to grow and maintain the cells. Suitable media formulations are known in the art and can be obtained from commercial suppliers. The cells are grown up from an inoculation density of approximately $2-5 \times 10^5$ cells to a density of $1-2 \times 10^6$ cells, at which time a recombinant viral stock is added at a multiplicity of infection (MOI) of 0.1 to 10, more typically near 3. Procedures used are generally described in available laboratory manuals (e.g., King and Possee, *ibid.*; O'Reilly et al., *ibid.*; Richardson, *ibid.*). See also, Guarino et al., U.S. Patent No. 5,162,222 and WIPO publication WO 94/06463.

Fungal cells, including yeast cells, can also be used within the present invention. Yeast species of particular interest in this regard include *Saccharomyces cerevisiae*, *Pichia pastoris*, and *Pichia methanolica*. Methods for transforming *S. cerevisiae* cells with exogenous DNA and producing recombinant polypeptides therefrom are disclosed by, for example, Kawasaki, U.S. Patent No. 4,599,311; Kawasaki et al., U.S. Patent No. 4,931,373; Brake, U.S. Patent No. 4,870,008; Welch et al., U.S. Patent No. 5,037,743; and Murray et al., U.S. Patent No. 4,845,075. Transformed cells are selected by phenotype determined by the selectable marker, commonly drug resistance or the ability to grow in the absence of a particular nutrient (e.g., leucine). A preferred vector system for use in *Saccharomyces cerevisiae* is the *POT1* vector system disclosed by Kawasaki et al. (U.S. Patent No. 4,931,373), which allows transformed cells to be selected by growth in glucose-containing media. Suitable promoters and terminators for use in yeast include those from glycolytic enzyme genes (see, e.g., Kawasaki, U.S. Patent No. 4,599,311; Kingsman et al., U.S. Patent No. 4,615,974; and Bitter, U.S. Patent No. 4,977,092) and alcohol dehydrogenase genes. See also U.S. Patents Nos. 4,990,446; 5,063,154; 5,139,936 and 4,661,454.

Transformation systems for other yeasts, including *Hansenula polymorpha*, *Schizosaccharomyces pombe*, *Kluyveromyces lactis*, *Kluyveromyces fragilis*, *Ustilago maydis*, *Pichia pastoris*, *Pichia methanolica*, *Pichia guilliermondii* and *Candida maltosa* are known in the art. See, for example, Gleeson et al., *J. Gen. Microbiol.* 132:3459-3465, 1986 and Cregg, U.S. Patent No. 4,882,279. Aspergillus cells may be utilized according to the methods of McKnight et al., U.S. Patent No. 4,935,349. Methods for transforming *Acremonium chrysogenum* are disclosed by Sumino et al., U.S. Patent No. 5,162,228. Methods for transforming *Neurospora* are disclosed by Lambowitz, U.S. Patent No. 4,486,533. Production of recombinant proteins in *Pichia methanolica* is disclosed in U.S. Patents No. 5,716,808, 5,736,383, 5,854,039, and 5,888,768; and WIPO publications WO 99/14347 and WO 99/14320.

Other higher eukaryotic cells, including plant cells and avian cells, can also be used as hosts according to methods commonly known in the art. For example, the use of *Agrobacterium rhizogenes* as a vector for expressing genes in plant cells has been reviewed by Sinkar et al., *J. Biosci. (Bangalore)* 11:47-58, 1987.

Prokaryotic host cells, including strains of the bacteria *Escherichia coli*, *Bacillus* and other genera are also useful host cells within the present invention. Techniques for transforming these hosts and expressing foreign DNA sequences cloned therein are well known in the art (see, e.g., Sambrook et al., *ibid.*). When expressing a polypeptide in bacteria such as *E. coli*, the polypeptide may be retained in the

cytoplasm, typically as insoluble granules, or may be directed to the periplasmic space by a bacterial secretion sequence. In the former case, the cells are lysed, and the granules are recovered and denatured using, for example, guanidine isothiocyanate or urea. The denatured polypeptide can then be refolded and dimerized by diluting the denaturant, such as by dialysis against a solution of urea and a combination of reduced and oxidized glutathione, followed by dialysis against a buffered saline solution. In the latter case, the polypeptide can be recovered from the periplasmic space in a soluble and functional form by disrupting the cells (by, for example, sonication or osmotic shock) to release the contents of the periplasmic space and recovering the protein, thereby obviating the need for denaturation and refolding.

Transformed or transfected host cells are cultured according to conventional procedures in a culture medium containing nutrients and other components required for the growth of the chosen host cells. A variety of suitable media, including defined media and complex media, are known in the art and generally include a carbon source, a nitrogen source, essential amino acids, vitamins and minerals. Media may also contain such components as growth factors or serum, as required. The growth medium will generally select for cells containing the exogenously added DNA by, for example, drug selection or deficiency in an essential nutrient which is complemented by the selectable marker carried on the expression vector or co-transfected into the host cell.

It is preferred to purify the polypeptides and proteins of the present invention to $\geq 80\%$ purity, more preferably to $\geq 90\%$ purity, even more preferably $\geq 95\%$ purity, and particularly preferred is a pharmaceutically pure state, that is greater than 99.9% pure with respect to contaminating macromolecules, particularly other proteins and nucleic acids, and free of infectious and pyrogenic agents. Preferably, a purified polypeptide or protein is substantially free of other polypeptides or proteins, particularly those of animal origin.

Expressed recombinant proteins (including single polypeptide chains, chimeric polypeptides, and polypeptide multimers) are purified by conventional protein purification methods, typically by a combination of chromatographic techniques. See, in general, Affinity Chromatography: Principles & Methods, Pharmacia LKB Biotechnology, Uppsala, Sweden, 1988; and Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York, 1994. Proteins comprising a polyhistidine affinity tag (typically about 6 histidine residues) are purified by affinity chromatography on a nickel chelate resin. See, for example, Houchuli et al., *Bio/Technol.* 6: 1321-1325, 1988. Proteins comprising a glu-glu tag can be purified by immunoaffinity chromatography essentially as disclosed by Grussenmeyer et al., *ibid.*

Proteins comprising other affinity tags can be purified by appropriate affinity chromatography methods, which are known in the art.

Proteins of the present invention and fragments thereof can also be prepared through chemical synthesis according to methods known in the art, including
5 exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. See, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149, 1963; Stewart et al., Solid Phase Peptide Synthesis (2nd edition), Pierce Chemical Co., Rockford, IL, 1984; Bayer and Rapp, *Chem. Pept. Prot.* 3:3, 1986; and Atherton et al., Solid Phase Peptide Synthesis: A Practical Approach, IRL Press, Oxford, 1989.

10 Using methods known in the art, the proteins of the present invention can be prepared in a variety of modified or derivatized forms. For example, the proteins can be prepared glycosylated or non-glycosylated; pegylated or non-pegylated; and may or may not include an initial methionine amino acid residue.

Biological activities of the proteins of the present invention can be
15 measured *in vitro* using cultured cells or *in vivo* by administering molecules of the claimed invention to the appropriate animal model. Many such assays and models are known in the art. Guidance in initial assay selection is provided by structural predictions and sequence alignments. However, even if no functional prediction is made, the activity of a protein can be elucidated by known methods, including, for
20 example, screening a variety of target cells for a biological response, other *in vitro* assays, expression in a host animal, or through the use of transgenic and/or "knockout" animals. Through the application of robotics, many *in vitro* assays can be adapted to rapid, high-throughput screening of a large number of samples. Target cells for use in activity assays include, without limitation, vascular cells (especially endothelial cells
25 and smooth muscle cells), hematopoietic (myeloid and lymphoid) cells, liver cells (including hepatocytes, fenestrated endothelial cells, Kupffer cells, and Ito cells), fibroblasts (including human dermal fibroblasts and lung fibroblasts), neurite cells (including astrocytes, glial cells, dendritic cells, and PC-12 cells), fetal lung cells, articular synoviocytes, pericytes, chondrocytes, osteoblasts, adipocytes, and prostate
30 epithelial cells. Endothelial cells and hematopoietic cells are derived from a common ancestral cell, the hemangioblast (Choi et al., *Development* 125:725-732, 1998).

Biological activity can be measured with a silicon-based biosensor microphysiometer that measures the extracellular acidification rate or proton excretion associated with receptor binding and subsequent physiologic cellular responses. An
35 exemplary such device is the Cytosensor™ Microphysiometer manufactured by Molecular Devices, Sunnyvale, CA. A variety of cellular responses, such as cell proliferation, ion transport, energy production, inflammatory response, regulatory and

receptor activation, and the like, can be measured by this method. See, for example, McConnell et al., *Science* 257:1906-1912, 1992; Pitchford et al., *Meth. Enzymol.* 228:84-108, 1997; Arimilli et al., *J. Immunol. Meth.* 212:49-59, 1998; and Van Liefde et al., *Eur. J. Pharmacol.* 346:87-95, 1998. The microphysiometer can be used for

5 assaying adherent or non-adherent eukaryotic or prokaryotic cells. By measuring extracellular acidification changes in cell media over time, the microphysiometer directly measures cellular responses to various stimuli, including agonistic and antagonistic stimuli. Preferably, the microphysiometer is used to measure responses of a eukaryotic cell known to be responsive to the protein of interest, compared to a

10 control eukaryotic cell that does not respond to the protein of interest. Responsive eukaryotic cells comprise cells into which a receptor for the protein of interest has been transfected, as well as naturally responsive cells. Differences in the response of cells exposed to the protein of interest, relative to a control not so exposed, are a direct measurement of protein-modulated cellular responses. Such responses can be assayed

15 under a variety of stimuli. The present invention thus provides methods of identifying agonists and antagonists of proteins of interest, comprising providing cells responsive to a selected protein, culturing a first portion of the cells in the absence of a test compound, culturing a second portion of the cells in the presence of a test compound, and detecting a change in a cellular response of the second portion of the cells as

20 compared to the first portion of the cells. The change in cellular response is shown as a measurable change in extracellular acidification rate. Culturing a third portion of the cells in the presence of the protein of interest and the absence of a test compound provides a positive control and a control to compare the agonist activity of a test compound with that of the protein of interest. Antagonists can be identified by

25 exposing the cells to the protein of interest in the presence and absence of the test compound, whereby a reduction in protein-stimulated activity is indicative of antagonist activity in the test compound.

Assays measuring cell proliferation or differentiation are well known in the art. For example, assays measuring proliferation include such assays as

30 chemosensitivity to neutral red dye (Cavanaugh et al., *Investigational New Drugs* 8:347-354, 1990), incorporation of radiolabelled nucleotides (as disclosed by, e.g., Raines and Ross, *Methods Enzymol.* 109:749-773, 1985; Wahl et al., *Mol. Cell Biol.* 8:5016-5025, 1988; and Cook et al., *Analytical Biochem.* 179:1-7, 1989), incorporation of 5-bromo-2'-deoxyuridine (BrdU) in the DNA of proliferating cells (Porstmann et al.,

35 *J. Immunol. Methods* 82:169-179, 1985), and use of tetrazolium salts (Mosmann, *J. Immunol. Methods* 65:55-63, 1983; Alley et al., *Cancer Res.* 48:589-601, 1988; Marshall et al., *Growth Reg.* 5:69-84, 1995; and Scudiero et al., *Cancer Res.* 48:4827-

4833, 1988). Differentiation can be assayed using suitable precursor cells that can be induced to differentiate into a more mature phenotype. Assays measuring differentiation include, for example, measuring cell-surface markers associated with stage-specific expression of a tissue, enzymatic activity, functional activity or morphological changes (Watt, *FASEB*, 5:281-284, 1991; Francis, *Differentiation* 57:63-75, 1994; Raes, *Adv. Anim. Cell Biol. Technol. Bioprocesses*, 161-171, 1989). Effects of a protein on tumor cell growth and metastasis can be analyzed using the Lewis lung carcinoma model, for example as described by Cao et al., *J. Exp. Med.* 182:2069-2077, 1995. Activity of a protein on cells of neural origin can be analyzed using assays that measure effects on neurite growth as disclosed below.

In vitro assays for pro- and anti-inflammatory activity are known in the art. Exemplary activity assays include mitogenesis assays in which IL-1 responsive cells (e.g., D10.N4.M cells) are incubated in the presence of IL-1 or a test protein for 72 hours at 37°C in a 5% CO₂ atmosphere. IL-2 (and optionally IL-4) is added to the culture medium to enhance sensitivity and specificity of the assay. ³H-thymidine is then added, and incubation is continued for six hours. The amount of label incorporated is indicative of agonist activity. See, Hopkins and Humphreys, *J. Immunol. Methods* 120:271-276, 1989; Greenfeder et al., *J. Biol. Chem.* 270:22460-22466, 1995. Stimulation of cell proliferation can also be measured using thymocytes cultured in a test protein in combination with phytohemagglutinin. IL-1 is used as a control. Proliferation is detected as ³H-thymidine incorporation or metabolic breakdown of (MTT) (Mosman, *ibid.*).

Protein activity may also be detected using assays designed to measure induction of one or more growth factors or other macromolecules. Preferred such assays include those for determining the presence of hepatocyte growth factor (HGF), epidermal growth factor (EGF), transforming growth factor alpha (TGFα), interleukin-6 (IL-6), VEGF, acidic fibroblast growth factor (aFGF), angiogenin, and other macromolecules produced by the liver. Suitable assays include mitogenesis assays using target cells responsive to the macromolecule of interest, receptor-binding assays, competition binding assays, immunological assays (e.g., ELISA), and other formats known in the art. Metalloprotease secretion is measured from treated primary human dermal fibroblasts, synoviocytes and chondrocytes. The relative levels of collagenase, gelatinase and stromalysin produced in response to culturing a target cell in the presence of a protein of interest is measured using zymogram gels (Loita and Stetler-Stevenson, *Cancer Biology* 1:96-106, 1990). Procollagen/collagen synthesis by dermal fibroblasts and chondrocytes in response to a test protein is measured using ³H-proline incorporation into nascent secreted collagen. ³H-labeled collagen is visualized by

SDS-PAGE followed by autoradiography (Unemori and Amento, *J. Biol. Chem.* 265: 10681-10685, 1990). Glycosaminoglycan (GAG) secretion from dermal fibroblasts and chondrocytes is measured using a 1,9-dimethylmethylene blue dye binding assay (Farndale et al., *Biochim. Biophys. Acta* 883:173-177, 1986). Collagen and GAG
5 assays are also carried out in the presence of IL-1 β or TGF- β to examine the ability of a protein to modify the established responses to these cytokines.

Monocyte activation assays are carried out (1) to look for the ability of a protein of interest to further stimulate monocyte activation, and (2) to examine the ability of a protein of interest to modulate attachment-induced or endotoxin-induced
10 monocyte activation (Fuhlbrigge et al., *J. Immunol.* 138: 3799-3802, 1987). IL-1 β and TNF α levels produced in response to activation are measured by ELISA (Biosource, Inc. Camarillo, CA). Monocyte/macrophage cells, by virtue of CD14 (LPS receptor), are exquisitely sensitive to endotoxin, and proteins with moderate levels of endotoxin-like activity will activate these cells.

15 Other metabolic effects of proteins can be measured by culturing target cells in the presence and absence of a protein and observing changes in adipogenesis, gluconeogenesis, glycogenolysis, lipogenesis, glucose uptake, or the like. Suitable assays are known in the art.

Hematopoietic activity of proteins can be assayed on various
20 hematopoietic cells in culture. Preferred assays include primary bone marrow colony assays and later stage lineage-restricted colony assays, which are known in the art (e.g., Holly et al., WIPO Publication WO 95/21920). Marrow cells plated on a suitable semi-solid medium (e.g., 50% methylcellulose containing 15% fetal bovine serum, 10% bovine serum albumin, and 0.6% PSN antibiotic mix) are incubated in the
25 presence of test polypeptide, then examined microscopically for colony formation. Known hematopoietic factors are used as controls. Mitogenic activity of a protein of interest on hematopoietic cell lines can be measured as disclosed above.

Cell migration is assayed essentially as disclosed by Kähler et al. (*Arteriosclerosis, Thrombosis, and Vascular Biology* 17:932-939, 1997). A protein is
30 considered to be chemotactic if it induces migration of cells from an area of low protein concentration to an area of high protein concentration. A typical assay is performed using modified Boyden chambers with a polystyrene membrane separating the two chambers (Transwell; Corning Costar Corp.). The test sample, diluted in medium containing 1% BSA, is added to the lower chamber of a 24-well plate
35 containing Transwells. Cells are then placed on the Transwell insert that has been pretreated with 0.2% gelatin. Cell migration is measured after 4 hours of incubation at 37°C. Non-migrating cells are wiped off the top of the Transwell membrane, and cells

attached to the lower face of the membrane are fixed and stained with 0.1% crystal violet. Stained cells are then extracted with 10% acetic acid and absorbance is measured at 600 nm. Migration is then calculated from a standard calibration curve. Cell migration can also be measured using the matrigel method of Grant et al.
5 ("Angiogenesis as a component of epithelial-mesenchymal interactions" in Goldberg and Rosen, *Epithelial-Mesenchymal Interaction in Cancer*, Birkhäuser Verlag, 1995, 235-248; Baatout, *Anticancer Research* 17:451-456, 1997).

Proteins can be assayed for the ability to modulate axon guidance and growth. Suitable assays that detect changes in neuron growth patterns include, for
10 example, those disclosed in Hastings, WIPO Publication WO 97/29189 and Walter et al., *Development* 101:685-96, 1987. Assays to measure the effects on neuron growth are well known in the art. For example, the C assay (e.g., Raper and Kapfhammer, *Neuron* 4:21-9, 1990 and Luo et al., *Cell* 75:217-27, 1993) can be used to determine collapsing activity of a protein of interest on growing neurons. Other methods that can
15 assess protein-induced inhibition of neurite extension or divert such extension are also known. See, Goodman, *Annu. Rev. Neurosci.* 19:341-77, 1996. Conditioned media from cells expressing a protein of interest, or aggregates of such cells, can be placed in a gel matrix near suitable neural cells, such as dorsal root ganglia (DRG) or sympathetic ganglia explants, which have been co-cultured with nerve growth factor.
20 Compared to control cells, protein-induced changes in neuron growth can be measured (as disclosed by, for example, Messersmith et al., *Neuron* 14:949-59, 1995 and Puschel et al., *Neuron* 14:941-8, 1995). Neurite outgrowth can be measured using neuronal cell suspensions grown in the presence of molecules of the present invention. See, for example, O'Shea et al., *Neuron* 7:231-7, 1991 and DeFreitas et al., *Neuron* 15:333-43,
25 1995.

Cell adhesion activity is assayed essentially as disclosed by LaFleur et al. (*J. Biol. Chem.* 272:32798-32803, 1997). Briefly, microtiter plates are coated with the test protein, non-specific sites are blocked with BSA, and cells (such as smooth
30 muscle cells, leukocytes, or endothelial cells) are plated at a density of approximately 10^4 - 10^5 cells/well. The wells are incubated at 37°C (typically for about 60 minutes), then non-adherent cells are removed by gentle washing. Adhered cells are quantitated by conventional methods (e.g., by staining with crystal violet, lysing the cells, and determining the optical density of the lysate). Control wells are coated with a known adhesive protein, such as fibronectin or vitronectin.

35 Assays for angiogenic activity are also known in the art. For example, the effect of a protein of interest on primordial endothelial cells in angiogenesis can be assayed in the chick chorioallantoic membrane angiogenesis assay (Leung, *Science*

246:1306-1309, 1989; Ferrara, *Ann. NY Acad. Sci.* 752:246-256, 1995). Briefly, a small window is cut into the shell of an eight-day old fertilized egg, and a test substance is applied to the chorioallantoic membrane. After 72 hours, the membrane is examined for neovascularization. Other suitable assays include microinjection of early stage quail (*Coturnix coturnix japonica*) embryos as disclosed by Drake et al. (*Proc. Natl. Acad. Sci. USA* 92:7657-7661, 1995); the rodent model of corneal neovascularization disclosed by Muthukkaruppan and Auerbach (*Science* 205:1416-1418, 1979), wherein a test substance is inserted into a pocket in the cornea of an inbred mouse; and the hamster cheek pouch assay (Höckel et al., *Arch. Surg.* 128:423-429, 1993). Induction of vascular permeability, which is indicative of angiogenic activity, is measured in assays designed to detect leakage of protein from the vasculature of a test animal (e.g., mouse or guinea pig) after administration of a test compound (Miles and Miles, *J. Physiol.* 118:228-257, 1952; Feng et al., *J. Exp. Med.* 183:1981-1986, 1996). *In vitro* assays for angiogenic activity include the tridimensional collagen gel matrix model (Pepper et al. *Biochem. Biophys. Res. Comm.* 189:824-831, 1992 and Ferrara et al., *Ann. NY Acad. Sci.* 732:246-256, 1995), which measures the formation of tube-like structures by microvascular endothelial cells; and matrigel models (Grant et al., "Angiogenesis as a component of epithelial-mesenchymal interactions" in Goldberg and Rosen, *Epithelial-Mesenchymal Interaction in Cancer*, Birkhäuser Verlag, 1995, 235-248; Baatout, *Anticancer Research* 17:451-456, 1997), which are used to determine effects on cell migration and tube formation by endothelial cells seeded in matrigel, a basement membrane extract enriched in laminin. It is preferred to carry out angiogenesis assays in the presence and absence of vascular endothelial growth factor (VEGF) to assess possible combinatorial effects. It is also preferred to use VEGF as a control within *in vivo* assays.

Receptor binding can be measured by the competition binding method of Labriola-Tompkins et al., *Proc. Natl. Acad. Sci. USA* 88:11182-11186, 1991. In an exemplary assay for IL-1 receptor binding, membranes prepared from EL-4 thymoma cells (Paganelli et al., *J. Immunol.* 138:2249-2253, 1987) are incubated in the presence of the test protein for 30 minutes at 37°C. Labeled IL-1 α or IL-1 β is then added and the incubation is continued for 60 minutes. The assay is terminated by membrane filtration. The amount of bound label is determined by conventional means (e.g., γ counter). In an alternative assay, the ability of a test protein to compete with labeled IL-1 for binding to cultured human dermal fibroblasts is measured according to the method of Dower et al. (*Nature* 324:266-268, 1986). Briefly, cells are incubated in a round-bottomed, 96-well plate in a suitable culture medium (e.g., RPMI 1640 containing 1% BSA, 0.1% Na azide, and 20 mM HEPES pH 7.4) at 8°C on a rocker

platform in the presence of labeled IL-1. Various concentrations of test protein are added. After the incubation (typically about two hours), cells are separated from unbound label by centrifuging 60- μ l aliquots through 200 μ l of phthalate oils in 400- μ l polyethylene centrifuge tubes and excising the tips of the tubes with a razor blade as disclosed by Segal and Hurwitz, *J. Immunol.* 118:1338-1347, 1977. Receptor binding assays for other cell types are known in the art. See, for example, Bowen-Pope and Ross, *Methods Enzymol.* 109:69-100, 1985.

Receptor binding can also be measured using immobilized receptors or ligand-binding receptor fragments. For example, an immobilized receptor can be exposed to its labeled ligand and unlabeled test protein, whereby a reduction in labeled ligand binding compared to a control is indicative of receptor-binding activity in the test protein. Within another format, a receptor or ligand-binding receptor fragment is immobilized on a biosensor (e.g., BIAcore™, Pharmacia Biosensor, Piscataway, NJ) and binding is determined. Antagonists of the native ligand will exhibit receptor binding but will exhibit essentially no activity in appropriate activity assays or will reduce the ligand-mediated response when combined with the native ligand. In view of the low level of receptor occupancy required to produce a response to some ligands (e.g., IL-1), a large excess of antagonist (typically a 10- to 1000-fold molar excess) may be necessary to neutralize ligand activity.

Receptor activation can be detected in target cells by: (1) measurement of adenylate cyclase activity (Salomon et al., *Anal. Biochem.* 58:541-48, 1974; Alvarez and Daniels, *Anal. Biochem.* 187:98-103, 1990); (2) measurement of change in intracellular cAMP levels using conventional radioimmunoassay methods (Steiner et al., *J. Biol. Chem.* 247:1106-13, 1972; Harper and Brooker, *J. Cyc. Nucl. Res.* 1:207-18, 1975); or (3) through use of a cAMP scintillation proximity assay (SPA) method (such as available from Amersham Corp., Arlington Heights, IL).

Proteins can be tested for serine protease activity or proteinase inhibitory activity using conventional assays. Substrate cleavage is conveniently assayed using a tetrapeptide that mimics the cleavage site of the natural substrate and which is linked, via a peptide bond, to a carboxyl-terminal para-nitro-anilide (pNA) group. The protease hydrolyzes the bond between the fourth amino acid residue and the pNA group, causing the pNA group to undergo a dramatic increase in absorbance at 405 nm. Suitable substrates can be synthesized according to known methods or obtained from commercial suppliers. Inhibitory activity is measured by adding a test sample to a reaction mixture containing enzyme and substrate, and comparing the observed enzyme activity to a control (without the test sample). A variety of such assays are known in the art, including assays measuring inhibition of trypsin,

chymotrypsin, plasmin, cathepsin G, and human leukocyte elastase. See, for example, Petersen et al., *Eur. J. Biochem.* 235:310-316, 1996. In a typical procedure, the inhibitory activity of a test compound is measured by incubating the test compound with the proteinase, then adding an appropriate substrate, typically a chromogenic peptide substrate. See, for example, Norris et al. (*Biol. Chem. Hoppe-Seyler* 371:37-42, 1990). Various concentrations of the inhibitor are incubated in the presence of trypsin, plasmin, and plasma kallikrein in a low-salt buffer at pH 7.4, 25°C. After 30 minutes, the residual enzymatic activity is measured by the addition of a chromogenic substrate (e.g., S2251 (D-Val-Leu-Lys-Nan) or S2302 (D-Pro-Phe-Arg-Nan), available from Kabi, Stockholm, Sweden) and a 30-minute incubation. Inhibition of enzyme activity is indicated by a decrease in absorbance at 405 nm or fluorescence Em at 460 nm. From the results, the apparent inhibition constant K_i is calculated. When a serine protease is prepared as an active precursor (e.g., comprising N-terminal residues 1-109 of SEQ ID NO:2), it is activated by cleavage with a suitable protease (e.g., furin (Steiner et al., *J. Biol. Chem.* 267:23435-23438, 1992)) prior to assay. Assays of this type are well known in the art. See, for example, Lottenberg et al., *Thrombosis Research* 28:313-332, 1982; Cho et al., *Biochem.* 23:644-650, 1984; Foster et al., *Biochem.* 26:7003-7011, 1987). The inhibition of coagulation factors (e.g., factor VIIa, factor Xa) can be measured using chromogenic substrates or in conventional coagulation assays (e.g., clotting time of normal human plasma; Dennis et al., *J. Biol. Chem.* 270:25411-25417, 1995).

Blood coagulation and chromogenic assays, which can be used to detect both procoagulant, anticoagulant, and thrombolytic activities, are known in the art. For example, pro- and anticoagulant activities can be measured in a one-stage clotting assay using platelet-poor or factor-deficient plasma (Levy and Edgington, *J. Exp. Med.* 151:1232-1243, 1980; Schwartz et al., *J. Clin. Invest.* 67:1650-1658, 1981). As disclosed by Anderson et al. (*Proc. Natl. Acad. Sci. USA* 96:11189-11193, 1999), the effect of a test compound on platelet activation can be determined by a change in turbidity, and the procoagulant activity of activated platelets can be determined in a phospholipid-dependent coagulation assay. Activation of thrombin can be determined by hydrolysis of peptide p-nitroanilide substrates as disclosed by Lottenberg et al. (*Thrombosis Res.* 28:313-332, 1982). Other procoagulant, anticoagulant, and thrombolytic activities can be measured using appropriate chromogenic substrates, a variety of which are available from commercial suppliers. See, for example, Kettner and Shaw, *Methods Enzymol.* 80:826-842, 1981.

Anti-microbial activity of proteins is evaluated by techniques that are known in the art. For example, anti-microbial activity can be assayed by evaluating the

sensitivity of microbial cell cultures to test agents and by evaluating the protective effect of test agents on infected mice. See, for example, Musiek et al., *Antimicrob. Agents Chemother.* 3:40, 1973. Antiviral activity can also be assessed by protection of mammalian cell cultures. Known techniques for evaluating anti-microbial activity include, for example, Barsum et al., *Eur. Respir. J.* 8:709-714, 1995; Sandovsky-Losica et al., *J. Med. Vet. Mycol (England)* 28:279-287, 1990; Mehentee et al., *J. Gen. Microbiol (England)* 135(:2181-2188, 1989; and Segal and Savage, *J. Med. Vet. Mycol.* 24:477-479, 1986. Assays specific for anti-viral activity include, for example, those described by Daher et al., *J. Virol.* 60:1068-1074, 1986.

10 The assays disclosed above can be modified by those skilled in the art to detect the presence of agonists and antagonists of a selected protein of interest.

 Expression of a polynucleotide encoding a protein of interest in animals provides models for further study of the biological effects of overproduction or inhibition of protein activity *in vivo*. Polynucleotides and antisense polynucleotides
15 can be introduced into test animals, such as mice, using viral vectors or naked DNA, or transgenic animals can be produced.

 One *in vivo* approach for assaying proteins of the present invention utilizes viral delivery systems. Exemplary viruses for this purpose include adenovirus, herpesvirus, retroviruses, vaccinia virus, and adeno-associated virus (AAV).
20 Adenovirus, a double-stranded DNA virus, is currently the best studied gene transfer vector for delivery of heterologous nucleic acids. For review, see Becker et al., *Meth. Cell Biol.* 43:161-89, 1994; and Douglas and Curiel, *Science & Medicine* 4:44-53, 1997. The adenovirus system offers several advantages. Adenovirus can (i) accommodate relatively large DNA inserts; (ii) be grown to high-titer; (iii) infect a
25 broad range of mammalian cell types; and (iv) be used with many different promoters including ubiquitous, tissue specific, and regulatable promoters. Because adenoviruses are stable in the bloodstream, they can be administered by intravenous injection.

 By deleting portions of the adenovirus genome, larger inserts (up to 7 kb) of heterologous DNA can be accommodated. These inserts can be incorporated
30 into the viral DNA by direct ligation or by homologous recombination with a co-transfected plasmid. In an exemplary system, the essential E1 gene is deleted from the viral vector, and the virus will not replicate unless the E1 gene is provided by the host cell (e.g., the human 293 cell line). When intravenously administered to intact animals, adenovirus primarily targets the liver. If the adenoviral delivery system has an E1 gene
35 deletion, the virus cannot replicate in the host cells. However, the host's tissue (e.g., liver) will express and process (and, if a signal sequence is present, secrete) the

heterologous protein. Secreted proteins will enter the circulation in the highly vascularized liver, and effects on the infected animal can be determined.

An alternative method of gene delivery comprises removing cells from the body and introducing a vector into the cells as a naked DNA plasmid. The transformed cells are then re-implanted in the body. Naked DNA vectors are introduced into host cells by methods known in the art, including transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use of a DNA vector transporter. See, Wu et al., *J. Biol. Chem.* 263:14621-14624, 1988; Wu et al., *J. Biol. Chem.* 267:963-967, 1992; and Johnston and Tang, *Meth. Cell Biol.* 43:353-365, 1994.

Transgenic mice, engineered to express a gene encoding a protein of interest, and mice that exhibit a complete absence of gene function, referred to as "knockout mice" (Snouwaert et al., *Science* 257:1083, 1992), can also be generated (Lowell et al., *Nature* 366:740-742, 1993). These mice can be employed to study the gene of interest and the protein encoded thereby in an *in vivo* system. Transgenic mice are particularly useful for investigating the role of proteins in early development in that they allow the identification of developmental abnormalities or blocks resulting from the over- or underexpression of a specific factor. See also, Maisonpierre et al., *Science* 277:55-60, 1997 and Hanahan, *Science* 277:48-50, 1997. Preferred promoters for transgenic expression include promoters from metallothionein and albumin genes. As disclosed above, the human sequences provided herein can be used to clone orthologous polynucleotides, which may be preferred for use in generating transgenic and knockout animals.

Antisense methodology can be used to inhibit gene transcription to examine the effects of such inhibition *in vivo*. Polynucleotides that are complementary to a segment of a protein-encoding polynucleotide are designed to bind to the encoding mRNA and to inhibit translation of such mRNA. Such antisense oligonucleotides can also be used to inhibit expression of protein-encoding genes in cell culture.

Biological activities of test proteins can also be measured in animal models by administering the test protein, by itself or in combination with other agents, including other proteins. Using such models facilitates the assay of the test protein by itself or as an inhibitor or modulator of another agent, and also facilitates the measurement of combinatorial effects of bioactive compounds.

Anti-inflammatory activity can be tested in animal models of inflammatory disease. For example, animal models of psoriasis include the analysis of histological alterations in adult mouse tail epidermis (Hofbauer et al, *Brit. J. Dermatol.*

118:85-89, 1988; Bladon et al., *Arch Dermatol. Res.* 277:121-125, 1985). In this model, anti-psoriatic activity is indicated by the induction of a granular layer and orthokeratosis in areas of scale between the hinges of the tail epidermis. Typically, a topical ointment comprising a test compound is applied daily for seven consecutive days, then the animal is sacrificed, and tail skin is examined histologically. An additional model is provided by grafting psoriatic human skin to congenitally athymic (nude) mice (Krueger et al., *J. Invest. Dermatol.* 64:307-312, 1975). Such grafts have been shown to retain the characteristic histology for up to eleven weeks. As in the mouse tail model, the test composition is applied to the skin at predetermined intervals for a period of one to several weeks, at which time the animals are sacrificed and the skin grafts examined histologically. A third model has been disclosed by Fretland et al. (*Inflammation* 14:727-739, 1990). Briefly, inflammation is induced in guinea pig epidermis by topically applying phorbol ester (phorbol-12-myristate-13-acetate; PMA), typically at ca. 2 g/ml in acetone, to one ear and vehicle to the contralateral ear. Test compounds are applied concurrently with the PMA, or may be given orally. Histological analysis is performed at 96 hours after application of PMA. This model duplicates many symptoms of human psoriasis, including edema, inflammatory cell diapedesis and infiltration, high LTB₄ levels and epidermal proliferation.

Cerebral ischemia can be studied in a rat model as disclosed by Relton et al. (*ibid.*) and Loddick et al. (*ibid.*).

The effect of a test protein on primordial endothelial cells in angiogenesis can be assayed in the chick chorioallantoic membrane angiogenesis assay (Leung, *Science* 246:1306-1309, 1989; Ferrara, *Ann. NY Acad. Sci.* 752:246-256, 1995). Briefly, a small window is cut into the shell of an eight-day old fertilized egg, and a test substance is applied to the chorioallantoic membrane. After 72 hours, the membrane is examined for neovascularization. Embryo microinjection of early stage quail (*Coturnix coturnix japonica*) embryos can also be used (Drake et al., *Proc. Natl. Acad. Sci. USA* 92:7657-7661, 1995). Briefly, a solution containing the protein is injected into the interstitial space between the endoderm and the splanchnic mesoderm of early-stage embryos using a micropipette and micromanipulator system. After injection, embryos are placed ventral side down on a nutrient agar medium and incubated for 7 hours at 37°C in a humidified CO₂/air mixture (10%/90%). Vascular development is assessed by microscopy of fixed, whole-mounted embryos and sections.

Stimulation of coronary collateral growth can be measured in known animal models, including a rabbit model of peripheral limb ischemia and hind limb ischemia and a pig model of chronic myocardial ischemia (Ferrara et al., *Endocrine*

Reviews 18:4-25, 1997). Test proteins are assayed in the presence and absence of VEGF and basic FGF to test for combinatorial effects. These models can be modified by the use of adenovirus or naked DNA for gene delivery as disclosed in more detail above, resulting in local expression of the test protein(s).

5 Angiogenic activity can also be tested in a rodent model of corneal neovascularization as disclosed by Muthukkaruppan and Auerbach, *Science* 205:1416-1418, 1979, wherein a test substance is inserted into a pocket in the cornea of an inbred mouse. For use in this assay, proteins are combined with a solid or semi-solid, biocompatible carrier, such as a polymer pellet. Angiogenesis is followed
10 microscopically. Vascular growth into the corneal stroma can be detected in about 10 days.

 Angiogenic activity can also be tested in the hamster cheek pouch assay (Höckel et al., *Arch. Surg.* 128:423-429, 1993). A test substance is injected subcutaneously into the cheek pouch, and after five days the pouch is examined under
15 low magnification to determine the extent of neovascularization. Tissue sections can also be examined histologically.

 Induction of vascular permeability is measured in assays designed to detect leakage of protein from the vasculature of a test animal (e.g., mouse or guinea pig) after administration of a test compound (Miles and Miles, *J. Physiol.* 118:228-257,
20 1952; Feng et al., *J. Exp. Med.* 183:1981-1986, 1996).

 Wound-healing models include the linear skin incision model of Mustoe et al. (*Science* 237:1333, 1987). In a typical procedure, a 6-cm incision is made in the dorsal pelt of an adult rat, then closed with wound clips. Test substances and controls (in solution, gel, or powder form) are applied before primary closure. It is preferred to
25 limit administration to a single application, although additional applications can be made on succeeding days by careful injection at several sites under the incision. Wound breaking strength is evaluated between 3 and 21 days post wounding. In a second model, multiple, small, full-thickness excisions are made on the ear of a rabbit. The cartilage in the ear splints the wound, removing the variable of wound contraction
30 from the evaluation of closure. Experimental treatments and controls are applied. The geometry and anatomy of the wound site allow for reliable quantification of cell ingrowth and epithelial migration, as well as quantitative analysis of the biochemistry of the wounds (e.g., collagen content). See, Mustoe et al., *J. Clin. Invest.* 87:694, 1991. The rabbit ear model can be modified to create an ischemic wound environment,
35 which more closely resembles the clinical situation (Ahn et al., *Ann. Plast. Surg.* 24:17, 1990). Within a third model, healing of partial-thickness skin wounds in pigs or guinea pigs is evaluated (LeGrand et al., *Growth Factors* 8:307, 1993). Experimental

treatments are applied daily on or under dressings. Seven days after wounding, granulation tissue thickness is determined. This model is preferred for dose-response studies, as it is more quantitative than other *in vivo* models of wound healing. A full thickness excision model can also be employed. Within this model, the epidermis and dermis are removed down to the panniculus carnosum in rodents or the subcutaneous fat in pigs. Experimental treatments are applied topically on or under a dressing, and can be applied daily if desired. The wound closes by a combination of contraction and cell ingrowth and proliferation. Measurable endpoints include time to wound closure, histologic score, and biochemical parameters of wound tissue. Impaired wound healing models are also known in the art (e.g., Cromack et al., *Surgery* 113:36, 1993; Pierce et al., *Proc. Natl. Acad. Sci. USA* 86:2229, 1989; Greenhalgh et al., *Amer. J. Pathol.* 136:1235, 1990). Delay or prolongation of the wound healing process can be induced pharmacologically by treatment with steroids, irradiation of the wound site, or by concomitant disease states (e.g., diabetes). Linear incisions or full-thickness excisions are most commonly used as the experimental wound. Endpoints are as disclosed above for each type of wound. Subcutaneous implants can be used to assess compounds acting in the early stages of wound healing (Broadley et al., *Lab. Invest.* 61:571, 1985; Sprugel et al., *Amer. J. Pathol.* 129: 601, 1987). Implants are prepared in a porous, relatively non-inflammatory container (e.g., polyethylene sponges or expanded polytetrafluoroethylene implants filled with bovine collagen) and placed subcutaneously in mice or rats. The interior of the implant is empty of cells, producing a "wound space" that is well-defined and separable from the preexisting tissue. This arrangement allows the assessment of cell influx and cell type as well as the measurement of vasculogenesis/angiogenesis and extracellular matrix production.

Inhibition of tumor metastasis can be assessed in mice into which cancerous cells or tumor tissue have been introduced by implantation or injection (e.g., Brown, *Advan. Enzyme Regul.* 35:293-301, 1995; Conway et al., *Clin. Exp. Metastasis* 14:115-124, 1996).

Effects on fibrinolysis can be measured in a rat model wherein the enzyme batroxobin and radiolabeled fibrinogen are administered to test animals. Inhibition of fibrinogen activation by a test compound is seen as a reduction in the circulating level of the label as compared to animals not receiving the test compound. See, Lenfors and Gustafsson, *Semin. Thromb. Hemost.* 22:335-342, 1996.

The invention further provides polypeptides that comprise an epitope-bearing portion of a protein as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 436. An "epitope" is a region of a protein to which an antibody can bind. See, for example, Geysen et al., *Proc. Natl. Acad. Sci. USA* 81:3998-4002, 1984.

Epitopes can be linear or conformational, the latter being composed of discontinuous regions of the protein that form an epitope upon folding of the protein. Linear epitopes are generally at least 6 amino acid residues in length. Relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for example, Sutcliffe et al., *Science* 219:660-666, 1983. Antibodies that recognize short, linear epitopes are particularly useful in analytic and diagnostic applications that employ denatured protein, such as Western blotting (Tobin, *Proc. Natl. Acad. Sci. USA* 76:4350-4356, 1979). Antibodies to short peptides may also recognize proteins in native conformation and will thus be useful for monitoring protein expression and protein isolation, and in detecting proteins in solution, such as by ELISA or in immunoprecipitation studies.

Antigenic, epitope-bearing polypeptides of the present invention are useful for raising antibodies, including monoclonal antibodies, that specifically bind to the corresponding protein. Antigenic, epitope-bearing polypeptides contain a sequence of at least six, preferably at least nine, more preferably from 15 to about 30 contiguous amino acid residues of a protein. Within certain embodiments of the invention, the polypeptides comprise 40, 50, 100, or more contiguous residues of a protein as shown in SEQ ID NO:M, up to the entire predicted mature protein or the primary translation product. It is preferred that the amino acid sequence of the epitope-bearing polypeptide is selected to provide substantial solubility in aqueous solvents, that is the sequence includes relatively hydrophilic residues, and hydrophobic residues are substantially avoided. Table 10 lists preferred hexapeptides for use as antigens. Within Table 10, each the amino termini of the hexapeptides are specified. Those skilled in the art will recognize that longer polypeptides comprising these hexapeptides can also be used and will often be preferred.

Table 10

<u>Protein</u>		<u>Hexapeptide N-termini</u>			
AFP210015	389	405	97	388	359
AFP170681	51	334	113	49	140
AFP413680	221	207	220	206	198
AFP483037	219	218	82	216	215
AFP230872	189	188	73	156	68
AFP178828	211	210	209	208	207
AFP200134	150	149	146	132	145
AFP195796	99	97	111	208	240

AFP477303	64	126	63	54	112
AFP354334	269	268	267	266	265
AFP250287	34	33	48	2	143
AFP177000	133	132	104	37	68
AFP278176	234	145	284	91	291
AFP202885	134	244	170	133	243
AFP221312	31	29	28	51	43
AFP239757	329	200	556	107	328
AFP226311	293	74	250	86	184
AFP305901	340	194	451	192	120
AFP325549	293	74	250	86	184
AFP81988	151	167	147	165	173
AFP199200	150	149	148	92	147
AFP290395	31	29	28	329	326
AFP212675	67	66	65	204	396
AFP326051	49	56	23	78	95
AFP512441	94	93	41	39	38
AFP55098	140	34	139	120	32
AFP169796	177	173	156	32	155
AFP280706	33	54	32	31	53
AFP383165	25	82	52	24	178
AFP195467	113	112	71	2	80
AFP134225	114	280	113	455	417
AFP261193	120	66	65	85	119
AFP324422	147	145	66	65	85
AFP374312	125	124	79	123	77
AFP258118	64	63	116	115	62
AFP74517	1	72	124	123	22
AFP254653	134	36	62	14	23
AFP108666	79	76	74	49	48
AFP8766	140	34	139	120	298
AFP397185	265	35	264	34	48
AFP195042	192	535	191	259	533
AFP310695	49	75	190	5	94
AFP70022	38	64	179	83	37
AFP121670	184	183	121	118	182
AFP345861	151	89	75	135	149

AFP395942	60	14	59	13	21
AFP170291	144	72	56	55	63
AFP297548	145	73	57	56	64
AFP188135	152	148	158	147	144
AFP302388	478	431	416	414	429
AFP263430	92	23	64	91	110
AFP201273	373	384	163	372	44
AFP98983	3	2	35	34	32
AFP581958	71	66	80	26	25
AFP404202	1	31	115	30	92
AFP207203	427	258	204	426	48
AFP220790	139	92	51	187	91
AFP536326	87	146	105	73	103
AFP257473	270	205	203	245	244
AFP248380	283	62	54	272	100
AFP276202	50	48	35	46	33
AFP227568	199	23	238	363	224
AFP229039	226	91	116	161	225
AFP176297	261	382	183	119	182
AFP356885	622	45	525	175	466
AFP226938	118	108	117	79	107
AFP138504	77	255	75	254	292
AFP359196	4	76	3	2	37
AFP501809	141	139	9	169	2
AFP152733	258	204	48	47	257
AFP541394	31	29	28	235	232
AFP243183	272	110	106	3	2
AFP80739	398	397	224	223	155
AFP361806	4	78	139	3	76
AFP483930	107	124	123	88	45
AFP257336	124	42	122	182	158
AFP195800	40	39	65	38	96
AFP179530	57	251	249	315	55
AFP279267	106	62	216	187	59
AFP299766	127	168	165	29	126
AFP244615	171	196	326	255	179
AFP325761	138	137	2	144	109

AFP226024	79	317	159	140	45
AFP257094	71	116	115	3	144
AFP197103	200	198	215	195	177
AFP271855	92	44	42	18	27
AFP324816	9	252	120	8	63
AFP407963	202	201	156	200	155
AFP369635	98	398	255	97	254
AFP93743	4	254	3	294	293
AFP243230	28	129	128	127	44
AFP169316	294	170	293	36	157
AFP130852	82	59	117	145	66
AFP194191	363	112	271	69	267
AFP213472	103	102	69	2	37
AFP360430	177	75	183	74	130
AFP491309	107	106	69	2	37
AFP193428	129	87	343	60	128
AFP366534	72	4	2	59	39
AFP22706	229	227	65	64	188
AFP389012	216	27	289	34	17
AFP137186	2	1	182	216	43
AFP127023	86	56	131	178	55
AFP389687	57	56	117	370	369
AFP293220	186	194	105	146	182
AFP425535	264	181	163	370	149
AFP301494	159	4	2	84	25
AFP345421	500	592	639	652	849
AFP216667	92	435	329	422	47
AFP247951	27	34	33	25	94
AFP4464	365	363	362	55	209
AFP561930	108	107	104	52	66
AFP192851	300	276	299	298	496
AFP252759	311	310	64	21	157
AFP199044	143	2	209	206	125
AFP357958	167	338	165	324	362
AFP117501	135	87	362	86	418
AFP194554	318	170	54	105	169
AFP371069	332	1	283	365	279

AFP313600	341	340	240	48	176
AFP262739	25	24	142	23	207
AFP180730	58	37	30	27	36
AFP287227	596	592	591	374	525
AFP75785	128	127	136	99	71
AFP174843	152	323	150	309	347
AFP250422	100	140	99	138	182
AFP198645	145	144	143	64	56
AFP238111	123	50	20	137	35
AFP460626	153	151	71	150	70
AFP271081	68	112	39	202	67
AFP277752	109	106	220	238	92
AFP291338	347	342	97	362	339
AFP551038	134	131	186	130	173
AFP301579	105	153	130	152	67
AFP266188	121	235	61	180	120
AFP275580	193	77	192	2	148
AFP298054	148	234	146	233	144
AFP348226	148	103	85	309	59
AFP349106	208	118	117	207	116
AFP288248	376	342	340	339	312
AFP436476	18	39	139	38	99
AFP352125	53	59	163	142	104
AFP62060	247	187	73	426	72
AFP236718	100	99	249	248	184
AFP75775	201	90	239	173	199
AFP407487	148	103	85	59	58
AFP280451	141	294	6	209	139
AFP11675	58	56	90	64	89
AFP348656	160	159	158	103	149
AFP277451	118	2	1	146	241
AFP287436	53	59	223	142	104
AFP116043	212	239	138	186	183
AFP138740	264	263	31	72	232
AFP15192	47	46	216	85	212
AFP169968	64	117	63	2	81
AFP173341	65	64	102	101	100

AFP17588	43	42	2	41	1
AFP176427	311	290	308	155	288
AFP192633	58	56	162	349	44
AFP193013	47	90	87	46	68
AFP193881	274	295	402	273	292
AFP195562	274	295	339	473	273
AFP199922	57	55	74	180	50
AFP204736	89	58	43	28	23
AFP206179	74	80	73	71	70
AFP221877	32	31	30	50	75
AFP222758	44	43	75	42	19
AFP227032	47	55	46	65	54
AFP229269	147	127	146	63	60
AFP232213	44	41	28	27	40
AFP237679	2	1	34	58	55
AFP249599	48	47	45	43	42
AFP275215	82	80	70	2	55
AFP290397	149	148	2	1	29
AFP306591	45	44	84	83	65
AFP310297	23	31	37	47	30
AFP314720	47	44	26	25	23
AFP318671	55	54	51	64	63
AFP323575	75	73	72	70	18
AFP327160	37	68	47	67	96
AFP329002	78	77	76	75	74
AFP345415	41	40	133	106	39
AFP347179	30	4	29	86	177
AFP359138	77	2	76	75	74
AFP365372	13	1	62	69	79
AFP367284	61	60	36	5	59
AFP372822	49	48	25	8	24
AFP374595	154	153	165	3	56
AFP375952	36	35	53	52	69
AFP382913	67	32	30	20	66
AFP389184	24	31	78	30	39
AFP404208	69	68	67	39	36
AFP404279	81	31	72	30	62

AFP409112	97	96	56	94	55
AFP413111	65	85	96	64	94
AFP415635	35	26	25	34	32
AFP421092	27	1	46	57	35
AFP436666	5	95	59	4	58
AFP448623	14				
AFP454192	106	104	83	114	112
AFP49026	49	104	76	48	138
AFP51688	51	86	50	85	43
AFP525341	18	17	16	79	14
AFP545268	65	64	75	21	74
AFP592620	22	21	29	20	28
AFP62197	134	84	133	20	104
AFP68229	161	171	192	170	232
AFP71288	67	49	65	48	46
AFP77851	123	121	33	103	53
AFP81957	89	66	63	25	40
AFP85168	61	31	39	27	46

As used herein, the term "antibodies" includes polyclonal antibodies, monoclonal antibodies, antigen-binding fragments thereof such as F(ab')₂ and Fab fragments, single chain antibodies, and the like, including genetically engineered antibodies. Non-human antibodies can be humanized by grafting only non-human CDRs onto human framework and constant regions, or by incorporating the entire non-human variable domains (optionally "cloaking" them with a human-like surface by replacement of exposed residues, wherein the result is a "veneered" antibody). In some instances, humanized antibodies may retain non-human residues within the human variable region framework domains to enhance proper binding characteristics. Through humanizing antibodies, biological half-life may be increased, and the potential for adverse immune reactions upon administration to humans is reduced. One skilled in the art can generate humanized antibodies with specific and different constant domains (i.e., different Ig subclasses) to facilitate or inhibit various immune functions associated with particular antibody constant domains.

Alternative techniques for generating or selecting antibodies useful herein include *in vitro* exposure of lymphocytes to an immunogenic polypeptide, and selection of antibody display libraries in phage or similar vectors (for instance, through use of an immobilized or labeled polypeptide). Human antibodies can be produced in

transgenic, non-human animals that have been engineered to contain human immunoglobulin genes as disclosed in WIPO Publication WO 98/24893. It is preferred that the endogenous immunoglobulin genes in these animals be inactivated or eliminated, such as by homologous recombination.

5 Antibodies are defined to be specifically binding if they bind to a target polypeptide with an affinity at least 10-fold greater than the binding affinity to control (non-target) polypeptide. It is preferred that the antibodies exhibit a binding affinity (K_a) of 10^6 M^{-1} or greater, preferably 10^7 M^{-1} or greater, more preferably 10^8 M^{-1} or greater, and most preferably 10^9 M^{-1} or greater. The affinity of a monoclonal antibody
10 can be readily determined by one of ordinary skill in the art (see, for example, Scatchard, *Ann. NY Acad. Sci.* 51: 660-672, 1949).

 Methods for preparing polyclonal and monoclonal antibodies are well known in the art (see for example, Hurrell, J. G. R., Ed., *Monoclonal Hybridoma Antibodies: Techniques and Applications*, CRC Press, Inc., Boca Raton, FL, 1982). As
15 would be evident to one of ordinary skill in the art, polyclonal antibodies can be generated from a variety of warm-blooded animals such as horses, cows, goats, sheep, dogs, chickens, rabbits, mice, and rats. The immunogenicity of a polypeptide immunogen may be increased through the use of an adjuvant such as alum (aluminum hydroxide) or Freund's complete or incomplete adjuvant. Polypeptides useful for
20 immunization also include fusion polypeptides, such as fusions of a polypeptide of interest or a portion thereof with an immunoglobulin polypeptide or with maltose binding protein. The polypeptide immunogen may be a full-length molecule or a portion thereof. If the polypeptide portion is "hapten-like", such portion may be advantageously joined or linked to a macromolecular carrier (such as keyhole limpet
25 hemocyanin (KLH), bovine serum albumin (BSA) or tetanus toxoid) for immunization.

 A variety of assays known to those skilled in the art can be utilized to detect antibodies that specifically bind to a polypeptide of interest. Exemplary assays are described in detail in *Antibodies: A Laboratory Manual*, Harlow and Lane (Eds.), Cold Spring Harbor Laboratory Press, 1988. Representative examples of such assays
30 include concurrent immunoelectrophoresis, radio-immunoassays, radio-immunoprecipitations, enzyme-linked immunosorbent assays (ELISA), dot blot assays, Western blot assays, inhibition or competition assays, and sandwich assays.

 Antibodies can be used, for example, to isolate target polypeptides by affinity purification, for diagnostic assays for determining circulating or localized
35 levels of target polypeptides, for tissue typing, for cell sorting, for screening expression libraries; for generating anti-idiotypic antibodies, and as neutralizing antibodies or as antagonists to block protein activity *in vitro* and *in vivo*.

The present invention also provides reagents for use in diagnostic and therapeutic applications. Such reagents include polynucleotide probes and primers; antibodies, including antibody fragments, single-chain antibodies, and other genetically engineered forms; soluble receptors and other polypeptide binding partners; and the proteins of the invention themselves, including fragments thereof. Those skilled in the art will recognize that diagnostic reagents will commonly be labeled to provide a detectable signal or other second function. Thus, polypeptides, antibodies, receptors, and other binding partners disclosed herein can be directly or indirectly conjugated to drugs, toxins, radionuclides, enzymes, enzyme substrates, cofactors, inhibitors, fluorescent markers, chemiluminescent markers, magnetic particles, and the like, and these conjugates used for *in vivo* diagnostic or therapeutic applications. Cytotoxic molecules, for example, can be directly or indirectly attached to the binding partner (e.g., by chemical coupling or as a fusion protein), and include bacterial or plant toxins (e.g., diphtheria toxin, *Pseudomonas* exotoxin, ricin, saporin, abrin, and the like); therapeutic radionuclides (e.g., iodine-131, rhenium-188 or yttrium-90) which can be directly attached to a polypeptide or antibody or indirectly attached through means of a chelating moiety; and cytotoxic drugs (e.g., adriamycin). Methods for preparing labeled reagents are known in the art. Within an alternative embodiment, the detectable signal or other function can be provided by a second member of a complement-anticomplement pair, which second member binds to the diagnostic reagent. For example, a first (unlabeled) antibody can be used to bind to a cell-surface polypeptide, after which a second, labeled antibody which binds to the first antibody is added. Other complement-anticomplement pairs are known in the art and include biotin/streptavidin.

Diagnostic reagents as disclosed herein can be used *in vivo* or *in vitro*. *In vitro* diagnostic assays include assays of tissue and fluid samples. Assays for protein in serum, for example, may be used to detect metabolic abnormalities characterized by over- or under-production of the protein, such as cancers, immune system abnormalities, infections, organ failure, metabolic imbalances, inborn errors of metabolism and other disease states. Proteins of the present invention can also be used in the detection of circulating autoantibodies, which are indicative of autoimmune disorders. Those skilled in the art will recognize that conditions related to protein underexpression or overexpression may be amenable to treatment by therapeutic manipulation of the relevant protein level(s). Proteins in serum can be quantitated by known methods known in the art, which include the use of antibodies in a variety of formats. Non-antibody binding partners, such as ligand-binding receptor fragments (commonly referred to as "soluble receptors") can also be used.

In general, diagnostic methods employing oligonucleotide probes or primers comprise the steps of (a) obtaining a genetic sample from a patient; (b) incubating the genetic sample with an oligonucleotide probe or primer as disclosed above, under conditions wherein the probe or primer will hybridize to a complementary polynucleotide sequence, to produce a first reaction product; and (c) comparing the first reaction product to a control reaction product. A difference between the first reaction product and the control reaction product is indicative of a genetic abnormality in the patient. Genetic samples for use within such methods include genomic DNA, cDNA, and RNA. Suitable assay methods in this regard include molecular genetic techniques known to those in the art, such as restriction fragment length polymorphism (RFLP) analysis, short tandem repeat (STR) analysis employing PCR techniques, ligation chain reaction (Barany, *PCR Methods and Applications* 1:5-16, 1991), ribonuclease protection assays, and other genetic linkage analysis techniques known in the art (Sambrook et al., *ibid.*; Ausubel et al., *ibid.*; A.J. Marian, *Chest* 108:255-65, 1995). Ribonuclease protection assays (see, e.g., Ausubel et al., *ibid.*, ch. 4) comprise the hybridization of an RNA probe to a patient RNA sample, after which the reaction product (RNA-RNA hybrid) is exposed to RNase. Hybridized regions of the RNA are protected from digestion. Within PCR assays, a patient genetic sample is incubated with a pair of oligonucleotide primers, and the region between the primers is amplified and recovered. Changes in size, amount, or sequence of recovered product are indicative of mutations in the patient. Another PCR-based technique that can be employed is single strand conformational polymorphism (SSCP) analysis (Hayashi, *PCR Methods and Applications* 1:34-38, 1991). Chromosomal localization data can be used to correlate AFP gene locations with known genetic disorders using, for example, the OMIM™ Database, Johns Hopkins University, 2000 (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM>).

Relative chromosomal sublocalization shown in Table 11 was determined using the Draft Human Genome Browser (Kent, J., University of California Santa Cruz, <http://genome.ucsc.edu/goldenPath/hgTracks.html>) displaying the draft assembly of the July 17, 2000 version of the human genome. Table 11 also correlates AFP sequences with corresponding sequences in public databases by GenBank Accession Number, source clone ID number, and EST accession number. Also see Table 5, above.

Table 11

AFP	GenBank Acc. No.	Source Clone ID No.	EST Acc. No.	Chr.	Band	Start	Stop
AFP127023	AP001155	RP11-594B10	*	18	18q12	35729370	35952786
AFP138504	AP001931	RP11-691N7	*	11	11p11.11	53438038	53888802
AFP138740	AC024059	RP11-79121	AW580814	15	15q22.1	58185489	58481462
AFP138740	*	*	AW580814	15		58258653	58308652
AFP177000	AL118506	RP4-591C20	*	20	20q12	48950838	49160243
AFP178828	AC007686	CTD-2289B16;RP11-116N21;RP11-7F17	*	14	14q23.3	62132030	62313415
AFP179530	AC011475	CTC-539A10	*	12	12q12	41234876	41456630
AFP188135	AC013740	*	*	9	9q31.2	91150313	91361876
AFP194534	AC024888	RP11-901L	*	16	16q22.1	71944378	72167142
AFP199044	AC012180	RP11-311I0	*	16	16q11.2	44574019	44904017
AFP199200	CNS01DV7	BAC-R-1070N10	*	14		82330266	82541053
AFP229269	AL161670	BAC-R-804M7	*	14	14q21.3	46135365	46299284
AFP236718	AC010319	CTD-2521M24	*	19	19p13.3	4839920	5087628
AFP237679	Z69709	*	*	4	4p16.3	4521455	4544888
AFP244615	*	*	AI494556;AW85055 3	3	3q13.12	116466893	116517043
AFP249599	AL157714	RP11-541H12	*	1	1q22-23.3	161893354	162136704
AFP250422	AC012046	RP11-312P12	*	10	10q22.1	81289799	81650062
AFP262739	AC005884	hRPK.264_B_14	*	17	17q23.3	64245127	64365313
AFP275580	AC016773	*	*	3	3q21.3	141329005	141513510
AFP277451	AC055822	RP11-707M3	*	8	8q13.3	75395740	75583383
AFP279267	*	*	AI566086	10	10q11.1	52859924	52861338
AFP280451	AL133355	RP11-541N10	*	10	10q24.32	115276306	115467187
AFP290397	*	*	AA421069	15	15q15.3	48427462	48427830
AFP293220	AC012476	RP11-532F12	*	15	15p11.1	17263661	17480097
AFP297548	*	*	W52728	11	11q11	57918740	57927327
AFP306591	AQ079258	2366B9	AW118928	6	6p22.3	19812023	19812791
AFP313600	AC005037	NH0469M07	*	2	2q33.1	205320800	205511307
AFP324816	AC011687	RP11-15120	*	2	2p21	49054619	49249783
AFP325761	AC012485	RP11-5024	*	2	2p24.3	17554756	17765537

AFP326051	AL132639	BAC-R-407N17	AI525611	14	14p11.1	19959493	20153358
AFP345861	AC015936	CTD-2534I21	*	17	17q21.2	44087441	44286594
AFP347179	AC025740	*	*	12	12q24.23	125918909	126134148
AFP372822	AL022240	3.28E+21	*	1	1q12-21.2	138667522	138765140
AFP374312	*	*	AI253088	11	11q23.3	128134250	128134589
AFP375952	*	*	AI741157	16	16p13.3	3479999	3500834
AFP395942	AC004235	*	*	16	16p13.3	4189155	4222465
AFP404202	*	*	AI133727	7		142961410	143641730
AFP404279	*	*	AI341602	4	4p16.3	1512179	1514256
AFP413680	AC006942	cosmid-R31181	*	19	19q13.33	59897688	59940397
AFP436666	*	*	AI814257	8	8p21.3	18993217	19003942
AFP448623	*	*	AI140615	5	5q33.1	173540737	173547400
AFP460626	AC009131	RP11-502K10	*	16	16q22.1	70222075	70471703
AFP477303	AC008686	CTB-5E10	*	19	19p13.13	16491516	16677574
AFP501809	*	*	AW583171	6	6p21.1	50554924	50564907
AFP545268	AL138695	RP11-342J4	*	13	13q21.1	60450247	60714738
AFP561930	AL136221	RP11-391H12	*	13	13q34	108494503	108794286
AFP71288	*	*	AA493506	6	6q22.33	137477811	137478427
AFP74517	HS1056L3	RP5-1056L3	*	1	1p35.1-36.13	*	*
AFP93743	AC067942	RP11-791G16	*	4	4q21.22	77419530	77633569

If a mammal has an insufficiency of a protein of interest (due to, for example, a mutated or absent gene), the corresponding wild-type gene can be introduced into the cells of the mammal. In one embodiment, a gene encoding a protein of interest is introduced into the animal using a viral vector. Such vectors include an attenuated or defective DNA virus, such as, but not limited to, herpes simplex virus (HSV), papillomavirus, Epstein Barr virus (EBV), adenovirus, adeno-associated virus (AAV), and the like. Defective viruses, which entirely or almost entirely lack viral genes, are preferred. A defective virus is not infective after introduction into a cell. Use of defective viral vectors allows for administration to cells in a specific, localized area, without concern that the vector can infect other cells. Examples of particular vectors include, but are not limited to, a defective herpes simplex virus 1 (HSV1) vector (Kaplit et al., *Molec. Cell. Neurosci.* 2:320-30, 1991); an attenuated adenovirus vector, such as the vector described by Stratford-Perricaudet et al. (*J. Clin. Invest.* 90:626-30, 1992); and a defective adeno-associated virus vector (Samulski et al., *J. Virol.* 61:3096-101, 1987; Samulski et al., *J. Virol.* 63:3822-28, 1989).

Within another embodiment, a gene of interest is introduced into an animal by liposome-mediated transfection ("lipofection") essentially as disclosed above. Lipofection can be used to introduce exogenous genes into specific organs.

A gene of interest can also be introduced into an animal for gene therapy as a naked DNA plasmid using the methods disclosed above.

In another embodiment, polypeptide-toxin fusion proteins or antibody/fragment-toxin fusion proteins may be used for targeted cell or tissue inhibition or ablation, such as in cancer therapy. Of particular interest in this regard are conjugates of an AFP protein and a cytotoxin, which can be used to target the cytotoxin to a tumor or other tissue that is undergoing undesired angiogenesis or neovascularization.

In another embodiment, AFP-cytokine fusion proteins or antibody/fragment-cytokine fusion proteins may be used for enhancing *in vitro* cytotoxicity (for instance, that mediated by monoclonal antibodies against tumor targets) and for enhancing *in vivo* killing of target tissues (for example, blood and bone marrow cancers). See, generally, Hornick et al., *Blood* 89:4437-4447, 1997). In general, cytokines are toxic if administered systemically. The described fusion proteins enable targeting of a cytokine to a desired site of action, such as a cell having binding sites for an AFP protein, thereby providing an elevated local concentration of cytokine. Polypeptides, antibodies, or receptors target an undesirable cell or tissue

(e.g., a tumor), and the fused cytokine mediates improved target cell lysis by effector cells. Suitable cytokines for this purpose include, for example, interleukin-2 and granulocyte-macrophage colony-stimulating factor (GM-CSF).

In another embodiment, polypeptide-toxin fusion proteins or other
5 binding partner-linked toxins may be used for targeted cell or tissue inhibition or ablation (for instance, to treat cancer cells or tissues). Target cells (i.e., those displaying a receptor for a polypeptide of interest) bind the polypeptide-toxin conjugate, which is then internalized, killing the cell. The effects of receptor-specific cell killing (target ablation) are revealed by changes in whole animal physiology or
10 through histological examination. Thus, ligand-dependent, receptor-directed cytotoxicity can be used to enhance understanding of the physiological significance of a protein ligand. A preferred such toxin is saporin. Mammalian cells have no receptor for saporin, which is non-toxic when it remains extracellular. Alternatively, if the polypeptide of interest has multiple functional domains (i.e., an activation domain or a
15 ligand binding domain, plus a targeting domain), a fusion protein including only the targeting domain may be suitable for directing a detectable molecule, a cytotoxic molecule or a complementary molecule to a cell or tissue type of interest. In instances where the domain-only fusion protein includes a complementary molecule, the anti-complementary molecule can be conjugated to a detectable or cytotoxic molecule.
20 Such domain-complementary molecule fusion proteins thus represent a generic targeting vehicle for cell- or tissue-specific delivery of generic anti-complementary-detectable/cytotoxic molecule conjugates.

The bioactive conjugates described herein can be delivered intravenously, intraarterially or intraductally, or may be introduced locally at the
25 intended site of action.

For pharmaceutical use, the proteins of the present invention are formulated according to conventional methods. Routes of delivery include topical, mucosal, and parenteral, the latter including intravenous and subcutaneous delivery. Intravenous administration will be by bolus injection or infusion over a typical period
30 of one to several hours. In general, pharmaceutical formulations will include a protein of the present invention in combination with a pharmaceutically acceptable vehicle, such as saline, buffered saline, 5% dextrose in water or the like. Formulations may further include one or more excipients, diluents, fillers, emulsifiers, preservatives, solubilizers, buffering agents, wetting agents, stabilizers, colorings, penetration
35 enhancers, albumin to prevent protein loss on vial surfaces, etc. Topical formulations are typically provided as liquids, ointments, salves, gels, emulsions and the like. Methods of formulation are well known in the art and are disclosed, for example, in

Remington: The Science and Practice of Pharmacy, Gennaro, ed., Mack Publishing Co., Easton, PA, 19th ed., 1995. Therapeutic doses will be determined by the clinician according to accepted standards, taking into account the nature and severity of the condition to be treated, patient traits, etc. Proteins of the present invention will
5 generally be formulated to provide a dose of from 0.01 μ g to 100 mg per kg patient weight per day, more commonly from 0.1 μ g to 10 mg/kg/day, still more commonly from 0.1 μ g to 1.0 mg/kg/day. Determination of dose is within the level of ordinary skill in the art. The proteins may be administered for acute treatment, over one week or less, often over a period of one to three days or may be used in chronic treatment, over
10 several months or years. In general, a therapeutically effective amount is an amount sufficient to produce a clinically significant change in the targetted condition.

Within the laboratory research field, the proteins of the present invention can be used as molecular weight standards, or as standards in the analysis of cell phenotype, and as reagents for the study of cells, receptors, and other binding
15 molecules. Such reagents will generally further comprise a second moiety, such as a label, binding partner, or toxin, that facilitates the detection of the protein when bound to its target. Many such systems are known in the art and are summarized above. Receptors and other cell-surface binding sites for proteins of the present invention can be identified by exposing a population of cells to a labelled protein under physiologic
20 conditions, whereby the protein binds to the surface of the cell. Cells bearing receptors for a protein of interest can also be identified using the protein joined to a toxin, whereby receptor-bearing cells are killed by the toxin.

AFP proteins and antagonists thereof can be used as standards in assays of protein and protein inhibitors in both clinical and research settings. Such assays can
25 comprise any of a number of standard formats, include radioreceptor assays and ELISAs. Protein standards can be prepared in labeled form using a radioisotope, enzyme, fluorophore, or other compound that produces a detectable signal. The proteins can be packaged in kit form, such kits comprising one or more vials containing the AFP protein and, optionally, a diluent, an antibody, a labeled binding protein, etc.
30 Assay kits can be used in the research laboratory to detect protein and inhibitor activities produced by cultured cells or test animals.

Proteins of the present invention may also be used as protein and amino acid supplements, including hydrolysates. Specific uses in this regard include use as
35 animal feed supplements and as cell culture components. Proteins rich in a particular amino acid can be used as a source of that amino acid.

Polynucleotides and polypeptides of the present invention will additionally find use as educational tools as a laboratory practicum kits for courses

related to genetics and molecular biology, protein chemistry and antibody production and analysis. Due to their unique polynucleotide and polypeptide sequences, molecules of AFP protein or polynucleotide can be used as standards or as "unknowns" for testing purposes. For example, AFP polynucleotides can be used as aids in
5 teaching students how to prepare expression constructs for bacterial, viral, and/or mammalian expression, including fusion constructs, wherein an AFP polynucleotide is the gene to be expressed; for determining the restriction endonuclease cleavage sites of the polynucleotides (which can be determined from the sequence using conventional computer software, such as MapDraw™ (DNASTAR, Madison, WI)); determining
10 mRNA and DNA localization of AFP polynucleotides in tissues (e.g., by Northern and Southern blotting as well as polymerase chain reaction); and for identifying related polynucleotides and polypeptides by nucleic acid hybridization.

AFP polypeptides can be used educationally as aids to teach preparation of antibodies; identifying proteins by Western blotting; protein purification;
15 determining the weight of expressed AFP polypeptides as a ratio to total protein expressed; identifying peptide cleavage sites; coupling amino and carboxyl terminal tags; amino acid sequence analysis, as well as, but not limited to monitoring biological activities of both the native and tagged protein (i.e., receptor binding, signal transduction, proliferation, and differentiation) *in vitro* and *in vivo*. AFP polypeptides
20 can also be used to teach analytical skills such as mass spectrometry, circular dichroism to determine conformation, in particular the locations of the disulfide bonds, x-ray crystallography to determine the three-dimensional structure in atomic detail, nuclear magnetic resonance spectroscopy to reveal the structure of proteins in solution. For example, a kit containing an AFP protein can be given to the student to analyze.
25 Since the amino acid sequence would be known by the professor, the protein can be given to the student as a test to determine the skills or develop the skills of the student, the teacher would then know whether or not the student has correctly analyzed the polypeptide. Since every polypeptide is unique, the educational utility of zcub5 would be unique unto itself.

30 Antibodies that bind specifically to an AFP polypeptide can be used as a teaching aid to instruct students how to prepare affinity chromatography columns to purify the cognate polypeptide, cloning and sequencing the polynucleotide that encodes an antibody and thus as a practicum for teaching a student how to design humanized antibodies. The AFP polynucleotide, polypeptide or antibody would then be packaged
35 by reagent companies and sold to universities so that the students gain skill in art of molecular biology. Because each polynucleotide and protein is unique, each polynucleotide and protein creates unique challenges and learning experiences for

students in a lab practicum. Such educational kits containing an AFP polynucleotide, polypeptide or antibody are considered within the scope of the present invention.

The invention is further illustrated by the following non-limiting examples.

5

EXAMPLES

Example 1

A protein of the present invention ("AFP") is produced in *E. coli* using a His₆ tag/maltose binding protein (MBP) double affinity fusion system as generally disclosed by Pryor and Leiting, *Prot. Expr. Pur.* 10:309-319, 1997. A thrombin cleavage site is placed at the junction between the affinity tag and AFP sequences.

The fusion construct is assembled in the vector pTAP98, which comprises sequences for replication and selection in *E. coli* and yeast, the *E. coli* *tac* promoter, and a unique SmaI site just downstream of the MBP-His₆-thrombin site coding sequences. The AFP cDNA is amplified by PCR using primers each comprising 40 bp of sequence homologous to vector sequence and 25 bp of sequence that anneals to the cDNA. The reaction is run using Taq DNA polymerase (Boehringer Mannheim, Indianapolis, IN) for 30 cycles of 94°C, 30 seconds; 60°C, 60 seconds; and 72°C, 60 seconds. One microgram of the resulting fragment is mixed with 100 ng of SmaI-cut pTAP98, and the mixture is transformed into yeast to assemble the vector by homologous recombination (Oldenburg et al., *Nucl. Acids. Res.* 25:451-452, 1997). Ura⁺ transformants are selected.

Plasmid DNA is prepared from yeast transformants and transformed into *E. coli* MC1061. Pooled plasmid DNA is then prepared from the MC1061 transformants by the miniprep method after scraping an entire plate. Plasmid DNA is analyzed by restriction digestion.

E. coli strain BL21 is used for expression of AFP. Cells are transformed by electroporation and grown on minimal glucose plates containing casamino acids and ampicillin.

Protein expression is analyzed by gel electrophoresis. Cells are grown in liquid glucose media containing casamino acids and ampicillin. After one hour at 37°C, IPTG is added to a final concentration of 1mM, and the cells are grown for an additional 2-3 hours at 37°C. Cells are disrupted using glass beads, and extracts are prepared.

35

Example 2

Larger scale cultures of AFP transformants are prepared by the method of Pryor and Leiting (*ibid.*). 100-ml cultures in minimal glucose media containing casamino acids and 100 µg/ml ampicillin are grown at 37°C in 500-ml baffled flasks to
5 OD₆₀₀ ≈ 0.5. Cells are harvested by centrifugation and resuspended in 100 ml of the same media at room temperature. After 15 minutes, IPTG is added to 0.5 mM, and cultures are incubated at room temperature (ca. 22.5°C) for 16 to 20 hours with shaking at 125 rpm. The culture is harvested by centrifugation, and cell pellets are stored at -70°C.

10

Example 3

For larger-scale protein preparation, 500-ml cultures of *E. coli* BL21 expressing the AFP-MBP-His₆ fusion protein are prepared essentially as disclosed in Example 2. Cell pellets are resuspended in 100 ml of binding buffer (20 mM Tris, pH
15 7.58, 100 mM NaCl, 20 mM NaH₂PO₄, 0.4 mM 4-(2-Aminoethyl)-benzenesulfonyl fluoride hydrochloride [Pefabloc® SC; Boehringer-Mannheim], 2 µg/ml Leupeptin, 2 µg/ml Aprotinin). The cells are lysed in a French press at 30,000 psi, and the lysate is centrifuged at 18,000 x g for 45 minutes at 4°C to clarify it. Protein concentration is estimated by gel electrophoresis with a BSA standard.

20

Recombinant AFP fusion protein is purified from the lysate by affinity chromatography. Immobilized cobalt resin (Talon® resin; Clontech Laboratories, Inc., Palo Alto, CA) is equilibrated in binding buffer. One ml of packed resin per 50 mg protein is combined with the clarified supernatant in a tube, and the tube is capped and sealed, then placed on a rocker overnight at 4°C. The resin is then pelleted by
25 centrifugation at 4°C and washed three times with binding buffer. Protein is eluted with binding buffer containing 0.2 M imidazole. The resin and elution buffer are mixed for at least one hour at 4°C, the resin is pelleted, and the supernatant is removed. An aliquot is analyzed by gel electrophoresis, and concentration is estimated. Amylose resin is equilibrated in amylose binding buffer (20 mM Tris-HCl, pH 7.0, 100 mM
30 NaCl, 10 mM EDTA) and combined with the supernatant from the Talon resin at a ratio of 2 mg fusion protein per ml of resin. Binding and washing steps are carried out as disclosed above. Protein is eluted with amylose binding buffer containing 10 mM maltose using as small a volume as possible to minimize the need for subsequent concentration. The eluted protein is analyzed by gel electrophoresis and staining with
35 Coomassie blue using a BSA standard, and by Western blotting using an anti-MBP antibody.

Example 4

An expression plasmid containing all or part of a polynucleotide encoding AFP is constructed via homologous recombination. An AFP coding sequence comprising the ORF with 5' and 3' ends corresponding to the vector sequences flanking the insertion point is prepared by PCR. The primers for PCR each include from 5' to 3' end: 40 bp of flanking sequence from the vector and 17 bp corresponding to the amino or carboxyl termini from the open reading frame of AFP.

Ten μ l of the 100 μ l PCR reaction mixture is run on a 0.8% low-melting-temperature agarose (SeaPlaque GTG®; FMC BioProducts, Rockland, ME) gel with 1 x TBE buffer for analysis. The remaining 90 μ l of the reaction mixture is precipitated with the addition of 5 μ l 1 M NaCl and 250 μ l of absolute ethanol. The plasmid pZMP6, which has been cut with SmaI, is used for recombination with the PCR fragment. Plasmid pZMP6 is a mammalian expression vector containing an expression cassette having the cytomegalovirus immediate early promoter, multiple restriction sites for insertion of coding sequences, a stop codon, and a human growth hormone terminator; an *E. coli* origin of replication; a mammalian selectable marker expression unit comprising an SV40 promoter, enhancer and origin of replication, a DHFR gene, and the SV40 terminator; and URA3 and CEN-ARS sequences required for selection and replication in *S. cerevisiae*. It was constructed from pZP9 (deposited at the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209, under Accession No. 98668) with the yeast genetic elements taken from pRS316 (available from the American Type Culture Collection, 10801 University Boulevard, Manassas, VA, under Accession No. 77145), an internal ribosome entry site (IRES) element from poliovirus, and the extracellular domain of CD8 truncated at the C-terminal end of the transmembrane domain.

One hundred microliters of competent yeast (*S. cerevisiae*) cells are independently combined with 10 μ l of the various DNA mixtures from above and transferred to a 0.2-cm electroporation cuvette. The yeast/DNA mixtures are electropulsed using power supply (BioRad Laboratories, Hercules, CA) settings of 0.75 kV (5 kV/cm), ∞ ohms, 25 μ F. To each cuvette is added 600 μ l of 1.2 M sorbitol, and the yeast is plated in two 300- μ l aliquots onto two URA-D plates (1.8% agar in 2% D-glucose, 0.67% yeast nitrogen base without amino acids, 0.056% -Ura -Trp -Thr powder [made by combining 4.0 g L-adenine, 3.0 g L-arginine, 5.0 g L-aspartic acid, 2.0 g L-histidine, 6.0 g L-isoleucine, 8.0 g L-leucine, 4.0 g L-lysine, 2.0 g L-methionine, 6.0 g L-phenylalanine, 5.0 g L-serine, 5.0 g L-tyrosine, and 6.0 g L-valine], and 0.5% 200X tryptophan, threonine solution [3.0% L-threonine, 0.8% L-tryptophan in H₂O]) and incubated at 30°C. After about 48 hours, the Ura⁺ yeast

transformants from a single plate are resuspended in 1 ml H₂O and spun briefly to pellet the yeast cells. The cell pellet is resuspended in 1 ml of lysis buffer (2% Triton X-100, 1% SDS, 100 mM NaCl, 10 mM Tris, pH 8.0, 1 mM EDTA). Five hundred microliters of the lysis mixture is added to an Eppendorf tube containing 300 µl acid-washed glass beads and 200 µl phenol-chloroform, vortexed for 1 minute intervals two or three times, and spun for 5 minutes in an Eppendorf centrifuge at maximum speed. Three hundred microliters of the aqueous phase is transferred to a fresh tube, and the DNA is precipitated with 600 µl ethanol (EtOH), followed by centrifugation for 10 minutes at 4°C. The DNA pellet is resuspended in 10 µl H₂O.

10 Transformation of electrocompetent *E. coli* host cells (Electromax DH10B™ cells; obtained from Life Technologies, Inc., Gaithersburg, MD) is done with 0.5-2 ml yeast DNA prep and 40 µl of cells. The cells are electropulsed at 1.7 kV, 25 µF, and 400 ohms. Following electroporation, 1 ml SOC (2% Bacto™ Tryptone (Difco, Detroit, MI), 0.5% yeast extract (Difco), 10 mM NaCl, 2.5 mM KCl, 10 mM
15 MgCl₂, 10 mM MgSO₄, 20 mM glucose) is plated in 250-µl aliquots on four LB AMP plates (LB broth (Lennox), 1.8% Bacto™ Agar (Difco), 100 mg/L Ampicillin).

Individual clones harboring the correct expression construct for AFP are identified by restriction digest to verify the presence of the AFP insert and to confirm that the various DNA sequences have been joined correctly to one another. The inserts
20 of positive clones are subjected to sequence analysis. Larger scale plasmid DNA is isolated using a commercially available kit (QIAGEN Plasmid Maxi Kit, Qiagen, Valencia, CA) according to manufacturer's instructions. The correct construct is designated pZMP6/AFP.

Recombinant protein is produced in BHK cells transfected with
25 pZMP6/AFP. BHK 570 cells (ATCC CRL-10314) are plated in 10-cm tissue culture dishes and allowed to grow to approximately 50 to 70% confluence overnight at 37°C, 5% CO₂, in DMEM/FBS media (DMEM, Gibco/BRL High Glucose; Life Technologies), 5% fetal bovine serum (Hyclone, Logan, UT), 1 mM L-glutamine (JRH Biosciences, Lenexa, KS), 1 mM sodium pyruvate (Life Technologies). The cells are
30 then transfected with pZMP6/AFP by liposome-mediated transfection using a 3:1 (w/w) liposome formulation of the polycationic lipid 2,3-dioleoyloxy-N-[2(sperminecarboxamido)ethyl]-N,N-dimethyl-1-propaniminium-trifluoroacetate and the neutral lipid dioleoyl phosphatidylethanolamine in membrane-filtered water (Lipofectamine™ Reagent; Life Technologies, Gaithersburg, MD), in serum free (SF)
35 media (DMEM supplemented with 10 mg/ml transferrin, 5 mg/ml insulin, 2 mg/ml fetuin, 1% L-glutamine and 1% sodium pyruvate). The plasmid is diluted into 15-ml tubes to a total final volume of 640 µl with SF media. 35 µl of the lipid mixture is

mixed with 605 μ l of SF medium, and the resulting mixture is allowed to incubate approximately 30 minutes at room temperature. Five milliliters of SF media is then added to the DNA:lipid mixture. The cells are rinsed once with 5 ml of SF media, aspirated, and the DNA:lipid mixture is added. The cells are incubated at 37°C for five
5 hours, then 6.4 ml of DMEM/10% FBS, 1% PSN media is added to each plate. The plates are incubated at 37°C overnight, and the DNA:lipid mixture is replaced with fresh 5% FBS/DMEM media the next day. On day 5 post-transfection, the cells are split into T-162 flasks in selection medium (DMEM + 5% FBS, 1% L-Gln, 1% NaPyr, 1 μ M methotrexate). Approximately 10 days post-transfection, two 150-mm culture
10 dishes of methotrexate-resistant colonies from each transfection are trypsinized, and the cells are pooled and plated into a T-162 flask and transferred to large-scale culture.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration,
15 various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

We claim:

1. An isolated polypeptide comprising fifteen contiguous amino acid residues of a polypeptide as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422.

2. The isolated polypeptide of claim 1 wherein M is 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, or 416.

3. The isolated polypeptide of claim 1 or claim 2 which is from 15 to 2235 amino acid residues in length.

4. The isolated polypeptide of claim 3 which is operably linked via a peptide bond or polypeptide linker to a second polypeptide selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag, and a peptide as shown in SEQ ID NO:423.

5. The isolated polypeptide of any of claims 1-4 comprising at least 30 contiguous residues of SEQ ID NO:M.

6. The isolated polypeptide of any of claims 1-5 comprising at least 47 contiguous residues of SEQ ID NO:M.

7. An isolated, mature protein encoded by a sequence selected from the group consisting of SEQ ID NO:N, wherein N is an odd integer from 1 to 421.

8. The protein of claim 7 wherein N is 5, 7, 11, 17, 23, 41, 47, 53, 65, 67, 69, 71, 89, 91, 95, 97, 101, 105, 109, 121, 133, 137, 139, 155, 157, 161, 163, 167, 173, 177, 179, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 407, 411, or 415.

9. An isolated polynucleotide comprising a sequence of nucleotides as shown in SEQ ID NO:N, wherein N is an odd integer from 1 to 421.

10. The isolated polynucleotide of claim 9 wherein N is 5, 7, 11, 17, 23, 41, 47, 53, 65, 67, 69, 71, 89, 91, 95, 97, 101, 105, 109, 121, 133, 137, 139, 155, 157, 161, 163, 167, 173, 177, 179, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 407, 411, or 415.

11. An expression vector comprising the following operably linked elements:

a transcription promoter;

a DNA segment encoding a polypeptide as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422; and

a transcription terminator.

12. The expression vector of claim 11 wherein M is 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, or 416.

13. A cultured cell comprising the expression vector of claim 11 or claim 12.

14. A method of producing a polypeptide comprising culturing the cell of claim 13 under conditions whereby said sequence of nucleotides is expressed, and recovering said polypeptide.

15. A polypeptide produced by the method of claim 14.

16. An isolated polynucleotide encoding a fusion protein, said protein comprising a secretory peptide selected from the group consisting of secretory peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide.

17. An expression vector comprising the following operably linked elements:

a transcription promoter;

a DNA segment encoding a fusion protein, said protein comprising a secretory peptide selected from the group consisting of secretory peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide; and

a transcription terminator.

18. A cultured cell comprising the expression vector of claim 17, wherein the cell expresses the DNA segment and produces the encoded fusion protein.

19. A method of producing a protein comprising culturing the cell of claim 18 under conditions whereby said DNA segment is expressed, and recovering said second polypeptide.

20. An antibody that specifically binds to a protein selected from of the group consisting of SEQ ID NO:M, wherein M is an even integer from 2 to 422.

SEQUENCE LISTING

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 Pro Ala Ser Glu Ile Ala Lys Leu Leu Ala Ser Asp Asp Met Asn Ile
 20 25 30

cct aat gag gag aca ata ttg aat gca ctt ctt act tgg gtc cgt cat	144
Pro Asn Glu Glu Thr Ile Leu Asn Ala Leu Leu Thr Trp Val Arg His	
35 40 45	
gat ttg gaa cag aga cgg aaa gat cta agt aaa ctt ttg gct tat att	192
Asp Leu Glu Gln Arg Arg Lys Asp Leu Ser Lys Leu Leu Ala Tyr Ile	
50 55 60	
agg cta cct ctt ctt gca cca cag ttc ctg gca gac atg gaa aat aat	240
Arg Leu Pro Leu Leu Ala Pro Gln Phe Leu Ala Asp Met Glu Asn Asn	
65 70 75 80	
gta ctt ttt cgg gat gat ata gaa tgt cag aaa ctc att atg gaa gca	288
Val Leu Phe Arg Asp Asp Ile Glu Cys Gln Lys Leu Ile Met Glu Ala	
85 90 95	
atg aag tac cat tta tta cca gag aga cga ccc atg tta caa agt cct	336
Met Lys Tyr His Leu Leu Pro Glu Arg Arg Pro Met Leu Gln Ser Pro	
100 105 110	
cgg aca aaa cct agg aag tca act gtt ggt aca tta ttt gca gtt ggg	384
Arg Thr Lys Pro Arg Lys Ser Thr Val Gly Thr Leu Phe Ala Val Gly	
115 120 125	
gga atg gat tca aca aaa gga gca aca agc att gaa aag tat gat ctc	432
Gly Met Asp Ser Thr Lys Gly Ala Thr Ser Ile Glu Lys Tyr Asp Leu	
130 135 140	
cgt aca aat atg tgg act cca gta gca aat atg aat ggg agg ngg cta	480
Arg Thr Asn Met Trp Thr Pro Val Ala Asn Met Asn Gly Arg Xaa Leu	
145 150 155 160	
cag ttc ggt gtt gca gtg cta gat gac aaa ctg tat gtg gtt gga gga	528
Gln Phe Gly Val Ala Val Leu Asp Asp Lys Leu Tyr Val Val Gly Gly	
165 170 175	
aga gat gga ctg aag act ttg aat act gta gag tgc tac aac ccc aaa	576
Arg Asp Gly Leu Lys Thr Leu Asn Thr Val Glu Cys Tyr Asn Pro Lys	
180 185 190	
aca aaa act tgg agt gtg atg cca cct atg tcc aca cat aga cat ggc	624
Thr Lys Thr Trp Ser Val Met Pro Pro Met Ser Thr His Arg His Gly	
195 200 205	

ctt ggt gtg gct gta ctg gaa ggt ccc atg tat gcc gta gga gga cat Leu Gly Val Ala Val Leu Glu Gly Pro Met Tyr Ala Val Gly Gly His 210 215 220	672
gat ggc tgg agc tat ctg aac aca gtg gaa aga tgg gac cct cag gct Asp Gly Trp Ser Tyr Leu Asn Thr Val Glu Arg Trp Asp Pro Gln Ala 225 230 235 240	720
cgc cag tgg aat ttt gtt gcc act atg tct acc cct agg agt aca gta Arg Gln Trp Asn Phe Val Ala Thr Met Ser Thr Pro Arg Ser Thr Val 245 250 255	768
ggt gtg gca gta cta agt gga aaa ctt tat gca gtt ggt ggt cgt gat Gly Val Ala Val Leu Ser Gly Lys Leu Tyr Ala Val Gly Gly Arg Asp 260 265 270	816
gga agt tct tgt ctc aaa tca gta gaa tgt ttt gat cct cat act aat Gly Ser Ser Cys Leu Lys Ser Val Glu Cys Phe Asp Pro His Thr Asn 275 280 285	864
aag tgg aca ctg tgt gca cag atg tca aaa agg aga ggt ggc gta gga Lys Trp Thr Leu Cys Ala Gln Met Ser Lys Arg Arg Gly Gly Val Gly 290 295 300	912
gtg acg acc tgg aat gga ctg ctg tat gct ata ggg ggg cac gat gct Val Thr Thr Trp Asn Gly Leu Leu Tyr Ala Ile Gly Gly His Asp Ala 305 310 315 320	960
ccc gca tcc aac ttg act tcc aga ctc tca gac tgt gtg gaa aga tat Pro Ala Ser Asn Leu Thr Ser Arg Leu Ser Asp Cys Val Glu Arg Tyr 325 330 335	1008
gat ccc aaa aca gac atg tgg act gca gta gca tcc atg agc atc agc Asp Pro Lys Thr Asp Met Trp Thr Ala Val Ala Ser Met Ser Ile Ser 340 345 350	1056
aga gat gca gtg ggg gtc tgt tta ctt ggt gat aag tta tat gct gtt Arg Asp Ala Val Gly Val Cys Leu Leu Gly Asp Lys Leu Tyr Ala Val 355 360 365	1104
ggg ggg tat gat gga cag gca tac ctt aat acc gtg gag gct tat gat Gly Gly Tyr Asp Gly Gln Ala Tyr Leu Asn Thr Val Glu Ala Tyr Asp 370 375 380	1152

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ccc cag aca aat gag tgg acc cag gtt gct cca ctg tgc cta gga aga      1200
Pro Gln Thr Asn Glu Trp Thr Gln Val Ala Pro Leu Cys Leu Gly Arg
385                      390                      395                      400

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gct gga gct tgt gtt gtg act gta aaa tta taa      1233
Ala Gly Ala Cys Val Val Thr Val Lys Leu *
405                      410

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<210> 4
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 <212> PRT
 <213> Homo sapiens

<220>
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 <223> Xaa = Any Amino Acid

<400> 4

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Met Glu His Phe Met Glu Val Ile Arg Asn Gln Glu Phe Val Leu Leu
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Pro Ala Ser Glu Ile Ala Lys Leu Leu Ala Ser Asp Asp Met Asn Ile
          20          25          30
Pro Asn Glu Glu Thr Ile Leu Asn Ala Leu Leu Thr Trp Val Arg His
          35          40          45
Asp Leu Glu Gln Arg Arg Lys Asp Leu Ser Lys Leu Leu Ala Tyr Ile
          50          55          60
Arg Leu Pro Leu Leu Ala Pro Gln Phe Leu Ala Asp Met Glu Asn Asn
65          70          75          80
Val Leu Phe Arg Asp Asp Ile Glu Cys Gln Lys Leu Ile Met Glu Ala
          85          90          95
Met Lys Tyr His Leu Leu Pro Glu Arg Arg Pro Met Leu Gln Ser Pro
          100          105          110
Arg Thr Lys Pro Arg Lys Ser Thr Val Gly Thr Leu Phe Ala Val Gly
          115          120          125
Gly Met Asp Ser Thr Lys Gly Ala Thr Ser Ile Glu Lys Tyr Asp Leu
          130          135          140
Arg Thr Asn Met Trp Thr Pro Val Ala Asn Met Asn Gly Arg Xaa Leu
145          150          155          160
Gln Phe Gly Val Ala Val Leu Asp Asp Lys Leu Tyr Val Val Gly Gly
          165          170          175
Arg Asp Gly Leu Lys Thr Leu Asn Thr Val Glu Cys Tyr Asn Pro Lys

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10

180										185					190				
Thr	Lys	Thr	Trp	Ser	Val	Met	Pro	Pro	Met	Ser	Thr	His	Arg	His	Gly				
195							200				205								
Leu	Gly	Val	Ala	Val	Leu	Glu	Gly	Pro	Met	Tyr	Ala	Val	Gly	Gly	His				
210							215				220								
Asp	Gly	Trp	Ser	Tyr	Leu	Asn	Thr	Val	Glu	Arg	Trp	Asp	Pro	Gln	Ala				
225							230				235								
Arg	Gln	Trp	Asn	Phe	Val	Ala	Thr	Met	Ser	Thr	Pro	Arg	Ser	Thr	Val				
245							250				255								
Gly	Val	Ala	Val	Leu	Ser	Gly	Lys	Leu	Tyr	Ala	Val	Gly	Gly	Arg	Asp				
260							265				270								
Gly	Ser	Ser	Cys	Leu	Lys	Ser	Val	Glu	Cys	Phe	Asp	Pro	His	Thr	Asn				
275							280				285								
Lys	Trp	Thr	Leu	Cys	Ala	Gln	Met	Ser	Lys	Arg	Arg	Gly	Gly	Val	Gly				
290							295				300								
Val	Thr	Thr	Trp	Asn	Gly	Leu	Leu	Tyr	Ala	Ile	Gly	Gly	His	Asp	Ala				
305							310				315								
Pro	Ala	Ser	Asn	Leu	Thr	Ser	Arg	Leu	Ser	Asp	Cys	Val	Glu	Arg	Tyr				
325							330				335								
Asp	Pro	Lys	Thr	Asp	Met	Trp	Thr	Ala	Val	Ala	Ser	Met	Ser	Ile	Ser				
340							345				350								
Arg	Asp	Ala	Val	Gly	Val	Cys	Leu	Leu	Gly	Asp	Lys	Leu	Tyr	Ala	Val				
355							360				365								
Gly	Gly	Tyr	Asp	Gly	Gln	Ala	Tyr	Leu	Asn	Thr	Val	Glu	Ala	Tyr	Asp				
370							375				380								
Pro	Gln	Thr	Asn	Glu	Trp	Thr	Gln	Val	Ala	Pro	Leu	Cys	Leu	Gly	Arg				
385							390				395								
Ala	Gly	Ala	Cys	Val	Val	Thr	Val	Lys	Leu										
405							410												

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<210> 5
<211> 1644
<212> DNA
<213> Homo sapiens
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<220>  
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<222> (1)...(1644)
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Met Leu Arg Tyr Leu Glu Thr Ala Asp Tyr Ala Ile Arg Glu Glu Ile
1 5 10 15

11

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tgg tac gtg gac acc atc ctc aac ctc atc cgc att gcg ggc gac tac Trp Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp Tyr 35 40 45	144
gtg agt gag gag gtg tgg tac cgt gtg cta cag atc gtc acc aac cgt Val Ser Glu Glu Val Trp Tyr Arg Val Leu Gln Ile Val Thr Asn Arg 50 55 60	192
gat gac gtc cag ggc tat gcc gcc aag acc gtc ttt gag gcg ctc cag Asp Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln 65 70 75 80	240
gcc cct gcc tgt cac gag aac atg gtg aag gtt ggc ggc tac atc ctt Ala Pro Ala Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu 85 90 95	288
ggg gag ttt ggg aac ctg att gct ggg gac ccc cgc tcc agc ccc cca Gly Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro Pro 100 105 110	336
gtg cag ttc tcc ctg ctc cac tcc aag ttc cat ctg tgc agc gtg gcc Val Gln Phe Ser Leu Leu His Ser Lys Phe His Leu Cys Ser Val Ala 115 120 125	384
acg cgg gcg ctg ctg ctg tcc acc tac atc aag ttc atc aac ctc ttc Thr Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Ile Asn Leu Phe 130 135 140	432
ccc gag acc aag gcc acc atc cag ggc gtc ctg cgg gcc ggc tcc cag Pro Glu Thr Lys Ala Thr Ile Gln Gly Val Leu Arg Ala Gly Ser Gln 145 150 155 160	480
ctg cgc aat gct gac gtg gag ctg cag cag cga gcc gtg gag tac ctc Leu Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu 165 170 175	528
acc ctc agc tca gtg gcc agc acc gac gtc ctg gcc acg gtg ctg gag Thr Leu Ser Ser Val Ala Ser Thr Asp Val Leu Ala Thr Val Leu Glu 180 185 190	576

12

gag atg ccg ccc ttc ccc gag cgc gag tcg tcc atc ctg gcc aag ctg Glu Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu 195 200 205	624
aaa cgc aag aag ggg cca ggg gcc ggc agc gcc ctg gac gat ggc cgg Lys Arg Lys Lys Gly Pro Gly Ala Gly Ser Ala Leu Asp Asp Gly Arg 210 215 220	672
agg gac ccc agc agc aac gac atc aac ggg ggc atg gag ccc acc ccc Arg Asp Pro Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro 225 230 235 240	720
agc act gtg tcg acg ccc tcg ccc tcc gcc gac ctc ctg ggg ctg cgg Ser Thr Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg 245 250 255	768
gca gcc cct ccc ccg gca gca ccc ccg gct tct gca gga gca ggg aac Ala Ala Pro Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn 260 265 270	816
ctt ctg gtg gac gtc ttc gat ggc ccg gcc gcc cag ccc agc ctg ggg Leu Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly 275 280 285	864
ccc acc ccc gag gag gcc ttc ctc agc cca ggt cct gag gac atc ggc Pro Thr Pro Glu Glu Ala Phe Leu Ser Pro Gly Pro Glu Asp Ile Gly 290 295 300	912
cct ccc att ccg gaa gcc gat gag ttg ctg aat aag ttt gtg tgt aag Pro Pro Ile Pro Glu Ala Asp Glu Leu Leu Asn Lys Phe Val Cys Lys 305 310 315 320	960
aac aac ggg gtc ctg ttc gag aac cag ctg ctg cag atc gga gtc aag Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys 325 330 335	1008
tca gag ttc cga cag aac ctg ggc cgc atg tat ctc ttc tat ggc aac Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn 340 345 350	1056
aag acc tcg gtg cag ttc cag aat ttc tca ccc act gtg gtt cac ccg Lys Thr Ser Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro 355 360 365	1104

gga gac ctc cag act cag ctg gct gtg cag acc aag cgc gtg gcg gcg	1152
Gly Asp Leu Gln Thr Gln Leu Ala Val Gln Thr Lys Arg Val Ala Ala	
370 375 380	
cag gtg gac ggc ggc gcg cag gtg cag cag gtg ctc aat atc gag tgc	1200
Gln Val Asp Gly Gly Ala Gln Val Gln Gln Val Leu Asn Ile Glu Cys	
385 390 395 400	
ctg cgg gac ttc ctg acg ccc ccg ctg ctg tcc gtg cgc ttc cgg tac	1248
Leu Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser Val Arg Phe Arg Tyr	
405 410 415	
ggt ggc gcc ccc cag gcc ctc acc ctg aag ctc cca gtg acc atc aac	1296
Gly Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu Pro Val Thr Ile Asn	
420 425 430	
aag ttc ttc cag ccc acc gag atg gcg gcc cag gat ttc ttc cag cgc	1344
Lys Phe Phe Gln Pro Thr Glu Met Ala Ala Gln Asp Phe Phe Gln Arg	
435 440 445	
tgg aag cag ctg agc ctc cct caa cag gag gcg cag aaa atc ttc aaa	1392
Trp Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala Gln Lys Ile Phe Lys	
450 455 460	
gcc aac cac ccc atg gac gca gaa gtt act aag gcc aag ctt ctg ggg	1440
Ala Asn His Pro Met Asp Ala Glu Val Thr Lys Ala Lys Leu Leu Gly	
465 470 475 480	
ttt ggc tct gct ctc ctg gac aat gtg gac ccc aac cct gag aac ttc	1488
Phe Gly Ser Ala Leu Leu Asp Asn Val Asp Pro Asn Pro Glu Asn Phe	
485 490 495	
gtg ggg gcg ggg atc atc cag act aaa gcc ctg cag gtg ggc tgt ctg	1536
Val Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu Gln Val Gly Cys Leu	
500 505 510	
ctt cgg ctg gag ccc aat gcc cag gcc cag atg tac cgg ctg acc ctg	1584
Leu Arg Leu Glu Pro Asn Ala Gln Ala Gln Met Tyr Arg Leu Thr Leu	
515 520 525	
cgc acc agc aag gag ccc gtc tcc cgt cac ctg tgt gag ctg ctg gca	1632
Arg Thr Ser Lys Glu Pro Val Ser Arg His Leu Cys Glu Leu Leu Ala	
530 535 540	

cag cag ttc tga
Gln Gln Phe *
545

1644

<210> 6
<211> 547
<212> PRT
<213> Homo sapiens

<400> 6

Met	Leu	Arg	Tyr	Leu	Glu	Thr	Ala	Asp	Tyr	Ala	Ile	Arg	Glu	Glu	Ile
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Val	Leu	Lys	Val	Ala	Ile	Leu	Ala	Glu	Lys	Tyr	Ala	Val	Asp	Tyr	Ser
			20					25					30		
Trp	Tyr	Val	Asp	Thr	Ile	Leu	Asn	Leu	Ile	Arg	Ile	Ala	Gly	Asp	Tyr
		35					40					45			
Val	Ser	Glu	Glu	Val	Trp	Tyr	Arg	Val	Leu	Gln	Ile	Val	Thr	Asn	Arg
	50					55				60					
Asp	Asp	Val	Gln	Gly	Tyr	Ala	Ala	Lys	Thr	Val	Phe	Glu	Ala	Leu	Gln
65				70					75					80	
Ala	Pro	Ala	Cys	His	Glu	Asn	Met	Val	Lys	Val	Gly	Gly	Tyr	Ile	Leu
			85						90					95	
Gly	Glu	Phe	Gly	Asn	Leu	Ile	Ala	Gly	Asp	Pro	Arg	Ser	Ser	Pro	Pro
			100					105					110		
Val	Gln	Phe	Ser	Leu	Leu	His	Ser	Lys	Phe	His	Leu	Cys	Ser	Val	Ala
	115						120					125			
Thr	Arg	Ala	Leu	Leu	Leu	Ser	Thr	Tyr	Ile	Lys	Phe	Ile	Asn	Leu	Phe
	130					135					140				
Pro	Glu	Thr	Lys	Ala	Thr	Ile	Gln	Gly	Val	Leu	Arg	Ala	Gly	Ser	Gln
145				150					155					160	
Leu	Arg	Asn	Ala	Asp	Val	Glu	Leu	Gln	Gln	Arg	Ala	Val	Glu	Tyr	Leu
			165					170					175		
Thr	Leu	Ser	Ser	Val	Ala	Ser	Thr	Asp	Val	Leu	Ala	Thr	Val	Leu	Glu
		180						185					190		
Glu	Met	Pro	Pro	Phe	Pro	Glu	Arg	Glu	Ser	Ser	Ile	Leu	Ala	Lys	Leu
	195					200						205			
Lys	Arg	Lys	Lys	Gly	Pro	Gly	Ala	Gly	Ser	Ala	Leu	Asp	Asp	Gly	Arg
	210					215					220				
Arg	Asp	Pro	Ser	Ser	Asn	Asp	Ile	Asn	Gly	Gly	Met	Glu	Pro	Thr	Pro
225					230				235					240	
Ser	Thr	Val	Ser	Thr	Pro	Ser	Pro	Ser	Ala	Asp	Leu	Leu	Gly	Leu	Arg
			245						250				255		
Ala	Ala	Pro	Pro	Pro	Ala	Ala	Pro	Pro	Ala	Ser	Ala	Gly	Ala	Gly	Asn

15

260 265 270
 Leu Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly
 275 280 285
 Pro Thr Pro Glu Glu Ala Phe Leu Ser Pro Gly Pro Glu Asp Ile Gly
 290 295 300
 Pro Pro Ile Pro Glu Ala Asp Glu Leu Leu Asn Lys Phe Val Cys Lys
 305 310 315 320
 Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys
 325 330 335
 Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn
 340 345 350
 Lys Thr Ser Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro
 355 360 365
 Gly Asp Leu Gln Thr Gln Leu Ala Val Gln Thr Lys Arg Val Ala Ala
 370 375 380
 Gln Val Asp Gly Gly Ala Gln Val Gln Gln Val Leu Asn Ile Glu Cys
 385 390 395 400
 Leu Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser Val Arg Phe Arg Tyr
 405 410 415
 Gly Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu Pro Val Thr Ile Asn
 420 425 430
 Lys Phe Phe Gln Pro Thr Glu Met Ala Ala Gln Asp Phe Phe Gln Arg
 435 440 445
 Trp Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala Gln Lys Ile Phe Lys
 450 455 460
 Ala Asn His Pro Met Asp Ala Glu Val Thr Lys Ala Lys Leu Leu Gly
 465 470 475 480
 Phe Gly Ser Ala Leu Leu Asp Asn Val Asp Pro Asn Pro Glu Asn Phe
 485 490 495
 Val Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu Gln Val Gly Cys Leu
 500 505 510
 Leu Arg Leu Glu Pro Asn Ala Gln Ala Gln Met Tyr Arg Leu Thr Leu
 515 520 525
 Arg Thr Ser Lys Glu Pro Val Ser Arg His Leu Cys Glu Leu Leu Ala
 530 535 540
 Gln Gln Phe
 545

<210> 7

<211> 711

<212> DNA

<213> Homo sapiens

<220>

16

<221> CDS

<222> (1)...(711)

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cca atg atg ctg ggt tca ccc aca tct cca aag cca gga gtt aat gcc	96
Pro Met Met Leu Gly Ser Pro Thr Ser Pro Lys Pro Gly Val Asn Ala	
20 25 30	
cag ttc tta cct gga ttt tta atg ggg gat ttg cca gct ccg gtg act	144
Gln Phe Leu Pro Gly Phe Leu Met Gly Asp Leu Pro Ala Pro Val Thr	
35 40 45	
cca caa cct cga tca att agt ggc cct tca gta gga gta atg gaa atg	192
Pro Gln Pro Arg Ser Ile Ser Gly Pro Ser Val Gly Val Met Glu Met	
50 55 60	
aga tca cct tta ctt gca ggt ggg tca cca cca caa cca gtt gta cca	240
Arg Ser Pro Leu Leu Ala Gly Gly Ser Pro Pro Gln Pro Val Val Pro	
65 70 75 80	
gct cat aaa gat aaa agt ggc gct cca cca gtt aga agt ata tat gat	288
Ala His Lys Asp Lys Ser Gly Ala Pro Pro Val Arg Ser Ile Tyr Asp	
85 90 95	
gac att tct agc cca gga ctt gga tca aca cct tta act tca aga aga	336
Asp Ile Ser Ser Pro Gly Leu Gly Ser Thr Pro Leu Thr Ser Arg Arg	
100 105 110	
cag atg tct aat aca gga aat tgg atg cat att cgt tat caa tct aaa	384
Gln Met Ser Asn Thr Gly Asn Trp Met His Ile Arg Tyr Gln Ser Lys	
115 120 125	
ctg cag gct cgg aaa gcc tta agc aaa gat ggg agg att ttt gga gaa	432
Leu Gln Ala Arg Lys Ala Leu Ser Lys Asp Gly Arg Ile Phe Gly Glu	
130 135 140	
tcc atc atg att ggt gta aaa cca tgt att gac aaa agt gtt atg gaa	480
Ser Ile Met Ile Gly Val Lys Pro Cys Ile Asp Lys Ser Val Met Glu	
145 150 155 160	

17

agc agt gac aga tgt gct tta tca tct cca tct tta gcc ttt aca cca 528
 Ser Ser Asp Arg Cys Ala Leu Ser Ser Pro Ser Leu Ala Phe Thr Pro
 165 170 175

cca atc aaa act cta ggt aca cca aca caa cct gga agt act cct agg 576
 Pro Ile Lys Thr Leu Gly Thr Pro Thr Gln Pro Gly Ser Thr Pro Arg
 180 185 190

att tct acc atg aga cct ctt gct aca gca tac aaa gcc tct act agt 624
 Ile Ser Thr Met Arg Pro Leu Ala Thr Ala Tyr Lys Ala Ser Thr Ser
 195 200 205

gat tat cag gtt att tct gac aga caa acg cca aaa aaa gat gaa agt 672
 Asp Tyr Gln Val Ile Ser Asp Arg Gln Thr Pro Lys Lys Asp Glu Ser
 210 215 220

ctt gta tcc aaa gca atg gag tac atg ttt ggc tgg tag 711
 Leu Val Ser Lys Ala Met Glu Tyr Met Phe Gly Trp *
 225 230 235

<210> 8

<211> 236

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Ala Phe Ala Val Glu Pro Gln Gly Pro Ala Leu Gly Ser Glu
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 Pro Met Met Leu Gly Ser Pro Thr Ser Pro Lys Pro Gly Val Asn Ala
 20 25 30
 Gln Phe Leu Pro Gly Phe Leu Met Gly Asp Leu Pro Ala Pro Val Thr
 35 40 45
 Pro Gln Pro Arg Ser Ile Ser Gly Pro Ser Val Gly Val Met Glu Met
 50 55 60
 Arg Ser Pro Leu Leu Ala Gly Gly Ser Pro Pro Gln Pro Val Val Pro
 65 70 75 80
 Ala His Lys Asp Lys Ser Gly Ala Pro Pro Val Arg Ser Ile Tyr Asp
 85 90 95
 Asp Ile Ser Ser Pro Gly Leu Gly Ser Thr Pro Leu Thr Ser Arg Arg
 100 105 110
 Gln Met Ser Asn Thr Gly Asn Trp Met His Ile Arg Tyr Gln Ser Lys
 115 120 125
 Leu Gln Ala Arg Lys Ala Leu Ser Lys Asp Gly Arg Ile Phe Gly Glu

18

130	135	140
Ser Ile Met Ile Gly Val Lys Pro Cys Ile Asp Lys Ser Val Met Glu		
145	150	155
Ser Ser Asp Arg Cys Ala Leu Ser Ser Pro Ser Leu Ala Phe Thr Pro		160
	165	170
Pro Ile Lys Thr Leu Gly Thr Pro Thr Gln Pro Gly Ser Thr Pro Arg		175
	180	185
Ile Ser Thr Met Arg Pro Leu Ala Thr Ala Tyr Lys Ala Ser Thr Ser		190
	195	200
Asp Tyr Gln Val Ile Ser Asp Arg Gln Thr Pro Lys Lys Asp Glu Ser		205
	210	220
Leu Val Ser Lys Ala Met Glu Tyr Met Phe Gly Trp		
225	230	235

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(636)

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1 5 10 15	
ttg gtg tca tgc atg atc ctg tgg ata tct gtg act ccc aca cca tat	96
Leu Val Ser Cys Met Ile Leu Trp Ile Ser Val Thr Pro Thr Pro Tyr	
20 25 30	
gac cag atg tcc aat gag gag ctg tat gac aat ctg ctt tcc tgt tct	144
Asp Gln Met Ser Asn Glu Glu Leu Tyr Asp Asn Leu Leu Ser Cys Ser	
35 40 45	
cat cgc acc cat gta gtt gcc cga aaa atg tat aaa att tta gac tta	192
His Arg Thr His Val Val Ala Arg Lys Met Tyr Lys Ile Leu Asp Leu	
50 55 60	
aat gta gct gag aga aga tgt ttt aag aat aaa aga aac aac acc tgc	240
Asn Val Ala Glu Arg Arg Cys Phe Lys Asn Lys Arg Asn Asn Thr Cys	
65 70 75 80	

19

cac acc act tct acc cat act gca aaa aca aat gaa gat ctt ctg aaa	288
His Thr Thr Ser Thr His Thr Ala Lys Thr Asn Glu Asp Leu Leu Lys	
85 90 95	
gtc atc atc agt gtt tcg aat gca tgg ata tat cca ctg aaa atg ctc	336
Val Ile Ile Ser Val Ser Asn Ala Trp Ile Tyr Pro Leu Lys Met Leu	
100 105 110	
ata cct gca gtg ttg act cat ttg ggc tcc tat gat ggt atg atg gca	384
Ile Pro Ala Val Leu Thr His Leu Gly Ser Tyr Asp Gly Met Met Ala	
115 120 125	
aga gcc ata gag ctt aac tat gga aat caa aaa att ctg gag gga gca	432
Arg Ala Ile Glu Leu Asn Tyr Gly Asn Gln Lys Ile Leu Glu Gly Ala	
130 135 140	
aaa ttt tta ctc agc agg att cag cct gga att gaa gaa aat gac tat	480
Lys Phe Leu Leu Ser Arg Ile Gln Pro Gly Ile Glu Glu Asn Asp Tyr	
145 150 155 160	
cct gtc tgg tca agc tta aaa gaa ttg agg tct tcc aat aaa agc att	528
Pro Val Trp Ser Ser Leu Lys Glu Leu Arg Ser Ser Asn Lys Ser Ile	
165 170 175	
cac ctt ttt gca ttt tgt aaa ttc ttc tac tgc ttg cgc aaa gat aca	576
His Leu Phe Ala Phe Cys Lys Phe Phe Tyr Cys Leu Arg Lys Asp Thr	
180 185 190	
aag aag att aag gat tat ctc cag atc ttg agg cct aac att att aaa	624
Lys Lys Ile Lys Asp Tyr Leu Gln Ile Leu Arg Pro Asn Ile Ile Lys	
195 200 205	
aac aag tgg taa	636
Asn Lys Trp *	
210	

<210> 10

<211> 211

<212> PRT

<213> Homo sapiens

<400> 10

Met Gln Leu Ser Leu Thr Gln Ala Arg Thr Trp Lys Gly Leu Leu Leu

20

1 5 10 15
 Leu Val Ser Cys Met Ile Leu Trp Ile Ser Val Thr Pro Thr Pro Tyr
 20 25 30
 Asp Gln Met Ser Asn Glu Glu Leu Tyr Asp Asn Leu Leu Ser Cys Ser
 35 40 45
 His Arg Thr His Val Val Ala Arg Lys Met Tyr Lys Ile Leu Asp Leu
 50 55 60
 Asn Val Ala Glu Arg Arg Cys Phe Lys Asn Lys Arg Asn Asn Thr Cys
 65 70 75 80
 His Thr Thr Ser Thr His Thr Ala Lys Thr Asn Glu Asp Leu Leu Lys
 85 90 95
 Val Ile Ile Ser Val Ser Asn Ala Trp Ile Tyr Pro Leu Lys Met Leu
 100 105 110
 Ile Pro Ala Val Leu Thr His Leu Gly Ser Tyr Asp Gly Met Met Ala
 115 120 125
 Arg Ala Ile Glu Leu Asn Tyr Gly Asn Gln Lys Ile Leu Glu Gly Ala
 130 135 140
 Lys Phe Leu Leu Ser Arg Ile Gln Pro Gly Ile Glu Glu Asn Asp Tyr
 145 150 155 160
 Pro Val Trp Ser Ser Leu Lys Glu Leu Arg Ser Ser Asn Lys Ser Ile
 165 170 175
 His Leu Phe Ala Phe Cys Lys Phe Phe Tyr Cys Leu Arg Lys Asp Thr
 180 185 190
 Lys Lys Ile Lys Asp Tyr Leu Gln Ile Leu Arg Pro Asn Ile Ile Lys
 195 200 205
 Asn Lys Trp
 210

<210> 11
 <211> 651
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(651)

<400> 11
 atg tcc gcc ggg ggc ttc gcg gcg ccg ggg cac gcg gcg ggg ggt ccg 48
 Met Ser Ala Gly Gly Phe Ala Ala Pro Gly His Ala Ala Gly Gly Pro
 1 5 10 15
 cct ccg ccg ccc cca cct ctg gga ccc cat tcc aac cgg acc acc cca 96
 Pro Pro Pro Pro Pro Pro Leu Gly Pro His Ser Asn Arg Thr Thr Pro

21

20	25	30	
cct gag tca gcc ccc cag aac ggt ccg tcc cct atg gcc gct ctc atg Pro Glu Ser Ala Pro Gln Asn Gly Pro Ser Pro Met Ala Ala Leu Met			144
35	40	45	
tcg gtg gca gat act ctg ggc aca gcg cac tcg ccc aag gat ggc agt Ser Val Ala Asp Thr Leu Gly Thr Ala His Ser Pro Lys Asp Gly Ser			192
50	55	60	
tcc gtg cac tct acc act gcg tcg gcg cgg cga aac agc agc agc cca Ser Val His Ser Thr Thr Ala Ser Ala Arg Arg Asn Ser Ser Ser Pro			240
65	70	75	80
gtc tcg ccg gcc tcc gtg ccg ggg cag cgc cgc ttg gca tca cgt aac Val Ser Pro Ala Ser Val Pro Gly Gln Arg Arg Leu Ala Ser Arg Asn			288
85	90	95	
ggg gac ctg aat tta cag gtg gcg ccc ccg ccg cct agc gcc cac ccg Gly Asp Leu Asn Leu Gln Val Ala Pro Pro Pro Pro Ser Ala His Pro			336
100	105	110	
ggc atg gac caa gtg cac ccc caa aac att ccg gat tcc ccc atg gcc Gly Met Asp Gln Val His Pro Gln Asn Ile Pro Asp Ser Pro Met Ala			384
115	120	125	
aac agc gga ccc ctc tgc tgc acc att tgc cac gaa cgt ttg gag gat Asn Ser Gly Pro Leu Cys Cys Thr Ile Cys His Glu Arg Leu Glu Asp			432
130	135	140	
acg cat ttc gtt cag tgc cct tcc gtc ccc agc cac aaa ttt tgc ttc Thr His Phe Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe			480
145	150	155	160
cct tgc tct aga gag agt atc aag gcc cag ggg gcc acc ggc gag gtg Pro Cys Ser Arg Glu Ser Ile Lys Ala Gln Gly Ala Thr Gly Glu Val			528
165	170	175	
tat tgc ccc agc gga gag aaa tgc ccc cta gtc ggg tcg aat gta cct Tyr Cys Pro Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro			576
180	185	190	
tgg gcc ttc atg cag ggc gaa atc gcg act atc tta gct ggg gat gtt Trp Ala Phe Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val			624

22

195 200 205 651

aaa gtg aaa aag gag aga gac cct tga
 Lys Val Lys Lys Glu Arg Asp Pro *

210 215

<210> 12
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 12

Met Ser Ala Gly Gly Phe Ala Ala Pro Gly His Ala Ala Gly Gly Pro
 1 5 10 15
 Pro Pro Pro Pro Pro Pro Leu Gly Pro His Ser Asn Arg Thr Thr Pro
 20 25 30
 Pro Glu Ser Ala Pro Gln Asn Gly Pro Ser Pro Met Ala Ala Leu Met
 35 40 45
 Ser Val Ala Asp Thr Leu Gly Thr Ala His Ser Pro Lys Asp Gly Ser
 50 55 60
 Ser Val His Ser Thr Thr Ala Ser Ala Arg Arg Asn Ser Ser Ser Pro
 65 70 75 80
 Val Ser Pro Ala Ser Val Pro Gly Gln Arg Arg Leu Ala Ser Arg Asn
 85 90 95
 Gly Asp Leu Asn Leu Gln Val Ala Pro Pro Pro Ser Ala His Pro
 100 105 110
 Gly Met Asp Gln Val His Pro Gln Asn Ile Pro Asp Ser Pro Met Ala
 115 120 125
 Asn Ser Gly Pro Leu Cys Cys Thr Ile Cys His Glu Arg Leu Glu Asp
 130 135 140
 Thr His Phe Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe
 145 150 155 160
 Pro Cys Ser Arg Glu Ser Ile Lys Ala Gln Gly Ala Thr Gly Glu Val
 165 170 175
 Tyr Cys Pro Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro
 180 185 190
 Trp Ala Phe Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val
 195 200 205
 Lys Val Lys Lys Glu Arg Asp Pro
 210 215

<210> 13
 <211> 468

23

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(468)

<400> 13

atg gcc tta att att cgt cca tcc aca gat ttc acg ttt ctg ttt cta	48
Met Ala Leu Ile Ile Arg Pro Ser Thr Asp Phe Thr Phe Leu Phe Leu	
1 5 10 15	
ccc tgt acg tca gtt gga tta ttt aat ttt ctg tgt agt aga ttc tac	96
Pro Cys Thr Ser Val Gly Leu Phe Asn Phe Leu Cys Ser Arg Phe Tyr	
20 25 30	
ctg acc aag ttc aat aaa gaa aat aat tgt gta tta cct cat tca aaa	144
Leu Thr Lys Phe Asn Lys Glu Asn Asn Cys Val Leu Pro His Ser Lys	
35 40 45	
gtt tca ttc cag ggc ttt ata tta caa gtt ggc agt gga gca gct gca	192
Val Ser Phe Gln Gly Phe Ile Leu Gln Val Gly Ser Gly Ala Ala Ala	
50 55 60	
gag cca tcc cga ggc aca gga agc tct ggg ccc tcc tct caa cat cca	240
Glu Pro Ser Arg Gly Thr Gly Ser Ser Gly Pro Ser Ser Gln His Pro	
65 70 75 80	
tta tct caa gct cat cga cag gga aac ttc gtg gac att gtt gat gcc	288
Leu Ser Gln Ala His Arg Gln Gly Asn Phe Val Asp Ile Val Asp Ala	
85 90 95	
aag ttg aag att cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac	336
Lys Leu Lys Ile Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr	
100 105 110	
gtc cac tca tcc aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag	384
Val His Ser Ser Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu	
115 120 125	
gtc ttt tta gag ctc aag gat ggt cag cag att cct gtg ttc aag ctc	432
Val Phe Leu Glu Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu	
130 135 140	

24

agt ggg gaa aac ggt gat gaa gtg aaa aag gag tag 468
 Ser Gly Glu Asn Gly Asp Glu Val Lys Lys Glu *
 145 150 155

<210> 14
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Leu Ile Ile Arg Pro Ser Thr Asp Phe Thr Phe Leu Phe Leu
 1 5 10 15
 Pro Cys Thr Ser Val Gly Leu Phe Asn Phe Leu Cys Ser Arg Phe Tyr
 20 25 30
 Leu Thr Lys Phe Asn Lys Glu Asn Asn Cys Val Leu Pro His Ser Lys
 35 40 45
 Val Ser Phe Gln Gly Phe Ile Leu Gln Val Gly Ser Gly Ala Ala Ala
 50 55 60
 Glu Pro Ser Arg Gly Thr Gly Ser Ser Gly Pro Ser Ser Gln His Pro
 65 70 75 80
 Leu Ser Gln Ala His Arg Gln Gly Asn Phe Val Asp Ile Val Asp Ala
 85 90 95
 Lys Leu Lys Ile Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr
 100 105 110
 Val His Ser Ser Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu
 115 120 125
 Val Phe Leu Glu Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu
 130 135 140
 Ser Gly Glu Asn Gly Asp Glu Val Lys Lys Glu
 145 150 155

<210> 15
 <211> 765
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(765)

<400> 15
 atg gtg tcc tgg atc atc tct cgc ctg gtg gtg ctc atc ttt ggc acc 48
 Met Val Ser Trp Ile Ile Ser Arg Leu Val Val Leu Ile Phe Gly Thr

25

1	5	10	15	
ctg tac cca gcc tat tct tcc tac aag gcc gtg aag aca aaa aac gtg				96
Leu Tyr Pro Ala Tyr Ser Ser Tyr Lys Ala Val Lys Thr Lys Asn Val				
	20	25	30	
aag gaa tat gtg aaa tgg atg atg tac tgg atc gtc ttt gcc ttc ttc				144
Lys Glu Tyr Val Lys Trp Met Met Tyr Trp Ile Val Phe Ala Phe Phe				
	35	40	45	
acc acg gcc gag acg ctc acg gat ata gtg ctc tcc tgg ttc ccc ttc				192
Thr Thr Ala Glu Thr Leu Thr Asp Ile Val Leu Ser Trp Phe Pro Phe				
	50	55	60	
tac ttt gaa ctg aag atc gcc ttc gtg ata tgg ctg ctg tcc cct tac				240
Tyr Phe Glu Leu Lys Ile Ala Phe Val Ile Trp Leu Leu Ser Pro Tyr				
	65	70	75	80
acc aag ggc tcc agc gtg ctc tac cgc aag ttc gtg cac cca acg ctg				288
Thr Lys Gly Ser Ser Val Leu Tyr Arg Lys Phe Val His Pro Thr Leu				
	85	90	95	
tcc aac aag gag aag gag atc gac gag tac atc acg cag gcc cga gac				336
Ser Asn Lys Glu Lys Glu Ile Asp Glu Tyr Ile Thr Gln Ala Arg Asp				
	100	105	110	
aag agc tat gag acc atg atg agg gtg ggc aag agg ggc ctg aac ctt				384
Lys Ser Tyr Glu Thr Met Met Arg Val Gly Lys Arg Gly Leu Asn Leu				
	115	120	125	
gcc gcc aat gct gca gtc aca gct gcc gcc aag ggc cag ggg gtg ctg				432
Ala Ala Asn Ala Ala Val Thr Ala Ala Ala Lys Gly Gln Gly Val Leu				
	130	135	140	
tca gag aag ctc cgc agc ttc agc atg cag gac ctg acc ctg atc cgg				480
Ser Glu Lys Leu Arg Ser Phe Ser Met Gln Asp Leu Thr Leu Ile Arg				
	145	150	155	160
gac gag gac gca ctg ccc ctg cag agg cct gac ggc cgc ctc cga ccc				528
Asp Glu Asp Ala Leu Pro Leu Gln Arg Pro Asp Gly Arg Leu Arg Pro				
	165	170	175	
agc cct ggc agc ctc ctg gac acc atc gag gac tta gga gat gac cct				576
Ser Pro Gly Ser Leu Leu Asp Thr Ile Glu Asp Leu Gly Asp Asp Pro				

26

180	185	190	
gcc ctg agt cta agg tcc agc aca aac ccg gca gat tcc cgg aca gag			624
Ala Leu Ser Leu Arg Ser Ser Thr Asn Pro Ala Asp Ser Arg Thr Glu			
195	200	205	
 gct tct gag gat gac atg gga gac aaa gct ccc aag agg gcc aaa ccc			 672
Ala Ser Glu Asp Asp Met Gly Asp Lys Ala Pro Lys Arg Ala Lys Pro			
210	215	220	
 atc aaa aaa gcg ccc aaa gct gag cca ctg gct tcc aag aca ctg aag			 720
Ile Lys Lys Ala Pro Lys Ala Glu Pro Leu Ala Ser Lys Thr Leu Lys			
225	230	235	240
 acc cgg ccc aag aag aag acc tct ggc ggg ggc gac tca gct tga			 765
Thr Arg Pro Lys Lys Lys Thr Ser Gly Gly Gly Asp Ser Ala *			
245	250		

<210> 16
 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 16

Met Val Ser Trp Ile Ile Ser Arg Leu Val Val Leu Ile Phe Gly Thr			
1	5	10	15
Leu Tyr Pro Ala Tyr Ser Ser Tyr Lys Ala Val Lys Thr Lys Asn Val			
20	25	30	
Lys Glu Tyr Val Lys Trp Met Met Tyr Trp Ile Val Phe Ala Phe Phe			
35	40	45	
Thr Thr Ala Glu Thr Leu Thr Asp Ile Val Leu Ser Trp Phe Pro Phe			
50	55	60	
Tyr Phe Glu Leu Lys Ile Ala Phe Val Ile Trp Leu Leu Ser Pro Tyr			
65	70	75	80
Thr Lys Gly Ser Ser Val Leu Tyr Arg Lys Phe Val His Pro Thr Leu			
85	90	95	
Ser Asn Lys Glu Lys Glu Ile Asp Glu Tyr Ile Thr Gln Ala Arg Asp			
100	105	110	
Lys Ser Tyr Glu Thr Met Met Arg Val Gly Lys Arg Gly Leu Asn Leu			
115	120	125	
Ala Ala Asn Ala Ala Val Thr Ala Ala Ala Lys Gly Gln Gly Val Leu			
130	135	140	
Ser Glu Lys Leu Arg Ser Phe Ser Met Gln Asp Leu Thr Leu Ile Arg			

27

145 150 155 160
 Asp Glu Asp Ala Leu Pro Leu Gln Arg Pro Asp Gly Arg Leu Arg Pro
 165 170 175
 Ser Pro Gly Ser Leu Leu Asp Thr Ile Glu Asp Leu Gly Asp Asp Pro
 180 185 190
 Ala Leu Ser Leu Arg Ser Ser Thr Asn Pro Ala Asp Ser Arg Thr Glu
 195 200 205
 Ala Ser Glu Asp Asp Met Gly Asp Lys Ala Pro Lys Arg Ala Lys Pro
 210 215 220
 Ile Lys Lys Ala Pro Lys Ala Glu Pro Leu Ala Ser Lys Thr Leu Lys
 225 230 235 240
 Thr Arg Pro Lys Lys Lys Thr Ser Gly Gly Gly Asp Ser Ala
 245 250

<210> 17
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(408)

<221> misc_feature
 <222> (1)...(408)
 <223> n = A,T,C or G

<400> 17
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 Met Ala His Arg Gly Val Ser Ala Val Val Val Gly Ala Asp Arg Val
 1 5 10 15

 gtt gcc aac ggn gac aca gcc aac aag gtg ggc acc tac cag ctg gcc 96
 Val Ala Asn Xaa Asp Thr Ala Asn Lys Val Gly Thr Tyr Gln Leu Ala
 20 25 30

 att gtc gcc aag cac cat ggc att ccc ttc tac gtg gct gcc ccc agc 144
 Ile Val Ala Lys His His Gly Ile Pro Phe Tyr Val Ala Ala Pro Ser
 35 40 45

 tct tca tgt gac ctc cgt ctg gag acc ggc aag gag atc att att gaa 192
 Ser Ser Cys Asp Leu Arg Leu Glu Thr Gly Lys Glu Ile Ile Ile Glu
 50 55 60

28

gag cga ccg ggc cag gag ctg acc gat gtt aat ggg gtc cgg att gca 240
 Glu Arg Pro Gly Gln Glu Leu Thr Asp Val Asn Gly Val Arg Ile Ala
 65 70 75 80

gca cct ggg att gga gtt tgg aat cct gcc ttc gat gtc acc ccc cac 288
 Ala Pro Gly Ile Gly Val Trp Asn Pro Ala Phe Asp Val Thr Pro His
 85 90 95

gac ctc atc act ggt ggc atc atc aca gaa ctg ggg gtc ttt gcc cct 336
 Asp Leu Ile Thr Gly Gly Ile Ile Thr Glu Leu Gly Val Phe Ala Pro
 100 105 110

gag gag ctc cgg aca gcc cta acc acc acc atc tct tcc agg gat gga 384
 Glu Glu Leu Arg Thr Ala Leu Thr Thr Thr Ile Ser Ser Arg Asp Gly
 115 120 125

acc cta gat gga ccc cag atg taa 408
 Thr Leu Asp Gly Pro Gln Met *
 130 135

<210> 18

<211> 135

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(135)

<223> Xaa = Any Amino Acid

<400> 18

Met Ala His Arg Gly Val Ser Ala Val Val Val Gly Ala Asp Arg Val
 1 5 10 15
 Val Ala Asn Xaa Asp Thr Ala Asn Lys Val Gly Thr Tyr Gln Leu Ala
 20 25 30
 Ile Val Ala Lys His His Gly Ile Pro Phe Tyr Val Ala Ala Pro Ser
 35 40 45
 Ser Ser Cys Asp Leu Arg Leu Glu Thr Gly Lys Glu Ile Ile Ile Glu
 50 55 60
 Glu Arg Pro Gly Gln Glu Leu Thr Asp Val Asn Gly Val Arg Ile Ala
 65 70 75 80
 Ala Pro Gly Ile Gly Val Trp Asn Pro Ala Phe Asp Val Thr Pro His
 85 90 95

29

Asp Leu Ile Thr Gly Gly Ile Ile Thr Glu Leu Gly Val Phe Ala Pro
 100 105 110
 Glu Glu Leu Arg Thr Ala Leu Thr Thr Thr Ile Ser Ser Arg Asp Gly
 115 120 125
 Thr Leu Asp Gly Pro Gln Met
 130 135

<210> 19
 <211> 828
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(828)

<400> 19

atg ggg aat ttc aga ggt cat gcc ctc cct gga acc ttc ttt ttt att 48
 Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile
 1 5 10 15

att ggt ctt tgg tgg tgt aca aag agt att ctg aag tat atc tgc aaa 96
 Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys
 20 25 30

aag caa aag cga acc tgc tat ctt ggt tcc aaa aca tta ttc tat cga 144
 Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg
 35 40 45

ttg gaa att ttg gag gga att aca ata gtt ggc atg gct tta act ggc 192
 Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly
 50 55 60

atg gct ggg gag cag ttt att cct gga ggg ccc cat ctg atg tta tat 240
 Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr
 65 70 75 80

gac tat aaa caa ggt cac tgg aat caa ctc ctg ggc tgg cat cat ttc 288
 Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe
 85 90 95

acc atg tat ttc ttc ttt ggg ctg ttg ggt gtg gca gat atc tta tgt 336
 Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys
 100 105 110

ttc acc atc agt tca ctt cct gtg tcc tta acc aag tta atg ttg tca Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser 115 120 125	384
aat gcc tta ttt gtg gag gcc ttt atc ttc tac aac cac act cat ggc Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly 130 135 140	432
cgg gaa atg ctg gac atc ttt gtg cac cag ctg ctg gtt ttg gtc gtc Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val 145 150 155 160	480
ttt ctg aca ggc ctc gtt gcc ttc cta gag ttc ctt gtt cgg aac aat Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn 165 170 175	528
gta ctt ctg gag cta ttg cgg tca agt ctc att ctg ctt cag ggg agc Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser 180 185 190	576
tgg ttc ttt cag att gga ttt gtc ctg tat ccc ccc agt gga ggt cct Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro 195 200 205	624
gca tgg gat ctg atg gat cat gaa aat att ttg ttt ctc acc ata tgc Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys 210 215 220	672
ttt tgt tgg cat tat gca gta acc att gtc atc gtt gga atg aat tat Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr 225 230 235 240	720
gct ttc att acc tgg ttg gtt aaa tct aga ctt aag agg ctc tgc tcc Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser 245 250 255	768
tca gaa gtt gga ctt ctg aaa aat gct gaa cga gaa caa gaa tca gaa Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu 260 265 270	816
gaa gaa atg tga Glu Glu Met *	828
275	


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<210> 20
<211> 275
<212> PRT
<213> Homo sapiens
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[illegible]

<210> 21
 <211> 1623
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1623)

<221> misc_feature
 <222> (1)...(1623)
 <223> n = A,T,C or G

<400> 21

atg gag cgg gag gcg ttg ccg tgg ggc ctc gag ccc cag gat gtg cag	48
Met Glu Arg Glu Ala Leu Pro Trp Gly Leu Glu Pro Gln Asp Val Gln	
1 5 10 15	

agt tct gac gaa atg agg agc ccc gaa ggt aac ctc aga ggc aac atg	96
Ser Ser Asp Glu Met Arg Ser Pro Glu Gly Asn Leu Arg Gly Asn Met	
20 25 30	

agt gag aat gag gaa gag gaa att tct cag caa gaa ggc agt ggg gac	144
Ser Glu Asn Glu Glu Glu Glu Ile Ser Gln Gln Glu Gly Ser Gly Asp	
35 40 45	

tat gaa gtc gaa gag ata cca ttt ggg ctt gaa ccc cag agc cct ggg	192
Tyr Glu Val Glu Glu Ile Pro Phe Gly Leu Glu Pro Gln Ser Pro Gly	
50 55 60	

ttt gag cca caa agc cca gag ttt gaa ccc caa agc ccc aga ttt gag	240
Phe Glu Pro Gln Ser Pro Glu Phe Glu Pro Gln Ser Pro Arg Phe Glu	
65 70 75 80	

cct gaa agc ccg ggg ttt gag tcc cga agc cct ggg ctt gtg ccc cca	288
Pro Glu Ser Pro Gly Phe Glu Ser Arg Ser Pro Gly Leu Val Pro Pro	
85 90 95	

agc cct gag ttt gca ccc aga agc cct gaa tca gat tct cag agc cct	336
Ser Pro Glu Phe Ala Pro Arg Ser Pro Glu Ser Asp Ser Gln Ser Pro	
100 105 110	

gag ttt gaa tcc cag agc cct agg tat gaa ccc caa agc cct ggc tat	384
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Glu Phe Glu Ser Gln Ser Pro Arg Tyr Glu Pro Gln Ser Pro Gly Tyr	115	120	125	
gaa cct cgg agc ccc ggg tat gaa ccc cgg agc cct ggc tat gaa tct				432
Glu Pro Arg Ser Pro Gly Tyr Glu Pro Arg Ser Pro Gly Tyr Glu Ser	130	135	140	
gag agc tct aga tat gaa tcc cag aac act gag ctc aaa acc caa agc				480
Glu Ser Ser Arg Tyr Glu Ser Gln Asn Thr Glu Leu Lys Thr Gln Ser	145	150	155	160
cca gaa ttt gaa gct caa agt tcc aaa ttc cag gaa ggt gcg gag atg				528
Pro Glu Phe Glu Ala Gln Ser Ser Lys Phe Gln Glu Gly Ala Glu Met	165	170	175	
ctt ctg aac ccc gan gaa aag agt cct ttg aat atc tcc gta gga gtt				576
Leu Leu Asn Pro Xaa Glu Lys Ser Pro Leu Asn Ile Ser Val Gly Val	180	185	190	
cac ccc ctg gac tcc ttc act cag ggg ttt ggg gag cag ccc aca ggg				624
His Pro Leu Asp Ser Phe Thr Gln Gly Phe Gly Glu Gln Pro Thr Gly	195	200	205	
gac ctg ccc ata ggg cca cct ttt gag atg ccc aca ggg gcc ctg ctg				672
Asp Leu Pro Ile Gly Pro Pro Phe Glu Met Pro Thr Gly Ala Leu Leu	210	215	220	
tct aca ccg cag ttt gag atg ctt cag aat ccc ctg ggt ctc aca gga				720
Ser Thr Pro Gln Phe Glu Met Leu Gln Asn Pro Leu Gly Leu Thr Gly	225	230	235	240
gcc ctt cga ggt cca ggt cgg cgg ggt ggc cgg gcc agg ggt ggg cag				768
Ala Leu Arg Gly Pro Gly Arg Arg Gly Gly Arg Ala Arg Gly Gly Gln	245	250	255	
ggc cct cgg cct aac atc tgt ggc atc tgc ggg aag agc ttc ggg cgg				816
Gly Pro Arg Pro Asn Ile Cys Gly Ile Cys Gly Lys Ser Phe Gly Arg	260	265	270	
ggc tcc acc ctg atc cag cac cag cgc atc cac acc ggt gag aag ccc				864
Gly Ser Thr Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro	275	280	285	
tac aaa tgt gag gtc tgc agc aag gcc ttc tcc cag agc tct gac ctc				912

Tyr	Lys	Cys	Glu	Val	Cys	Ser	Lys	Ala	Phe	Ser	Gln	Ser	Ser	Asp	Leu	
290						295					300					
atc	aaa	cac	cag	cgc	acc	cac	act	ggc	gag	cgg	ccc	tac	aaa	tgt	ccc	960
Ile	Lys	His	Gln	Arg	Thr	His	Thr	Gly	Glu	Arg	Pro	Tyr	Lys	Cys	Pro	
305					310					315					320	
cgt	tgc	ggc	aag	gcc	ttc	gcc	gac	agc	tct	tac	ctg	ctt	cgc	cac	cag	1008
Arg	Cys	Gly	Lys	Ala	Phe	Ala	Asp	Ser	Ser	Tyr	Leu	Leu	Arg	His	Gln	
				325					330					335		
cgc	act	cac	tct	ggc	cag	aag	ccc	tac	aag	tgc	cca	cat	tgt	ggc	aag	1056
Arg	Thr	His	Ser	Gly	Gln	Lys	Pro	Tyr	Lys	Cys	Pro	His	Cys	Gly	Lys	
			340					345					350			
gcc	ttc	ggc	gac	agc	tcc	tac	ctc	ctg	cga	cac	cag	cgc	acc	cac	agc	1104
Ala	Phe	Gly	Asp	Ser	Ser	Tyr	Leu	Leu	Arg	His	Gln	Arg	Thr	His	Ser	
		355					360					365				
cac	gag	cgg	ccc	tac	agc	tgc	acc	gag	tgc	ggc	aag	tgc	tat	agc	cag	1152
His	Glu	Arg	Pro	Tyr	Ser	Cys	Thr	Glu	Cys	Gly	Lys	Cys	Tyr	Ser	Gln	
	370					375					380					
aac	tcg	tcc	ctg	cgc	agc	cat	cag	agg	gtg	cac	acc	ggt	cag	agg	ccc	1200
Asn	Ser	Ser	Leu	Arg	Ser	His	Gln	Arg	Val	His	Thr	Gly	Gln	Arg	Pro	
385					390					395					400	
ttc	agc	tgt	ggc	atc	tgc	ggc	aag	agc	ttc	tcc	cag	cgg	tcg	gcc	ctt	1248
Phe	Ser	Cys	Gly	Ile	Cys	Gly	Lys	Ser	Phe	Ser	Gln	Arg	Ser	Ala	Leu	
				405					410					415		
atc	ccc	cat	gcc	cgc	agc	cac	gcc	cgg	gag	aag	ccc	ttc	aag	tgc	cct	1296
Ile	Pro	His	Ala	Arg	Ser	His	Ala	Arg	Glu	Lys	Pro	Phe	Lys	Cys	Pro	
			420					425					430			
gag	tgc	ggc	aag	cgc	ttt	ggc	cag	agc	tcg	gtg	ctg	gcc	atc	cac	gcc	1344
Glu	Cys	Gly	Lys	Arg	Phe	Gly	Gln	Ser	Ser	Val	Leu	Ala	Ile	His	Ala	
		435					440					445				
cgc	acc	cac	ctg	cca	ggc	cgc	acc	tac	agc	tgc	ccc	gac	tgc	ggc	aag	1392
Arg	Thr	His	Leu	Pro	Gly	Arg	Thr	Tyr	Ser	Cys	Pro	Asp	Cys	Gly	Lys	
	450					455					460					
acc	ttc	aat	cgc	tcc	tcc	act	ctc	atc	cag	cac	cag	cgc	tcc	cac	acg	1440

35

Thr Phe Asn Arg Ser Ser Thr Leu Ile Gln His Gln Arg Ser His Thr
 465 470 475 480

 ggc gag cgg ccc tac agg tgc gcc gtg tgc ggc aag ggc ttc tgc cgc 1488
 Gly Glu Arg Pro Tyr Arg Cys Ala Val Cys Gly Lys Gly Phe Cys Arg
 485 490 495

 tcc tcc acg ctt ctg cag cat cac cgg gtc cac agt ggc gag cgg cct 1536
 Ser Ser Thr Leu Leu Gln His His Arg Val His Ser Gly Glu Arg Pro
 500 505 510

 tac aag tgc gat gac tgc gga aag gcc ttc tcc cag agc tcc gac ctc 1584
 Tyr Lys Cys Asp Asp Cys Gly Lys Ala Phe Ser Gln Ser Ser Asp Leu
 515 520 525

 atc cgc cac cag cgg acc cac gcg gcg ggc cgg cgc tga 1623
 Ile Arg His Gln Arg Thr His Ala Ala Gly Arg Arg *
 530 535 540

<210> 22
 <211> 540
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(540)
 <223> Xaa = Any Amino Acid

<400> 22
 Met Glu Arg Glu Ala Leu Pro Trp Gly Leu Glu Pro Gln Asp Val Gln
 1 5 10 15
 Ser Ser Asp Glu Met Arg Ser Pro Glu Gly Asn Leu Arg Gly Asn Met
 20 25 30
 Ser Glu Asn Glu Glu Glu Glu Ile Ser Gln Gln Glu Gly Ser Gly Asp
 35 40 45
 Tyr Glu Val Glu Glu Ile Pro Phe Gly Leu Glu Pro Gln Ser Pro Gly
 50 55 60
 Phe Glu Pro Gln Ser Pro Glu Phe Glu Pro Gln Ser Pro Arg Phe Glu
 65 70 75 80
 Pro Glu Ser Pro Gly Phe Glu Ser Arg Ser Pro Gly Leu Val Pro Pro
 85 90 95
 Ser Pro Glu Phe Ala Pro Arg Ser Pro Glu Ser Asp Ser Gln Ser Pro

100										105					110				
Glu	Phe	Glu	Ser	Gln	Ser	Pro	Arg	Tyr	Glu	Pro	Gln	Ser	Pro	Gly	Tyr				
115										120					125				
Glu	Pro	Arg	Ser	Pro	Gly	Tyr	Glu	Pro	Arg	Ser	Pro	Gly	Tyr	Glu	Ser				
130										135					140				
Glu	Ser	Ser	Arg	Tyr	Glu	Ser	Gln	Asn	Thr	Glu	Leu	Lys	Thr	Gln	Ser				
145										150					155				
Pro	Glu	Phe	Glu	Ala	Gln	Ser	Ser	Lys	Phe	Gln	Glu	Gly	Ala	Glu	Met				
165										170					175				
Leu	Leu	Asn	Pro	Xaa	Glu	Lys	Ser	Pro	Leu	Asn	Ile	Ser	Val	Gly	Val				
180										185					190				
His	Pro	Leu	Asp	Ser	Phe	Thr	Gln	Gly	Phe	Gly	Glu	Gln	Pro	Thr	Gly				
195										200					205				
Asp	Leu	Pro	Ile	Gly	Pro	Pro	Phe	Glu	Met	Pro	Thr	Gly	Ala	Leu	Leu				
210										215					220				
Ser	Thr	Pro	Gln	Phe	Glu	Met	Leu	Gln	Asn	Pro	Leu	Gly	Leu	Thr	Gly				
225										230					235				
Ala	Leu	Arg	Gly	Pro	Gly	Arg	Arg	Gly	Gly	Arg	Ala	Arg	Gly	Gly	Gln				
245										250					255				
Gly	Pro	Arg	Pro	Asn	Ile	Cys	Gly	Ile	Cys	Gly	Lys	Ser	Phe	Gly	Arg				
260										265					270				
Gly	Ser	Thr	Leu	Ile	Gln	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro				
275										280					285				
Tyr	Lys	Cys	Glu	Val	Cys	Ser	Lys	Ala	Phe	Ser	Gln	Ser	Ser	Asp	Leu				
290										295					300				
Ile	Lys	His	Gln	Arg	Thr	His	Thr	Gly	Glu	Arg	Pro	Tyr	Lys	Cys	Pro				
305										310					315				
Arg	Cys	Gly	Lys	Ala	Phe	Ala	Asp	Ser	Ser	Tyr	Leu	Leu	Arg	His	Gln				
325										330					335				
Arg	Thr	His	Ser	Gly	Gln	Lys	Pro	Tyr	Lys	Cys	Pro	His	Cys	Gly	Lys				
340										345					350				
Ala	Phe	Gly	Asp	Ser	Ser	Tyr	Leu	Leu	Arg	His	Gln	Arg	Thr	His	Ser				
355										360					365				
His	Glu	Arg	Pro	Tyr	Ser	Cys	Thr	Glu	Cys	Gly	Lys	Cys	Tyr	Ser	Gln				
370										375					380				
Asn	Ser	Ser	Leu	Arg	Ser	His	Gln	Arg	Val	His	Thr	Gly	Gln	Arg	Pro				
385										390					395				
Phe	Ser	Cys	Gly	Ile	Cys	Gly	Lys	Ser	Phe	Ser	Gln	Arg	Ser	Ala	Leu				
405										410					415				
Ile	Pro	His	Ala	Arg	Ser	His	Ala	Arg	Glu	Lys	Pro	Phe	Lys	Cys	Pro				
420										425					430				
Glu	Cys	Gly	Lys	Arg	Phe	Gly	Gln	Ser	Ser	Val	Leu	Ala	Ile	His	Ala				
435										440					445				
Arg	Thr	His	Leu	Pro	Gly	Arg	Thr	Tyr	Ser	Cys	Pro	Asp	Cys	Gly	Lys				

37

450 455 460
 Thr Phe Asn Arg Ser Ser Thr Leu Ile Gln His Gln Arg Ser His Thr
 465 470 475 480
 Gly Glu Arg Pro Tyr Arg Cys Ala Val Cys Gly Lys Gly Phe Cys Arg
 485 490 495
 Ser Ser Thr Leu Leu Gln His His Arg Val His Ser Gly Glu Arg Pro
 500 505 510
 Tyr Lys Cys Asp Asp Cys Gly Lys Ala Phe Ser Gln Ser Ser Asp Leu
 515 520 525
 Ile Arg His Gln Arg Thr His Ala Ala Gly Arg Arg
 530 535 540

<210> 23
 <211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(432)

<400> 23
 atg gag ccc gcg ctg cgc gct gtg tgc aaa gac gtg cgc atc ggc acc 48
 Met Glu Pro Ala Leu Arg Ala Val Cys Lys Asp Val Arg Ile Gly Thr
 1 5 10 15

 atc ctc atc cag acc aac cag ctt acc ggg gag ccc gag ctc cac tac 96
 Ile Leu Ile Gln Thr Asn Gln Leu Thr Gly Glu Pro Glu Leu His Tyr
 20 25 30

 ctg agg ctg ccc aag gac atc agc gat gac cac gtg atc ctc atg gac 144
 Leu Arg Leu Pro Lys Asp Ile Ser Asp Asp His Val Ile Leu Met Asp
 35 40 45

 tgc acc gtg tcc acg ggc gcg gcg gcc atg atg gca gtg cgc gtg ctc 192
 Cys Thr Val Ser Thr Gly Ala Ala Ala Met Met Ala Val Arg Val Leu
 50 55 60

 ctg gac cac gac gtg cct gag gac aag atc ttt ttg ctg tcg ctg ctc 240
 Leu Asp His Asp Val Pro Glu Asp Lys Ile Phe Leu Leu Ser Leu Leu
 65 70 75 80

 atg gca gag atg ggc gtg cac tca gtg gcc tat gca ttt ccg cga gtg 288
 Met Ala Glu Met Gly Val His Ser Val Ala Tyr Ala Phe Pro Arg Val

38

85

90

95

aga atc atc acc acg gcg gtc gac aag cgg gtc aat gac ctt ttc cgc 336
 Arg Ile Ile Thr Thr Ala Val Asp Lys Arg Val Asn Asp Leu Phe Arg
 100 105 110

atc atc cca ggc att ggg aac ttt ggc gac cgc tac ttt ggg aca gac 384
 Ile Ile Pro Gly Ile Gly Asn Phe Gly Asp Arg Tyr Phe Gly Thr Asp
 115 120 125

gcg gtc ccc gat ggc agt gac gag gag gaa gtc gcc tac acg ggt tag 432
 Ala Val Pro Asp Gly Ser Asp Glu Glu Glu Val Ala Tyr Thr Gly *
 130 135 140

<210> 24

<211> 143

<212> PRT

<213> Homo sapiens

<400> 24

Met Glu Pro Ala Leu Arg Ala Val Cys Lys Asp Val Arg Ile Gly Thr
 1 5 10 15
 Ile Leu Ile Gln Thr Asn Gln Leu Thr Gly Glu Pro Glu Leu His Tyr
 20 25 30
 Leu Arg Leu Pro Lys Asp Ile Ser Asp Asp His Val Ile Leu Met Asp
 35 40 45
 Cys Thr Val Ser Thr Gly Ala Ala Ala Met Met Ala Val Arg Val Leu
 50 55 60
 Leu Asp His Asp Val Pro Glu Asp Lys Ile Phe Leu Leu Ser Leu Leu
 65 70 75 80
 Met Ala Glu Met Gly Val His Ser Val Ala Tyr Ala Phe Pro Arg Val
 85 90 95
 Arg Ile Ile Thr Thr Ala Val Asp Lys Arg Val Asn Asp Leu Phe Arg
 100 105 110
 Ile Ile Pro Gly Ile Gly Asn Phe Gly Asp Arg Tyr Phe Gly Thr Asp
 115 120 125
 Ala Val Pro Asp Gly Ser Asp Glu Glu Glu Val Ala Tyr Thr Gly
 130 135 140

<210> 25

<211> 912

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(912)

<400> 25

atg	ctg	gcc	ggc	cac	ggc	ggc	gtc	ttc	gcg	ctc	acg	ctg	ctg	ctc	atc	48
Met	Leu	Ala	Gly	His	Gly	Gly	Val	Phe	Ala	Leu	Thr	Leu	Leu	Leu	Ile	
1				5				10						15		

ctc	acc	acc	acc	ggc	ctc	ttc	ttc	gtc	ttt	gac	tgt	ccc	tac	ctg	gct	96
Leu	Thr	Thr	Thr	Gly	Leu	Phe	Phe	Val	Phe	Asp	Cys	Pro	Tyr	Leu	Ala	
				20				25					30			

cgc	aag	ctg	acc	ctt	gcc	atc	ccc	atc	atc	gct	gcc	atc	ctc	ttc	ttc	144
Arg	Lys	Leu	Thr	Leu	Ala	Ile	Pro	Ile	Ile	Ala	Ala	Ile	Leu	Phe	Phe	
		35					40					45				

ttc	gtc	atg	agc	tgc	ctg	ctg	cag	aca	agc	ttc	acc	gac	cct	ggg	atc	192
Phe	Val	Met	Ser	Cys	Leu	Leu	Gln	Thr	Ser	Phe	Thr	Asp	Pro	Gly	Ile	
	50					55					60					

ctg	ccc	cgg	gcc	act	gtc	tgt	gaa	gca	gcc	gcc	ctg	gag	aaa	cag	atc	240
Leu	Pro	Arg	Ala	Thr	Val	Cys	Glu	Ala	Ala	Ala	Leu	Glu	Lys	Gln	Ile	
	65				70					75					80	

gac	aac	aca	ggc	agt	tct	aca	tac	cgg	cca	ccc	cct	cgg	acc	cgg	gag	288
Asp	Asn	Thr	Gly	Ser	Ser	Thr	Tyr	Arg	Pro	Pro	Pro	Arg	Thr	Arg	Glu	
			85					90					95			

gtg	ctg	atc	aac	ggg	cag	atg	gtg	aag	ctg	aag	tac	tgc	ttc	acc	tgc	336
Val	Leu	Ile	Asn	Gly	Gln	Met	Val	Lys	Leu	Lys	Tyr	Cys	Phe	Thr	Cys	
			100					105					110			

aag	atg	ttc	cgg	cca	ccc	cga	acc	tca	cac	tgc	agt	gtc	tgc	gac	aac	384
Lys	Met	Phe	Arg	Pro	Pro	Arg	Thr	Ser	His	Cys	Ser	Val	Cys	Asp	Asn	
		115					120					125				

tgt	gtg	gaa	cga	ttt	gac	cat	cac	tgc	ccc	tgg	gtg	ggc	aac	tgt	gtg	432
Cys	Val	Glu	Arg	Phe	Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	
	130					135				140						

ggg	aga	cgg	aac	tat	cgc	ttc	ttc	tac	gcg	ttt	att	ctc	tcc	ctc	tca	480
Gly	Arg	Arg	Asn	Tyr	Arg	Phe	Phe	Tyr	Ala	Phe	Ile	Leu	Ser	Leu	Ser	

40

145	150	155	160	
ttc ctg acg gcc ttc atc ttc gcc tgt gtg gtc acc cac ctg acg ttg				528
Phe Leu Thr Ala Phe Ile Phe Ala Cys Val Val Thr His Leu Thr Leu				
	165	170	175	
cgc gct cag gga agc aac ttc ctc tcc act ctg aag gag aca cca gca				576
Arg Ala Gln Gly Ser Asn Phe Leu Ser Thr Leu Lys Glu Thr Pro Ala				
	180	185	190	
agc gtg ctg gag ttg gtg atc tgc ttc ttc tcc atc tgg tcc att ctg				624
Ser Val Leu Glu Leu Val Ile Cys Phe Phe Ser Ile Trp Ser Ile Leu				
	195	200	205	
ggc ctc tca ggg ttt cac acg tac ctc gtc gcc tcc aac ctg act act				672
Gly Leu Ser Gly Phe His Thr Tyr Leu Val Ala Ser Asn Leu Thr Thr				
	210	215	220	
aat gaa gac atc aaa ggc tcg tgg tcc agc aag agg ggc ggt gag gcc				720
Asn Glu Asp Ile Lys Gly Ser Trp Ser Ser Lys Arg Gly Gly Glu Ala				
	225	230	235	240
tct gtc aac ccc tac agc cat aaa agt att atc acc aac tgc tgt gct				768
Ser Val Asn Pro Tyr Ser His Lys Ser Ile Ile Thr Asn Cys Cys Ala				
	245	250	255	
gtg ctc tgt ggc ccc cta cct ccc agc cta att gac cgg agg gga ttt				816
Val Leu Cys Gly Pro Leu Pro Pro Ser Leu Ile Asp Arg Arg Gly Phe				
	260	265	270	
gtg cag tcc gac acc gtg ttg ccc tca ccc atc aga agc gat gag cca				864
Val Gln Ser Asp Thr Val Leu Pro Ser Pro Ile Arg Ser Asp Glu Pro				
	275	280	285	
gcc tgc aga gcc aag cct gat gcc agc atg gta gga ggc cac ccc tga				912
Ala Cys Arg Ala Lys Pro Asp Ala Ser Met Val Gly Gly His Pro *				
	290	295	300	

<210> 26

<211> 303

<212> PRT

<213> Homo sapiens

<400> 26
 Met Leu Ala Gly His Gly Gly Val Phe Ala Leu Thr Leu Leu Leu Ile
 1 5 10 15
 Leu Thr Thr Thr Gly Leu Phe Phe Val Phe Asp Cys Pro Tyr Leu Ala
 20 25 30
 Arg Lys Leu Thr Leu Ala Ile Pro Ile Ile Ala Ala Ile Leu Phe Phe
 35 40 45
 Phe Val Met Ser Cys Leu Leu Gln Thr Ser Phe Thr Asp Pro Gly Ile
 50 55 60
 Leu Pro Arg Ala Thr Val Cys Glu Ala Ala Ala Leu Glu Lys Gln Ile
 65 70 75 80
 Asp Asn Thr Gly Ser Ser Thr Tyr Arg Pro Pro Pro Arg Thr Arg Glu
 85 90 95
 Val Leu Ile Asn Gly Gln Met Val Lys Leu Lys Tyr Cys Phe Thr Cys
 100 105 110
 Lys Met Phe Arg Pro Pro Arg Thr Ser His Cys Ser Val Cys Asp Asn
 115 120 125
 Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
 130 135 140
 Gly Arg Arg Asn Tyr Arg Phe Phe Tyr Ala Phe Ile Leu Ser Leu Ser
 145 150 155 160
 Phe Leu Thr Ala Phe Ile Phe Ala Cys Val Val Thr His Leu Thr Leu
 165 170 175
 Arg Ala Gln Gly Ser Asn Phe Leu Ser Thr Leu Lys Glu Thr Pro Ala
 180 185 190
 Ser Val Leu Glu Leu Val Ile Cys Phe Phe Ser Ile Trp Ser Ile Leu
 195 200 205
 Gly Leu Ser Gly Phe His Thr Tyr Leu Val Ala Ser Asn Leu Thr Thr
 210 215 220
 Asn Glu Asp Ile Lys Gly Ser Trp Ser Ser Lys Arg Gly Gly Glu Ala
 225 230 235 240
 Ser Val Asn Pro Tyr Ser His Lys Ser Ile Ile Thr Asn Cys Cys Ala
 245 250 255
 Val Leu Cys Gly Pro Leu Pro Pro Ser Leu Ile Asp Arg Arg Gly Phe
 260 265 270
 Val Gln Ser Asp Thr Val Leu Pro Ser Pro Ile Arg Ser Asp Glu Pro
 275 280 285
 Ala Cys Arg Ala Lys Pro Asp Ala Ser Met Val Gly Gly His Pro
 290 295 300

<210> 27

<211> 795

<212> DNA

<213> Homo sapiens

$\langle 220 \rangle$

<221> CDS

<222> (1)...(795)

<221> misc feature

<222> (1) ... (795)

<223> n = A, T, C or G

<400> 27

atg aat tca aag cac act ttt ctg gcc ttg tgt gcc ctt cgc ttt atg 48
Met Asn Ser Lys His Thr Phe Leu Ala Leu Cys Ala Leu Arg Phe Met
1 5 10 15

agg cgg ata att gga ctt aaa gat gaa ttt tat aat cgt tac atc acc 96
Arg Arg Ile Ile Gly Leu Lys Asp Glu Phe Tyr Asn Arg Tyr Ile Thr
20 25 30

aag gga aat ctt ttt gag cca gtt ata aat gca ctt ctg gat aat gga 144
Lys Gly Asn Leu Phe Glu Pro Val Ile Asn Ala Leu Leu Asp Asn Gly
35 40 45

act cgg tat aat ctg ttg aat tca gct gtt att gag ttg ttt gaa ttt 192
Thr Arg Tyr Asn Leu Leu Asn Ser Ala Val Ile Glu Leu Phe Glu Phe
50 55 60

ata aga gtg gaa gat atc aag tct ctt act gcc cat ata gtt gaa aac 240
Ile Arg Val Glu Asp Ile Lys Ser Leu Thr Ala His Ile Val Glu Asn
65 70 75 80

ttt tat aaa gca ctt gaa tcg att gaa tat gtt cag aca ttc aaa gga 288
Phe Tyr Lys Ala Leu Glu Ser Ile Glu Tyr Val Gln Thr Phe Lys Gly
85 90 95

ttg aag act aaa tat gag cag aaa aag aac agt gta cca tct ata ttg 336
 Leu Lys Thr Lys Tyr Glu Gln Lys Lys Asn Ser Val Pro Ser Ile Leu
 100 105 110

cgt agt aac aga ttt cgc aga gat gca aaa gcc ttg gaa gag gat gaa 384
Arg Ser Asn Arg Phe Arg Arg Asp Ala Lys Ala Leu Glu Glu Asp Glu
115 120 125

gaa atg tgg ttt aat gaa gat gaa gaa gag gaa gga aaa gca gtt gtg 432
Glu Met Trp Phe Asn Glu Asp Glu Glu Glu Glu Gly Lys Ala Val Val

130	135	140	
gca cca gtg gaa aaa cct aag cca gaa gat gat ttt cca gat aat tat			480
Ala Pro Val Glu Lys Pro Lys Pro Glu Asp Asp Phe Pro Asp Asn Tyr			
145	150	155	160
gaa aag ttt atg gag act aaa aaa gca aaa gaa agt gaa gac aag gaa			528
Glu Lys Phe Met Glu Thr Lys Lys Ala Lys Glu Ser Glu Asp Lys Glu			
	165	170	175
aac ctt ccc aaa agg aca tct cct ggt ggc ttc aaa ttt act ttc tcc			576
Asn Leu Pro Lys Arg Thr Ser Pro Gly Gly Phe Lys Phe Thr Phe Ser			
	180	185	190
cac tct gcc agt gct gct aat gga aca aac agt aaa tct gta gtg gct			624
His Ser Ala Ser Ala Ala Asn Gly Thr Asn Ser Lys Ser Val Val Ala			
	195	200	205
cag ata cca cca gca act tct aat gga tcc tct tcc aaa acc aca aac			672
Gln Ile Pro Pro Ala Thr Ser Asn Gly Ser Ser Ser Lys Thr Thr Asn			
	210	215	220
ttg cct acg tca gta aca gcc acc aag gga agt ttg gtt ggc tta gtg			720
Leu Pro Thr Ser Val Thr Ala Thr Lys Gly Ser Leu Val Gly Leu Val			
	225	230	240
gat tat cca gat gat gaa gag gaa gat gaa gaa gaa gnn tcg tcc ccc			768
Asp Tyr Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Xaa Ser Ser Pro			
	245	250	255
agg aaa aga cct cgt ctt ggc tca taa			795
Arg Lys Arg Pro Arg Leu Gly Ser *			
	260		

<210> 28

<211> 264

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(264)

<223> Xaa = Any Amino Acid

<400> 28
 Met Asn Ser Lys His Thr Phe Leu Ala Leu Cys Ala Leu Arg Phe Met
 1 5 10 15
 Arg Arg Ile Ile Gly Leu Lys Asp Glu Phe Tyr Asn Arg Tyr Ile Thr
 20 25 30
 Lys Gly Asn Leu Phe Glu Pro Val Ile Asn Ala Leu Leu Asp Asn Gly
 35 40 45
 Thr Arg Tyr Asn Leu Leu Asn Ser Ala Val Ile Glu Leu Phe Glu Phe
 50 55 60
 Ile Arg Val Glu Asp Ile Lys Ser Leu Thr Ala His Ile Val Glu Asn
 65 70 75 80
 Phe Tyr Lys Ala Leu Glu Ser Ile Glu Tyr Val Gln Thr Phe Lys Gly
 85 90 95
 Leu Lys Thr Lys Tyr Glu Gln Lys Lys Asn Ser Val Pro Ser Ile Leu
 100 105 110
 Arg Ser Asn Arg Phe Arg Arg Asp Ala Lys Ala Leu Glu Glu Asp Glu
 115 120 125
 Glu Met Trp Phe Asn Glu Asp Glu Glu Glu Glu Gly Lys Ala Val Val
 130 135 140
 Ala Pro Val Glu Lys Pro Lys Pro Glu Asp Asp Phe Pro Asp Asn Tyr
 145 150 155 160
 Glu Lys Phe Met Glu Thr Lys Lys Ala Lys Glu Ser Glu Asp Lys Glu
 165 170 175
 Asn Leu Pro Lys Arg Thr Ser Pro Gly Gly Phe Lys Phe Thr Phe Ser
 180 185 190
 His Ser Ala Ser Ala Ala Asn Gly Thr Asn Ser Lys Ser Val Val Ala
 195 200 205
 Gln Ile Pro Pro Ala Thr Ser Asn Gly Ser Ser Ser Lys Thr Thr Asn
 210 215 220
 Leu Pro Thr Ser Val Thr Ala Thr Lys Gly Ser Leu Val Gly Leu Val
 225 230 235 240
 Asp Tyr Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Xaa Ser Ser Pro
 245 250 255
 Arg Lys Arg Pro Arg Leu Gly Ser
 260

<210> 29

<211> 711

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

45

<222> (1)...(711)

<400> 29

atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg ggc ctg ctg ctc	48
Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu	
1 5 10 15	
ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc cgg ggt cgg cgg	96
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg	
20 25 30	
cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag tcc gca gaa gac	144
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp	
35 40 45	
tta act gat ggt tca tat gat gat gtt cta aat gct gaa caa ctt cag	192
Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln	
50 55 60	
aaa ctc ctt tac ctg ctg gag tca acg gag gat cct gta att att gaa	240
Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu	
65 70 75 80	
aga gct ttg att act ttg ggt aac aat gca gcc ttt tca gtt aac caa	288
Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln	
85 90 95	
gct att att cgt gaa ttg ggt ggt att cca att gtt gca aac aaa atc	336
Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile	
100 105 110	
aac cat tcc aac cag agt att aaa gag aaa gct tta aat gca cta aat	384
Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn	
115 120 125	
aac ctg agt gtg aat gtt gaa aat caa atc aag ata aag ata tac atc	432
Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Ile Tyr Ile	
130 135 140	
agt caa gta tgt gag gat gtc ttc tct ggt cct ctg aac tct gct gtg	480
Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn Ser Ala Val	
145 150 155 160	
cag ctg gct gga ctg aca ttg ttg aca aac atg act gtt acc aat gac	528

46

Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val Thr Asn Asp
 165 170 175

cac cag cac atg ctt cac agt tac att aca gac ctg ttc cag gtg tta 576
 His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe Gln Val Leu
 180 185 190

ctt act gga aat gga aac acg aag gtg caa gtt ttg aaa ctg ctt ttg 624
 Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys Leu Leu Leu
 195 200 205

aat ttg tct gaa aat cca gcc atg aca gaa gga ctt ctc cgt gcc caa 672
 Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu Arg Ala Gln
 210 215 220

gtg gat tca tca ttc ctt tcc ctt atg aca gcc acg tag 711
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 35 40 45
 Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
 50 55 60
 Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
 65 70 75 80
 Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln
 85 90 95
 Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile
 100 105 110
 Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
 115 120 125
 Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Ile Tyr Ile
 130 135 140

47

Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn Ser Ala Val
 145 150 155 160
 Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val Thr Asn Asp
 165 170 175
 His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe Gln Val Leu
 180 185 190
 Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys Leu Leu Leu
 195 200 205
 Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu Arg Ala Gln
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 Val Asp Ser Ser Phe Leu Ser Leu Met Thr Ala Thr
 225 230 235

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ggg ccg tgg ctg gag gct gcg ggc gtt gcg gag tcg ccg ctg ccc gcc	96
Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu Ser Pro Leu Pro Ala	
20 25 30	
gtg gtc ctt gcc atc ctg gcc cgc aat gcc gaa cac tcg ctg ccc cac	144
Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu His Ser Leu Pro His	
35 40 45	
tac ctg ggc gct ctg gag cgg ctg gac tac ccc cgg gcc agg atg gcc	192
Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro Arg Ala Arg Met Ala	
50 55 60	
ctc tgg tgt gcc acg gac cac aat gtg gac aac acc aca gag atg ctg	240
Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn Thr Thr Glu Met Leu	
65 70 75 80	
cag gag tgg ctg gcg gct gtg ggc gat gac tat gct gct gtg gtc tgg	288

48

Gln	Glu	Trp	Leu	Ala	Ala	Val	Gly	Asp	Asp	Tyr	Ala	Ala	Val	Val	Trp	
			85					90						95		
agg	cct	gag	ggc	gag	ccc	agg	ttc	tac	cca	gat	gaa	gag	ggt	ccc	aag	336
Arg	Pro	Glu	Gly	Glu	Pro	Arg	Phe	Tyr	Pro	Asp	Glu	Glu	Gly	Pro	Lys	
			100					105					110			
cac	tgg	acc	aaa	gaa	agg	cac	cag	ttt	ctg	atg	gag	ctg	aag	cag	gaa	384
His	Trp	Thr	Lys	Glu	Arg	His	Gln	Phe	Leu	Met	Glu	Leu	Lys	Gln	Glu	
			115					120					125			
gcc	ctc	acc	ttt	gcc	agg	aac	tgg	ggg	gcc	gac	tat	atc	ctg	ttt	gca	432
Ala	Leu	Thr	Phe	Ala	Arg	Asn	Trp	Gly	Ala	Asp	Tyr	Ile	Leu	Phe	Ala	
			130					135				140				
gac	aca	gac	aac	att	ctg	acc	aac	aat	cag	act	ctg	cgg	ctt	ctc	atg	480
Asp	Thr	Asp	Asn	Ile	Leu	Thr	Asn	Asn	Gln	Thr	Leu	Arg	Leu	Leu	Met	
					150				155						160	
ggg	cag	ggg	ctt	cca	gtg	gtg	gcc	cca	atg	ctg	gac	tcc	cag	acc	tac	528
Gly	Gln	Gly	Leu	Pro	Val	Val	Ala	Pro	Met	Leu	Asp	Ser	Gln	Thr	Tyr	
				165				170						175		
tac	tcc	aac	ttc	tgg	tgt	ggg	atc	acc	ccc	cag	ggc	tac	tac	cgc	cgc	576
Tyr	Ser	Asn	Phe	Trp	Cys	Gly	Ile	Thr	Pro	Gln	Gly	Tyr	Tyr	Arg	Arg	
			180					185						190		
aca	gcc	gag	tac	ttc	ccc	acc	aag	aac	cgc	cag	cgc	cgg	ggc	tgc	ttc	624
Thr	Ala	Glu	Tyr	Phe	Pro	Thr	Lys	Asn	Arg	Gln	Arg	Arg	Gly	Cys	Phe	
			195					200					205			
cgt	gtc	ccc	atg	gtc	cac	tcc	acc	ttc	ctt	gca	tcc	ctg	cgg	gct	gaa	672
Arg	Val	Pro	Met	Val	His	Ser	Thr	Phe	Leu	Ala	Ser	Leu	Arg	Ala	Glu	
			210					215				220				
ggg	gca	gac	cag	ctt	gct	ttc	tac	ccg	cca	cat	ccc	aac	tac	act	tgg	720
Gly	Ala	Asp	Gln	Leu	Ala	Phe	Tyr	Pro	Pro	His	Pro	Asn	Tyr	Thr	Trp	
				225			230			235					240	
cct	ttc	gac	gac	atc	atc	gtc	ttc	gcc	tat	gcc	tgc	cag	gct	gct	ggg	768
Pro	Phe	Asp	Asp	Ile	Ile	Val	Phe	Ala	Tyr	Ala	Cys	Gln	Ala	Ala	Gly	
				245				250						255		
gtc	tcc	gtc	cac	gtg	tgc	aat	gag	cac	cgt	tat	ggg	tac	atg	aat	gtg	816

Val	Ser	Val	His	Val	Cys	Asn	Glu	His	Arg	Tyr	Gly	Tyr	Met	Asn	Val	
			260					265					270			
ccg	gtg	aaa	tcc	cac	cag	ggg	ctg	gaa	gac	gag	agg	gtc	aac	ttc	atc	864
Pro	Val	Lys	Ser	His	Gln	Gly	Leu	Glu	Asp	Glu	Arg	Val	Asn	Phe	Ile	
		275					280					285				
cac	ctg	atc	tta	gaa	gca	cta	gtg	gac	ggc	ccc	cgc	atg	cag	gcc	tca	912
His	Leu	Ile	Leu	Glu	Ala	Leu	Val	Asp	Gly	Pro	Arg	Met	Gln	Ala	Ser	
	290					295					300					
gct	cat	gtg	act	cgg	ccc	tct	aag	agg	ccc	agc	aag	ata	ggg	ttt	gac	960
Ala	His	Val	Thr	Arg	Pro	Ser	Lys	Arg	Pro	Ser	Lys	Ile	Gly	Phe	Asp	
305					310					315					320	
gag	gtc	ttt	gtc	atc	agc	ctg	gct	cgc	agg	cct	gac	cgt	cgg	gaa	cgc	1008
Glu	Val	Phe	Val	Ile	Ser	Leu	Ala	Arg	Arg	Pro	Asp	Arg	Arg	Glu	Arg	
				325					330					335		
atg	ctc	gcc	tcg	ctc	tgg	gag	atg	gag	atc	tct	ggg	agg	gtg	gtg	gac	1056
Met	Leu	Ala	Ser	Leu	Trp	Glu	Met	Glu	Ile	Ser	Gly	Arg	Val	Val	Asp	
		340					345						350			
gct	gtg	gat	ggc	tgg	atg	ctc	aac	agc	agt	gcc	atc	agg	aac	ctc	ggc	1104
Ala	Val	Asp	Gly	Trp	Met	Leu	Asn	Ser	Ser	Ala	Ile	Arg	Asn	Leu	Gly	
		355					360					365				
gta	gac	ctg	ctc	ccg	ggc	tac	cag	gac	cct	tac	tcg	ggc	cgc	act	ctg	1152
Val	Asp	Leu	Leu	Pro	Gly	Tyr	Gln	Asp	Pro	Tyr	Ser	Gly	Arg	Thr	Leu	
	370					375					380					
acc	aag	ggc	gag	gtg	ggc	tgc	ttc	ctc	agc	cat	tac	tcc	atc	tgg	gaa	1200
Thr	Lys	Gly	Glu	Val	Gly	Cys	Phe	Leu	Ser	His	Tyr	Ser	Ile	Trp	Glu	
385					390					395				400		
gag	gtg	gtt	gcc	agg	ggc	ctg	gcc	cgg	gtc	ctg	gtg	ttt	gag	gat	gac	1248
Glu	Val	Val	Ala	Arg	Gly	Leu	Ala	Arg	Val	Leu	Val	Phe	Glu	Asp	Asp	
			405					410					415			
gtg	cgc	ttt	gag	agc	aac	ttc	agg	ggg	cgg	ctg	gag	cgg	ctg	atg	gag	1296
Val	Arg	Phe	Glu	Ser	Asn	Phe	Arg	Gly	Arg	Leu	Glu	Arg	Leu	Met	Glu	
		420					425						430			
gat	gtg	gag	gca	gag	aaa	ctg	tct	tgg	gac	ctg	atc	tac	ctc	gga	cgg	1344

50

Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg	
435 440 445	
aag cag gtg aac cct gag aag gag acg gcc gtg gag ggg ctg ccg ggc	1392
Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu Pro Gly	
450 455 460	
ctg gtg gtg gct ggg tac tcc tac tgg acg ctg gcc tat gcc ctg cgt	1440
Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala Leu Arg	
465 470 475 480	
ctg gcg ggt gcc cgc aag ctg ctg gcc tca cag cct ctg cgc cgc atg	1488
Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg Arg Met	
485 490 495	
ctg ccc gtg gac gag ttc ctg ccc atc atg ttc gac cag cac ccc aac	1536
Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His Pro Asn	
500 505 510	
gag cag tac aag gca cac ttc tgg cca cgg gac ctg gtg gcc ttc tcc	1584
Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser	
515 520 525	
gcc cag ccc ctg ctc gct gcc cct acc cac tat gcc ggg gac gcc gag	1632
Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu	
530 535 540	
tgg ctc agt gac acg gag aca tcc tct cca tgg gat gat gac agc ggc	1680
Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly	
545 550 555 560	
cgc ctc atc agc tgg agc ggc tcc caa aag acc ctg cgc agc ccc gcc	1728
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tgg acc tga	1737
Trp Thr *	

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      20           25           30
Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu His Ser Leu Pro His
      35           40           45
Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro Arg Ala Arg Met Ala
 50           55           60
Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn Thr Thr Glu Met Leu
65           70           75           80
Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr Ala Ala Val Val Trp
      85           90           95
Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly Pro Lys
      100          105          110
His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys Gln Glu
      115          120          125
Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu Phe Ala
      130          135          140
Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu Leu Met
      145          150          155          160
Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln Thr Tyr
      165          170          175
Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr Arg Arg
      180          185          190
Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly Cys Phe
      195          200          205
Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg Ala Glu
      210          215          220
Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr Thr Trp
      225          230          235          240
Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala Ala Gly
      245          250          255
Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met Asn Val
      260          265          270
Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn Phe Ile
      275          280          285
His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln Ala Ser
      290          295          300
Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp
      305          310          315          320
Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg
      325          330          335

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52

Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp
 340 345 350
 Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly
 355 360 365
 Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu
 370 375 380
 Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu
 385 390 395 400
 Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu Asp Asp
 405 410 415
 Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu Met Glu
 420 425 430
 Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg
 435 440 445
 Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu Pro Gly
 450 455 460
 Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala Leu Arg
 465 470 475 480
 Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg Arg Met
 485 490 495
 Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His Pro Asn
 500 505 510
 Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
 515 520 525
 Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
 530 535 540
 Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly
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 565 570 575
 Trp Thr

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48

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ggt	gca	agc	cgt	ggc	att	ggc	aaa	gct	att	gca	ttg	aaa	gca	gca	aag		96
Gly	Ala	Ser	Arg	Gly	Ile	Gly	Lys	Ala	Ile	Ala	Leu	Lys	Ala	Ala	Lys		
			20					25					30				
gat	gga	gca	aat	att	gtt	att	gct	gca	aag	acc	gcc	cag	cca	cat	cca		144
Asp	Gly	Ala	Asn	Ile	Val	Ile	Ala	Ala	Lys	Thr	Ala	Gln	Pro	His	Pro		
			35				40					45					
aaa	ctt	cta	ggc	aca	atc	tat	act	gct	gct	gaa	gaa	att	gaa	gca	gtt		192
Lys	Leu	Leu	Gly	Thr	Ile	Tyr	Thr	Ala	Ala	Glu	Glu	Ile	Glu	Ala	Val		
	50					55				60							
gga	gga	aag	gcc	ttg	cca	tgt	att	gtt	gat	gtg	aga	gat	gaa	cag	cag		240
Gly	Gly	Lys	Ala	Leu	Pro	Cys	Ile	Val	Asp	Val	Arg	Asp	Glu	Gln	Gln		
65				70				75					80				
atc	agt	gct	gca	gtg	gag	aaa	gcc	atc	aag	aaa	ttt	gga	gga	att	gat		288
Ile	Ser	Ala	Ala	Val	Glu	Lys	Ala	Ile	Lys	Lys	Phe	Gly	Gly	Ile	Asp		
				85				90					95				
att	ctg	gta	aat	aat	gcc	agt	gcc	att	agt	ttg	acc	aat	aca	ttg	gac		336
Ile	Leu	Val	Asn	Asn	Ala	Ser	Ala	Ile	Ser	Leu	Thr	Asn	Thr	Leu	Asp		
			100				105					110					
aca	cct	acc	aag	aga	ttg	gat	ctg	atg	atg	aac	gtg	aac	acc	aga	ggc		384
Thr	Pro	Thr	Lys	Arg	Leu	Asp	Leu	Met	Met	Asn	Val	Asn	Thr	Arg	Gly		
			115				120					125					
acc	tac	ctt	gca	tct	aaa	gca	tgt	att	cct	tat	ttg	aaa	aag	agc	aaa		432
Thr	Tyr	Leu	Ala	Ser	Lys	Ala	Cys	Ile	Pro	Tyr	Leu	Lys	Lys	Ser	Lys		
	130					135					140						
gtt	gct	cat	atc	ctc	aat	atc	agt	cca	cca	ctg	aac	cta	aat	cca	gtt		480
Val	Ala	His	Ile	Leu	Asn	Ile	Ser	Pro	Pro	Leu	Asn	Leu	Asn	Pro	Val		
145				150				155					160				
tgg	ttc	aaa	cag	cac	tgt	gct	tat	acc	att	gct	aag	tat	ggg	atg	tct		528
Trp	Phe	Lys	Gln	His	Cys	Ala	Tyr	Thr	Ile	Ala	Lys	Tyr	Gly	Met	Ser		
			165				170						175				
atg	tat	gtg	ctt	gga	atg	gca	gaa	gaa	ttt	aaa	ggg	gaa	att	gca	gtc		576

Met Tyr Val	Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val	
180	185	190
aat gca tta tgg cct aaa aca gcc ata cac act gct gct atg gat atg		624
Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met		
195	200	205
ctg gga gga cct ggt atc gaa agc cag tgt aga aaa gtt gat atc att		672
Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile		
210	215	220
gca gat gca gca tat tcc att ttc caa aag cca aaa agt ttt act ggc		720
Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly		
225	230	235 240
aac ttt gtc att gat gaa aat atc tta aaa gaa gaa gga ata gaa aat		768
Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn		
245	250	255
ttt gac gtt tat gca att aaa cca ggt cat cct ttg caa cca gat ttc		816
Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe		
260	265	270
ttc tta gat gaa tac cca gaa gca gtt agc aag aaa gtg gaa tca act		864
Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr		
275	280	285
ggt gct gtt cca gaa ttc aaa gaa gag aaa ctg cag ctg caa cca aaa		912
Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys		
290	295	300
cca cgt tct gga gct gtg gaa gaa aca ttt aga att gtt aag gac tct		960
Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser		
305	310	315 320
ctc agt gat gat gtt gtt aaa gcc act caa gca atc tat ctg ttt gaa		1008
Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu		
325	330	335
ctc tcc ggt gaa gat ggt ggc acg tgg ttt ctt gat ctg aaa agc aag		1056
Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys		
340	345	350
ggt ggg aat gtc gga tat gga gag cct tct gat cag gca gat gtg gtg		1104

55

Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val
 355 360 365

atg agt atg act act gat gac ttt gta aaa atg ttt tca ggg aac taa 1152
 Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Asn *
 370 375 380

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 20 25 30
 Asp Gly Ala Asn Ile Val Ile Ala Ala Lys Thr Ala Gln Pro His Pro
 35 40 45
 Lys Leu Leu Gly Thr Ile Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val
 50 55 60
 Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln
 65 70 75 80
 Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp
 85 90 95
 Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp
 100 105 110
 Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly
 115 120 125
 Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys
 130 135 140
 Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val
 145 150 155 160
 Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser
 165 170 175
 Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val
 180 185 190
 Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met
 195 200 205
 Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile
 210 215 220
 Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly
 225 230 235 240

56

Asn	Phe	Val	Ile	Asp	Glu	Asn	Ile	Leu	Lys	Glu	Glu	Gly	Ile	Glu	Asn
				245					250					255	
Phe	Asp	Val	Tyr	Ala	Ile	Lys	Pro	Gly	His	Pro	Leu	Gln	Pro	Asp	Phe
			260					265					270		
Phe	Leu	Asp	Glu	Tyr	Pro	Glu	Ala	Val	Ser	Lys	Lys	Val	Glu	Ser	Thr
		275					280					285			
Gly	Ala	Val	Pro	Glu	Phe	Lys	Glu	Glu	Lys	Leu	Gln	Leu	Gln	Pro	Lys
	290					295					300				
Pro	Arg	Ser	Gly	Ala	Val	Glu	Glu	Thr	Phe	Arg	Ile	Val	Lys	Asp	Ser
305					310					315					320
Leu	Ser	Asp	Asp	Val	Val	Lys	Ala	Thr	Gln	Ala	Ile	Tyr	Leu	Phe	Glu
			325						330					335	
Leu	Ser	Gly	Glu	Asp	Gly	Gly	Thr	Trp	Phe	Leu	Asp	Leu	Lys	Ser	Lys
		340						345					350		
Gly	Gly	Asn	Val	Gly	Tyr	Gly	Glu	Pro	Ser	Asp	Gln	Ala	Asp	Val	Val
	355						360					365			
Met	Ser	Met	Thr	Thr	Asp	Asp	Phe	Val	Lys	Met	Phe	Ser	Gly	Asn	
	370					375					380				

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<210> 35
<211> 1371
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(1371)
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<221> misc_feature
<222> (1)...(1371)
<223> n = A,T,C or G
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<400> 35																
atg	ggg	gcc	tgc	ctg	gga	gcc	tgc	tcc	ctg	ctc	agc	tgc	gcg	tcc	tgc	48
Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser	Cys	
1			5			10			15							
ctc	tgc	ggc	tct	gcc	ccc	tgc	atc	ctg	tgc	agc	tgc	tgc	ccc	gcc	agc	96
Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro	Ala	Ser	
			20			25						30				
cgc	aac	tcc	acc	gtg	agc	cgc	ctc	atc	ttc	acg	ttc	ttc	ctc	ttc	ctg	144
Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe	Leu	Phe	Leu	
35						40						45				

ggg gtg ctg gtg tcc atc att atg ctg agc ccg ggc gtg gag agt cag Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly Val Glu Ser Gln 50 55 60	192
ctc tac aag ctg ccc tgg gtg tgt gag gag ggg gcc ggg atc ccc acc Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly Ala Gly Ile Pro Thr 65 70 75 80	240
gtc ctg cag ggc cac atc gac tgt ggc tcc ctg ctt ggc tac cgc gct Val Leu Gln Gly His Ile Asp Cys Gly Ser Leu Leu Gly Tyr Arg Ala 85 90 95	288
gtc tac cgc atg tgc ttc gcc acg gcg gcc ttc ttc ttc ttt ttc acc Val Tyr Arg Met Cys Phe Ala Thr Ala Ala Phe Phe Phe Phe Thr 100 105 110	336
ctg ctc atg ctc tgc gtg agc agc agc cgg gac ccc cgg gct gcc atc Leu Leu Met Leu Cys Val Ser Ser Ser Arg Asp Pro Arg Ala Ala Ile 115 120 125	384
cag aat ggg ttt tgg ttc ttt aag ttc ctg atc ctg gtg ggc ctc acc Gln Asn Gly Phe Trp Phe Phe Lys Phe Leu Ile Leu Val Gly Leu Thr 130 135 140	432
gtg ggt gcc ttc tac atc cct gac ggc tcc ttc acc aac atc tgg ttc Val Gly Ala Phe Tyr Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe 145 150 155 160	480
tac ttc ggc gtc gtg ggc tcc ttc ctc ttc atc ctc atc cag ctg gtg Tyr Phe Gly Val Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val 165 170 175	528
ctg ctc atc gac ttt gcg cac tcc tgg aac cag cgg tgg ctg ggc aag Leu Leu Ile Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys 180 185 190	576
gcc gag gag tgc gat tcc cgt gcc tgg tac gca ggc ctc ttc ttc ttc Ala Glu Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe 195 200 205	624
act ctc ctc ttc tac ttg ctg tcg atc gcg gcc gtg gcg ctg atg ttc Thr Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe 210 215 220	672

atg	tac	tac	act	gag	ccc	agc	ggc	tgc	cac	gag	ggc	aag	gtc	ttc	atc	720
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe	Ile	
225					230					235					240	
agc	ctc	aac	ctc	acc	ttc	tgt	gtc	tgc	gtg	tcc	atc	gct	gct	gtc	ctg	768
Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	Val	Leu	
				245					250						255	
ccc	aag	gtc	cag	gac	gcc	cag	ccc	aac	tcg	ggt	ctg	ctg	cag	gcc	tcg	816
Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	Gln	Ala	Ser	
			260					265						270		
gtc	atc	acc	ctc	tac	acc	atg	ttt	gtc	acc	tgg	tca	gcc	cta	tcc	agt	864
Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	Ala	Leu	Ser	Ser	
		275					280						285			
atc	cct	gaa	cag	aaa	tgc	aac	ccc	cat	ttg	cca	acc	cag	ctg	ggc	aac	912
Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	Thr	Gln	Leu	Gly	Asn	
	290					295					300					
gag	aca	gtt	gtg	gca	ggc	ccc	gag	ggc	tat	gag	acc	cag	tgg	tgg	gat	960
Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	Glu	Thr	Gln	Trp	Trp	Asp	
305					310					315					320	
gcc	ccg	agc	att	gtg	ggc	ctc	atc	atc	ttc	ctc	ctg	tgc	acc	ctc	ttc	1008
Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	Phe	Leu	Leu	Cys	Thr	Leu	Phe	
				325					330						335	
atc	agt	ctg	cgc	tcc	tca	gac	cac	cgg	cag	gtg	aac	agc	ctg	atg	cag	1056
Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	
			340					345					350			
acc	gag	gag	tgc	cca	cct	atg	cta	gac	gcc	aca	cng	cag	cag	cag	cag	1104
Thr	Glu	Glu	Cys	Pro	Pro	Met	Leu	Asp	Ala	Thr	Xaa	Gln	Gln	Gln	Gln	
			355				360					365				
cag	gtg	gca	gcc	tgt	gag	ggc	cgg	gcc	ttt	gac	aac	gag	cag	gac	ggc	1152
Gln	Val	Ala	Ala	Cys	Glu	Gly	Arg	Ala	Phe	Asp	Asn	Glu	Gln	Asp	Gly	
	370					375					380					
gtc	acc	tac	agc	tac	tcc	ttc	ttc	cac	ttc	tgc	ctg	gtg	ctg	gcc	tca	1200
Val	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	His	Phe	Cys	Leu	Val	Leu	Ala	Ser	
385					390					395					400	

ctg cac gtc atg atg acg ctc acc aac tgg tac aag ccc ggt gag acc 1248
 Leu His Val Met Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr
 405 410 415

cgg aag atg atc agc acg tgg acc gcc gtg tgg gtg aag atc tgt gcc 1296
 Arg Lys Met Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala
 420 425 430

agc tgg gca ggg ctg ctc ctc tac ctg tgg acc ctg gta gcc cca ctc 1344
 Ser Trp Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu
 435 440 445

ctc ctg cgc aac cgc gac ttc agc tga 1371
 Leu Leu Arg Asn Arg Asp Phe Ser *
 450 455

<210> 36
 <211> 456
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(456)
 <223> Xaa = Any Amino Acid

<400> 36
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser Cys
 1 5 10 15
 Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro Ala Ser
 20 25 30
 Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe Leu Phe Leu
 35 40 45
 Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly Val Glu Ser Gln
 50 55 60
 Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly Ala Gly Ile Pro Thr
 65 70 75 80
 Val Leu Gln Gly His Ile Asp Cys Gly Ser Leu Leu Gly Tyr Arg Ala
 85 90 95
 Val Tyr Arg Met Cys Phe Ala Thr Ala Ala Phe Phe Phe Phe Thr
 100 105 110
 Leu Leu Met Leu Cys Val Ser Ser Ser Arg Asp Pro Arg Ala Ala Ile

115	120	125
Gln Asn Gly Phe Trp Phe Phe Lys Phe Leu Ile Leu Val Gly Leu Thr		
130	135	140
Val Gly Ala Phe Tyr Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe		
145	150	155
Tyr Phe Gly Val Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val		
165	170	175
Leu Leu Ile Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys		
180	185	190
Ala Glu Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe		
195	200	205
Thr Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe		
210	215	220
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe Ile		
225	230	235
Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala Val Leu		
245	250	255
Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu Gln Ala Ser		
260	265	270
Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser Ala Leu Ser Ser		
275	280	285
Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro Thr Gln Leu Gly Asn		
290	295	300
Glu Thr Val Val Ala Gly Pro Glu Gly Tyr Glu Thr Gln Trp Trp Asp		
305	310	315
Ala Pro Ser Ile Val Gly Leu Ile Ile Phe Leu Leu Cys Thr Leu Phe		
325	330	335
Ile Ser Leu Arg Ser Ser Asp His Arg Gln Val Asn Ser Leu Met Gln		
340	345	350
Thr Glu Glu Cys Pro Pro Met Leu Asp Ala Thr Xaa Gln Gln Gln Gln		
355	360	365
Gln Val Ala Ala Cys Glu Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly		
370	375	380
Val Thr Tyr Ser Tyr Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser		
385	390	395
Leu His Val Met Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr		
405	410	415
Arg Lys Met Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala		
420	425	430
Ser Trp Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu		
435	440	445
Leu Leu Arg Asn Arg Asp Phe Ser		
450	455	

61

<210> 37
 <211> 1257
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1257)

<400> 37

atg tta ccc aac acc ggg agg ctg gca gga tgt aca gtt ttt atc aca	48
Met Leu Pro Asn Thr Gly Arg Leu Ala Gly Cys Thr Val Phe Ile Thr	
1 5 10 15	
ggg gca agc cgt ggc att ggc aaa gct att gca ttg aaa gca gca aag	96
Gly Ala Ser Arg Gly Ile Gly Lys Ala Ile Ala Leu Lys Ala Ala Lys	
20 25 30	
gat gga gca aat att gtt att gct gca aag acc gcc cag cca cat cca	144
Asp Gly Ala Asn Ile Val Ile Ala Ala Lys Thr Ala Gln Pro His Pro	
35 40 45	
aaa ctt cta ggc aca atc tat act gct gct gaa gaa att gaa gca gtt	192
Lys Leu Leu Gly Thr Ile Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val	
50 55 60	
gga gga aag gcc ttg cca tgt att gtt gat gtg aga gat gaa cag cag	240
Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln	
65 70 75 80	
atc agt gct gca gtg gag aaa gcc atc aag aaa ttt gga gga att gat	288
Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp	
85 90 95	
att ctg gta aat aat gcc agt gcc att agt ttg acc aat aca ttg gac	336
Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp	
100 105 110	
aca cct acc aag aga ttg gat ctg atg atg aac gtg aac acc aga ggc	384
Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly	
115 120 125	
acc tac ctt gca tct aaa gca tgt att cct tat ttg aaa aag agc aaa	432
Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys	

130	135	140	
ggt gct cat atc ctc aat atc agt cca cca ctg aac cta aat cca gtt			480
Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val			
145	150	155	160
tgg ttc aaa cag cac tgt gct tat acc att gct aag tat ggt atg tct			528
Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser			
	165	170	175
atg tat gtg ctt gga atg gca gaa gaa ttt aaa ggt gaa att gca gtc			576
Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val			
	180	185	190
aat gca tta tgg cct aaa aca gcc ata cac act gct gct atg gat atg			624
Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met			
	195	200	205
ctg gga gga cct ggt atc gaa agc cag tgt aga aaa gtt gat atc att			672
Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile			
	210	215	220
gca gat gca gca tat tcc att ttc caa aag cca aaa agt ttt act ggc			720
Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly			
225	230	235	240
aac ttt gtc att gat gaa aat atc tta aaa gaa gaa gga ata gaa aat			768
Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn			
	245	250	255
ttt gac gtt tat gca att aaa cca ggt cat cct ttg caa cca gat ttc			816
Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe			
	260	265	270
ttc tta gat gaa tac cca gaa gca gtt agc aag aaa gtg gaa tca act			864
Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr			
	275	280	285
ggt gct gtt cca gaa ttc aaa gaa gag aaa ctg cag ctg caa cca aaa			912
Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys			
	290	295	300
cca cgt tct gga gct gtg gaa gaa aca ttt aga att gtt aag gac tct			960
Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser			

63

305	310	315	320	
ctc agt gat gat gtt gtt aaa gcc act caa gca atc tat ctg ttt gaa	1008			
Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu				
325	330	335		
ctc tcc ggt gaa gat ggt ggc acg tgg ttt ctt gat ctg aaa agc aag	1056			
Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys				
340	345	350		
ggg aat gtc gga tat gga gag cct tct gat cag gca gat gtg gtg	1104			
Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val				
355	360	365		
atg agt atg act act gat gac ttt gta aaa atg ttt tca ggg aaa cta	1152			
Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Lys Leu				
370	375	380		
aaa cca aca atg gca ttc atg tca ggg aaa ttg aag att aaa ggt aac	1200			
Lys Pro Thr Met Ala Phe Met Ser Gly Lys Leu Lys Ile Lys Gly Asn				
385	390	395	400	
atg gcc cta gca atc aaa ttg gag aag cta atg aat cag atg aat gcc	1248			
Met Ala Leu Ala Ile Lys Leu Glu Lys Leu Met Asn Gln Met Asn Ala				
405	410	415		
aga ctg tga	1257			
Arg Leu *				

<210> 38

<211> 418

<212> PRT

<213> Homo sapiens

<400> 38

Met	Leu	Pro	Asn	Thr	Gly	Arg	Leu	Ala	Gly	Cys	Thr	Val	Phe	Ile	Thr
1				5				10					15		
Gly	Ala	Ser	Arg	Gly	Ile	Gly	Lys	Ala	Ile	Ala	Leu	Lys	Ala	Ala	Lys
		20					25					30			
Asp	Gly	Ala	Asn	Ile	Val	Ile	Ala	Ala	Lys	Thr	Ala	Gln	Pro	His	Pro
	35						40				45				
Lys	Leu	Leu	Gly	Thr	Ile	Tyr	Thr	Ala	Ala	Glu	Glu	Ile	Glu	Ala	Val

50	55	60
Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln		
65	70	75
Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp		80
	85	90
Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp		95
	100	105
Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly		110
	115	120
Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys		125
	130	135
Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val		140
145	150	155
Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser		160
	165	170
Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val		175
	180	185
Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met		190
	195	200
Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile		205
	210	215
Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly		220
225	230	235
Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn		240
	245	250
Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe		255
	260	265
Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr		270
	275	280
Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys		285
	290	295
Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser		300
305	310	315
Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu		320
	325	330
Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys		335
	340	345
Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val		350
	355	360
Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Lys Leu		365
	370	375
Lys Pro Thr Met Ala Phe Met Ser Gly Lys Leu Lys Ile Lys Gly Asn		380
385	390	395
Met Ala Leu Ala Ile Lys Leu Glu Lys Leu Met Asn Gln Met Asn Ala		400

65

Arg Leu 405 410 415

<210> 39
 <211> 627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(627)

<400> 39
 atg gtg ttc tac ttc acc agc agc agc gtt aat tca tct gcc tac act 48
 Met Val Phe Tyr Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr
 1 5 10 15

att tac atg gga aaa gat aaa tat gaa aat gaa gat ctg atc aag cat 96
 Ile Tyr Met Gly Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His
 20 25 30

ggc tgg cct gaa gat atc tgg ttt cat gtg gac aaa ctc tct tcg gct 144
 Gly Trp Pro Glu Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala
 35 40 45

cat gta tac ctt cga tta cat aag gga gag aat ata gaa gac atc cca 192
 His Val Tyr Leu Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro
 50 55 60

aag gaa gtg ctg atg gac tgt gcc cac ctt gtg aag gcc aat agc att 240
 Lys Glu Val Leu Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile
 65 70 75 80

caa ggc tgc aag atg aac aac gtt aat gtg gta tat acg ccg tgg tct 288
 Gln Gly Cys Lys Met Asn Asn Val Asn Val Val Tyr Thr Pro Trp Ser
 85 90 95

aac ctg aag aaa aca gct gac atg gat gtg ggg cag ata ggc ttt cac 336
 Asn Leu Lys Lys Thr Ala Asp Met Asp Val Gly Gln Ile Gly Phe His
 100 105 110

agg cag aag gat gta aaa att gtg aca gtg gag aag aaa gta aat gag 384
 Arg Gln Lys Asp Val Lys Ile Val Thr Val Glu Lys Lys Val Asn Glu

66

115	120	125	
atc ctg aac cga tta gaa aag acc aaa gtc gag cgg ttc cca gac cta			432
Ile Leu Asn Arg Leu Glu Lys Thr Lys Val Glu Arg Phe Pro Asp Leu			
130	135	140	
gca gca gag aaa gaa tgc aga gat cgt gaa gag agg aat gag aaa aaa			480
Ala Ala Glu Lys Glu Cys Arg Asp Arg Glu Glu Arg Asn Glu Lys Lys			
145	150	155	160
gcc caa att cag gaa atg aaa aag aga gaa aaa gaa gaa atg aag aag			528
Ala Gln Ile Gln Glu Met Lys Lys Arg Glu Lys Glu Glu Met Lys Lys			
165	170	175	
aag agg gaa atg gat gaa ctt agg agc tat tca tca cta atg aaa gtt			576
Lys Arg Glu Met Asp Glu Leu Arg Ser Tyr Ser Ser Leu Met Lys Val			
180	185	190	
gaa aat atg tct tca aat cag gat ggc aat gat tca gat gaa ttc atg			624
Glu Asn Met Ser Ser Asn Gln Asp Gly Asn Asp Ser Asp Glu Phe Met			
195	200	205	
taa			627
*			

<210> 40
 <211> 208
 <212> PRT
 <213> Homo sapiens

<400> 40
 Met Val Phe Tyr Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr
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 Ile Tyr Met Gly Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His
 20 25 30
 Gly Trp Pro Glu Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala
 35 40 45
 His Val Tyr Leu Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro
 50 55 60
 Lys Glu Val Leu Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile
 65 70 75 80
 Gln Gly Cys Lys Met Asn Asn Val Asn Val Val Tyr Thr Pro Trp Ser

67

				85				90				95			
Asn	Leu	Lys	Lys	Thr	Ala	Asp	Met	Asp	Val	Gly	Gln	Ile	Gly	Phe	His
100				105				110							
Arg	Gln	Lys	Asp	Val	Lys	Ile	Val	Thr	Val	Glu	Lys	Lys	Val	Asn	Glu
115				120				125							
Ile	Leu	Asn	Arg	Leu	Glu	Lys	Thr	Lys	Val	Glu	Arg	Phe	Pro	Asp	Leu
130				135				140							
Ala	Ala	Glu	Lys	Glu	Cys	Arg	Asp	Arg	Glu	Glu	Arg	Asn	Glu	Lys	Lys
145				150				155				160			
Ala	Gln	Ile	Gln	Glu	Met	Lys	Lys	Arg	Glu	Lys	Glu	Glu	Met	Lys	Lys
165				170				175							
Lys	Arg	Glu	Met	Asp	Glu	Leu	Arg	Ser	Tyr	Ser	Ser	Leu	Met	Lys	Val
180				185				190							
Glu	Asn	Met	Ser	Ser	Asn	Gln	Asp	Gly	Asn	Asp	Ser	Asp	Glu	Phe	Met
195				200				205							

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<210> 41
<211> 474
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(474)

<221> misc_feature
<222> (1)...(474)
<223> n = A.T.C or G
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<400> 41																
atg	agc	ggg	tcc	ctc	ggc	cga	gct	gct	gcg	gct	ctg	ctc	cgc	tgg	agg	48
Met	Ser	Gly	Ser	Leu	Gly	Arg	Ala	Ala	Ala	Ala	Leu	Leu	Arg	Trp	Arg	
1		5			10						15					
ctc	tgc	gcg	ggc	ggc	ggt	ggc	ctt	tgg	ggt	ccg	gtc	gtc	cgg	act	gcg	96
Leu	Cys	Ala	Gly	Gly	Gly	Gly	Leu	Trp	Gly	Pro	Val	Val	Arg	Thr	Ala	
			20		25					30						
gga	tcg	gcc	ccg	ggc	ggc	ggc	ggc	tcg	gcg	gan	nag	ttg	gac	gcg	ctg	144
Gly	Ser	Ala	Pro	Gly	Gly	Gly	Gly	Ser	Ala	Xaa	Xaa	Leu	Asp	Ala	Leu	
			35		40					45						
gtg	aag	aag	gac	aag	gtg	gtg	gtc	ttc	ctc	aag	ggg	acg	ccg	gag	cag	192
Val	Lys	Lys	Asp	Lys	Val	Val	Val	Phe	Leu	Lys	Gly	Thr	Pro	Glu	Gln	

68

50	55	60	
ccc cag tgc ggc ttc agc aac gcc gtg gtg cag atc ctg cgg ctg cac			240
Pro Gln Cys Gly Phe Ser Asn Ala Val Val Gln Ile Leu Arg Leu His			
65	70	75	80
ggc gtc cgc gat tac gcg gcc tac aac gtg ctg gac gac ccg gag ctc			288
Gly Val Arg Asp Tyr Ala Ala Tyr Asn Val Leu Asp Asp Pro Glu Leu			
	85	90	95
cga caa ggc att aaa gac tat tcc aac tgg ccc acc atc ccg caa gtg			336
Arg Gln Gly Ile Lys Asp Tyr Ser Asn Trp Pro Thr Ile Pro Gln Val			
	100	105	110
tac ctc aat ggc gag ttt gta ggg ggc tgt gac att ctt ctg cag atg			384
Tyr Leu Asn Gly Glu Phe Val Gly Gly Cys Asp Ile Leu Leu Gln Met			
	115	120	125
cac cag aat ggg gac ttg gtg gaa gaa ctg aaa aag ctg ggg atc cac			432
His Gln Asn Gly Asp Leu Val Glu Glu Leu Lys Lys Leu Gly Ile His			
	130	135	140
tcc gcc ctt tta gat gaa aag aaa gac caa gac tcc aag tga			474
Ser Ala Leu Leu Asp Glu Lys Lys Asp Gln Asp Ser Lys *			
145	150	155	

<210> 42

<211> 157

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 42

Met Ser Gly Ser Leu Gly Arg Ala Ala Ala Ala Leu Leu Arg Trp Arg			
1	5	10	15
Leu Cys Ala Gly Gly Gly Gly Leu Trp Gly Pro Val Val Arg Thr Ala			
	20	25	30
Gly Ser Ala Pro Gly Gly Gly Gly Ser Ala Xaa Xaa Leu Asp Ala Leu			
	35	40	45

69

Val Lys Lys Asp Lys Val Val Val Phe Leu Lys Gly Thr Pro Glu Gln
 50 55 60
 Pro Gln Cys Gly Phe Ser Asn Ala Val Val Gln Ile Leu Arg Leu His
 65 70 75 80
 Gly Val Arg Asp Tyr Ala Ala Tyr Asn Val Leu Asp Asp Pro Glu Leu
 85 90 95
 Arg Gln Gly Ile Lys Asp Tyr Ser Asn Trp Pro Thr Ile Pro Gln Val
 100 105 110
 Tyr Leu Asn Gly Glu Phe Val Gly Gly Cys Asp Ile Leu Leu Gln Met
 115 120 125
 His Gln Asn Gly Asp Leu Val Glu Glu Leu Lys Lys Leu Gly Ile His
 130 135 140
 Ser Ala Leu Leu Asp Glu Lys Lys Asp Gln Asp Ser Lys
 145 150 155

<210> 43
 <211> 1032
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1032)

<400> 43

atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg ggc ctg ctg ctc 48
 Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1 5 10 15

ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc cgg ggt cgg cgg 96
 Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
 20 25 30

cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag tcc gca ggt gcc 144
 Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Gly Ala
 35 40 45

ctg gaa gaa ggg acg tca gag ggt cag ttg tgc ggg cgc tcg gcc cgg 192
 Leu Glu Glu Gly Thr Ser Glu Gly Gln Leu Cys Gly Arg Ser Ala Arg
 50 55 60

cct cag acg gga ggt acc tgg gag tca cag tgg tcc aag acc tcg cag 240
 Pro Gln Thr Gly Gly Thr Trp Glu Ser Gln Trp Ser Lys Thr Ser Gln
 65 70 75 80

cct gaa gac tta act gat ggt tca tat gat gat gtt cta aat gct gaa Pro Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu	288
85 90 95	
caa ctt cag aaa ctc ctt tac ctg ctg gag tca acg gag gat cct gta Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val	336
100 105 110	
att att gaa aga gct ttg att act ttg ggt aac aat gca gcc ttt tca Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser	384
115 120 125	
gtt aac caa gct att att cgt gaa ttg ggt ggt att cca att gtt gca Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala	432
130 135 140	
aac aaa atc aac cat tcc aac cag agt att aaa gag aaa gct tta aat Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn	480
145 150 155 160	
gca cta aat aac ctg agt gtg aat gtt gaa aat caa atc aag ata aag Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys	528
165 170 175	
ata tac atc agt caa gta tgt gag gat gtc ttc tct ggt cct ctg aac Ile Tyr Ile Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn	576
180 185 190	
tct gct gtg cag ctg gct gga ctg aca ttg ttg aca aac atg act gtt Ser Ala Val Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val	624
195 200 205	
acc aat gac cac cag cac atg ctt cac agt tac att aca gac ctg ttc Thr Asn Asp His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe	672
210 215 220	
cag gtg tta ctt act gga aat gga aac acg aag gtg caa gtt ttg aaa Gln Val Leu Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys	720
225 230 235 240	
ctg ctt ttg aat ttg tct gaa aat cca gcc atg aca gaa gga ctt ctc Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu	768
245 250 255	

cgt gcc caa gtg gat tca tca ttc ctt tcc ctt tat gac agc cac gta 816
 Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser His Val
 260 265 270

gca aag gag att ctt ctt cga gta ctt acg cta ttt cag aat ata aag 864
 Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn Ile Lys
 275 280 285

aac tgc ctc aaa ata gaa ggc cat tta gct gtg cag cct act ttc act 912
 Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr Phe Thr
 290 295 300

gaa ggt tca ttg ttt ttc ctg tta cat gga gaa gaa tgt gcc cag aaa 960
 Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala Gln Lys
 305 310 315 320

ata aga gct tta gtt gat cac cat gat gca gag gtg aag gaa aag gtt 1008
 Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu Lys Val
 325 330 335

gta aca ata ata ccc aaa atc tga 1032
 Val Thr Ile Ile Pro Lys Ile *
 340

<210> 44
 <211> 343
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1 5 10 15
 Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
 20 25 30
 Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Gly Ala
 35 40 45
 Leu Glu Glu Gly Thr Ser Glu Gly Gln Leu Cys Gly Arg Ser Ala Arg
 50 55 60
 Pro Gln Thr Gly Gly Thr Trp Glu Ser Gln Trp Ser Lys Thr Ser Gln
 65 70 75 80
 Pro Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu
 85 90 95

Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val
 100 105 110
 Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser
 115 120 125
 Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala
 130 135 140
 Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn
 145 150 155 160
 Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys
 165 170 175
 Ile Tyr Ile Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn
 180 185 190
 Ser Ala Val Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val
 195 200 205
 Thr Asn Asp His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe
 210 215 220
 Gln Val Leu Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys
 225 230 235 240
 Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu
 245 250 255
 Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser His Val
 260 265 270
 Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn Ile Lys
 275 280 285
 Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr Phe Thr
 290 295 300
 Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala Gln Lys
 305 310 315 320
 Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu Lys Val
 325 330 335
 Val Thr Ile Ile Pro Lys Ile
 340

<210> 45
 <211> 1335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1335)

<221> misc_feature
 <222> (1)...(1335)

73

<223> n = A,T,C or G

<400> 45

atg tcg gga aga gat aca atc ctt ggc ctg tgt atc ctc gca tta gcc	48
Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu Ala	
1 5 10 15	
ttg tct ttg gcc atg atg ttt acc ttc aga ttc atc acc acc ctt ctg	96
Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr Leu Leu	
20 25 30	
gtt cac att ttc att tca ttg gtt att ttg gga ttg ttg ttt gtc tgc	144
Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu Phe Val Cys	
35 40 45	
ggt gtt tta tgg tgg ctg tat tat gac tat acc aac gac ctc agc ata	192
Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn Asp Leu Ser Ile	
50 55 60	
gaa ttg gac aca gaa agg gaa aat atg aag tgc gtg ctg ggg ttt gct	240
Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys Val Leu Gly Phe Ala	
65 70 75 80	
atc gta tcc aca ggc atc acg gca gtg ctg ctc gtc ttg att ttt gtt	288
Ile Val Ser Thr Gly Ile Thr Ala Val Leu Leu Val Leu Ile Phe Val	
85 90 95	
ctc aga aag aga ata aaa ttg aca gtt gag ctt ttc caa atc aca aat	336
Leu Arg Lys Arg Ile Lys Leu Thr Val Glu Leu Phe Gln Ile Thr Asn	
100 105 110	
aaa gcc atc agc agt gct ccc ttc ctg ctg ttc cag cca ctg tgg aca	384
Lys Ala Ile Ser Ser Ala Pro Phe Leu Leu Phe Gln Pro Leu Trp Thr	
115 120 125	
ttt gcc atc ctc att ttc ttc tgg gtc ctc tgg gtg gct gtg ctg ctg	432
Phe Ala Ile Leu Ile Phe Phe Trp Val Leu Trp Val Ala Val Leu Leu	
130 135 140	
agc ctg gga act gca gga gct gcc cag gtt atg gaa ggc ggc caa gtg	480
Ser Leu Gly Thr Ala Gly Ala Ala Gln Val Met Glu Gly Gly Gln Val	
145 150 155 160	
gaa tat aag ccc ctt tcg ggc att cgg tac atg tgg tcg tac cat tta	528

74

Glu Tyr Lys Pro Leu Ser Gly Ile Arg Tyr Met Trp Ser Tyr His Leu	
165 170 175	
att ggc ctc atc tgg act agt gaa ttc atc ctt gcg tgc cag caa atg	576
Ile Gly Leu Ile Trp Thr Ser Glu Phe Ile Leu Ala Cys Gln Gln Met	
180 185 190	
act ata gct ggg gca gtg gnt act tgt tat ttc aac aga agt aaa aat	624
Thr Ile Ala Gly Ala Val Xaa Thr Cys Tyr Phe Asn Arg Ser Lys Asn	
195 200 205	
gat cct cct gat cat ccc atc ctt tcg tct ctc tcc att ctc ttc ttc	672
Asp Pro Pro Asp His Pro Ile Leu Ser Ser Leu Ser Ile Leu Phe Phe	
210 215 220	
tac cat caa gga acc att gtg aaa ggg tca ttt tta atc tct gtg gtg	720
Tyr His Gln Gly Thr Ile Val Lys Gly Ser Phe Leu Ile Ser Val Val	
225 230 235 240	
agg att ccg aga atc att gtc atg tac atg caa aac gca ctg aaa gaa	768
Arg Ile Pro Arg Ile Ile Val Met Tyr Met Gln Asn Ala Leu Lys Glu	
245 250 255	
cag cat ggt gca ttg tcc agg tac ctg ttc cga tgc tgc tac tgc tgt	816
Gln His Gly Ala Leu Ser Arg Tyr Leu Phe Arg Cys Cys Tyr Cys Cys	
260 265 270	
ttc tgg tgt ctt gac aaa tac ctg ctc cat ctc aac cag aat gca tat	864
Phe Trp Cys Leu Asp Lys Tyr Leu Leu His Leu Asn Gln Asn Ala Tyr	
275 280 285	
act aca act gct att aat ggg aca gat ttc tgt aca tca gca aaa gat	912
Thr Thr Thr Ala Ile Asn Gly Thr Asp Phe Cys Thr Ser Ala Lys Asp	
290 295 300	
gca ttc aaa atc ttg tcc aag aac tca agt cac ttt aca tct att aac	960
Ala Phe Lys Ile Leu Ser Lys Asn Ser Ser His Phe Thr Ser Ile Asn	
305 310 315 320	
tgc ttt gga gac ttc ata att ttt cta gga aag gtg tta gtg gtg tgt	1008
Cys Phe Gly Asp Phe Ile Ile Phe Leu Gly Lys Val Leu Val Val Cys	
325 330 335	
ttc act gtt ttt gga gga ctc atg gct ttt aac tac aat cgg gca ttc	1056

75

Phe Thr Val Phe Gly Gly Leu Met Ala Phe Asn Tyr Asn Arg Ala Phe
 340 345 350

 cag gtg tgg gca gtc cct ctg tta ttg gta gct ttt ttt gcc tac tta 1104
 Gln Val Trp Ala Val Pro Leu Leu Leu Val Ala Phe Phe Ala Tyr Leu
 355 360 365

 gta gcc cat agt ttt tta tct gtg ttt gaa act gtg ctg gat gca ctt 1152
 Val Ala His Ser Phe Leu Ser Val Phe Glu Thr Val Leu Asp Ala Leu
 370 375 380

 ttc ctg tgt ttt gct gtt gat ctg gaa aca aat gat gga tcg tca gaa 1200
 Phe Leu Cys Phe Ala Val Asp Leu Glu Thr Asn Asp Gly Ser Ser Glu
 385 390 395 400

 aag ccc tac ttt atg gat caa gaa ttt ctg agt ttc gta aaa agg agc 1248
 Lys Pro Tyr Phe Met Asp Gln Glu Phe Leu Ser Phe Val Lys Arg Ser
 405 410 415

 aac aaa tta aac aat gca agg gca cag cag gac aag cac tca tta agg 1296
 Asn Lys Leu Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg
 420 425 430

 aat gag gag gga aca gaa ctc cag gcc att gtg aga tag 1335
 Asn Glu Glu Gly Thr Glu Leu Gln Ala Ile Val Arg *
 435 440

<210> 46

<211> 444

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(444)

<223> Xaa = Any Amino Acid

<400> 46

Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu Ala
 1 5 10 15
 Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr Leu Leu
 20 25 30
 Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu Phe Val Cys

35															40					45				
Gly	Val	Leu	Trp	Trp	Leu	Tyr	Tyr	Asp	Tyr	Thr	Asn	Asp	Leu	Ser	Ile									
50					55					60														
Glu	Leu	Asp	Thr	Glu	Arg	Glu	Asn	Met	Lys	Cys	Val	Leu	Gly	Phe	Ala									
65					70					75					80									
Ile	Val	Ser	Thr	Gly	Ile	Thr	Ala	Val	Leu	Leu	Val	Leu	Ile	Phe	Val									
85					90					95														
Leu	Arg	Lys	Arg	Ile	Lys	Leu	Thr	Val	Glu	Leu	Phe	Gln	Ile	Thr	Asn									
100					105					110														
Lys	Ala	Ile	Ser	Ser	Ala	Pro	Phe	Leu	Leu	Phe	Gln	Pro	Leu	Trp	Thr									
115					120					125														
Phe	Ala	Ile	Leu	Ile	Phe	Phe	Trp	Val	Leu	Trp	Val	Ala	Val	Leu	Leu									
130					135					140														
Ser	Leu	Gly	Thr	Ala	Gly	Ala	Ala	Gln	Val	Met	Glu	Gly	Gly	Gln	Val									
145					150					155					160									
Glu	Tyr	Lys	Pro	Leu	Ser	Gly	Ile	Arg	Tyr	Met	Trp	Ser	Tyr	His	Leu									
165					170					175														
Ile	Gly	Leu	Ile	Trp	Thr	Ser	Glu	Phe	Ile	Leu	Ala	Cys	Gln	Gln	Met									
180					185					190														
Thr	Ile	Ala	Gly	Ala	Val	Xaa	Thr	Cys	Tyr	Phe	Asn	Arg	Ser	Lys	Asn									
195					200					205														
Asp	Pro	Pro	Asp	His	Pro	Ile	Leu	Ser	Ser	Leu	Ser	Ile	Leu	Phe	Phe									
210					215					220														
Tyr	His	Gln	Gly	Thr	Ile	Val	Lys	Gly	Ser	Phe	Leu	Ile	Ser	Val	Val									
225					230					235					240									
Arg	Ile	Pro	Arg	Ile	Ile	Val	Met	Tyr	Met	Gln	Asn	Ala	Leu	Lys	Glu									
245					250					255														
Gln	His	Gly	Ala	Leu	Ser	Arg	Tyr	Leu	Phe	Arg	Cys	Cys	Tyr	Cys	Cys									
260					265					270														
Phe	Trp	Cys	Leu	Asp	Lys	Tyr	Leu	Leu	His	Leu	Asn	Gln	Asn	Ala	Tyr									
275					280					285														
Thr	Thr	Thr	Ala	Ile	Asn	Gly	Thr	Asp	Phe	Cys	Thr	Ser	Ala	Lys	Asp									
290					295					300														
Ala	Phe	Lys	Ile	Leu	Ser	Lys	Asn	Ser	Ser	His	Phe	Thr	Ser	Ile	Asn									
305					310					315					320									
Cys	Phe	Gly	Asp	Phe	Ile	Ile	Phe	Leu	Gly	Lys	Val	Leu	Val	Val	Cys									
325					330					335														
Phe	Thr	Val	Phe	Gly	Gly	Leu	Met	Ala	Phe	Asn	Tyr	Asn	Arg	Ala	Phe									
340					345					350														
Gln	Val	Trp	Ala	Val	Pro	Leu	Leu	Leu	Val	Ala	Phe	Phe	Ala	Tyr	Leu									
355					360					365														
Val	Ala	His	Ser	Phe	Leu	Ser	Val	Phe	Glu	Thr	Val	Leu	Asp	Ala	Leu									
370					375					380														
Phe	Leu	Cys	Phe	Ala	Val	Asp	Leu	Glu	Thr	Asn	Asp	Gly	Ser	Ser	Glu									

77

385 390 395 400
Lys Pro Tyr Phe Met Asp Gln Glu Phe Leu Ser Phe Val Lys Arg Ser
 405 410 415
Asn Lys Leu Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg
 420 425 430
Asn Glu Glu Gly Thr Glu Leu Gln Ala Ile Val Arg
 435 440

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<210> 47
<211> 351
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(351)
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<400> 47

atg gcg gat gag gcg ttg ttt ttg ctt ctc cat aac gag atg gtg tct 48
Met Ala Asp Glu Ala Leu Phe Leu Leu Leu His Asn Glu Met Val Ser
1 5 10 15

gga gtg tac aag tcc gcg gag cag ggg gag gtg gaa aac gga cga tgt 96
Gly Val Tyr Lys Ser Ala Glu Gln Gly Glu Val Glu Asn Gly Arg Cys
20 25 30

att act aag ctg gaa aac atg ggg ttt cga gtg gga caa gga ttg ata 144
Ile Thr Lys Leu Glu Asn Met Gly Phe Arg Val Gly Gln Gly Leu Ile
35 40 45

gaa agg ttt aca aaa gat act gca agg ttc aag gat gag tta gat atc 192
Glu Arg Phe Thr Lys Asp Thr Ala Arg Phe Lys Asp Glu Leu Asp Ile
50 55 60

atg aag ttc att tgt aaa gat ttt tgg act acg gta ttc aag aaa caa 240
Met Lys Phe Ile Cys Lys Asp Phe Trp Thr Thr Val Phe Lys Lys Gln
65 70 75 80

atc gac aat cta agg aca aat cat cag ggc atc tat gta ctt cag gac 288
Ile Asp Asn Leu Arg Thr Asn His Gln Gly Ile Tyr Val Leu Gln Asp
85 90 95

aac aaa ttt cgc ctg ctt act cag atg tct gca gga aaa cag tat tta 336
Asn Lys Phe Arg Leu Leu Thr Gln Met Ser Ala Gly Lys Gln Tyr Leu

78

100

105

110

gaa cat gca tcc taa

351

Glu His Ala Ser *

115

<210> 48

<211> 116

<212> PRT

<213> Homo sapiens

<400> 48

Met Ala Asp Glu Ala Leu Phe Leu Leu Leu His Asn Glu Met Val Ser

1

5

10

15

Gly Val Tyr Lys Ser Ala Glu Gln Gly Glu Val Glu Asn Gly Arg Cys

20

25

30

Ile Thr Lys Leu Glu Asn Met Gly Phe Arg Val Gly Gln Gly Leu Ile

35

40

45

Glu Arg Phe Thr Lys Asp Thr Ala Arg Phe Lys Asp Glu Leu Asp Ile

50

55

60

Met Lys Phe Ile Cys Lys Asp Phe Trp Thr Thr Val Phe Lys Lys Gln

65

70

75

80

Ile Asp Asn Leu Arg Thr Asn His Gln Gly Ile Tyr Val Leu Gln Asp

85

90

95

Asn Lys Phe Arg Leu Leu Thr Gln Met Ser Ala Gly Lys Gln Tyr Leu

100

105

110

Glu His Ala Ser

115

<210> 49

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(516)

<400> 49

atg aag aaa tgt ctt ttg ccc gtt ttg att acg tgc atg caa aca gcg

48

Met Lys Lys Cys Leu Leu Pro Val Leu Ile Thr Cys Met Gln Thr Ala

1

5

10

15

79

att tgc aaa gac cgt atg atg atg atc atg atc tta ctg gtg aat tac	96
Ile Cys Lys Asp Arg Met Met Met Ile Met Ile Leu Leu Val Asn Tyr	
20 25 30	
cta cct gat gaa ttt ata gaa tgt gaa gac cca gtg gat cat gtt gga	144
Leu Pro Asp Glu Phe Ile Glu Cys Glu Asp Pro Val Asp His Val Gly	
35 40 45	
aat gca act gca tcc cag gaa ctt ggt tat ggt tgt ctc aag ttc ggc	192
Asn Ala Thr Ala Ser Gln Glu Leu Gly Tyr Gly Cys Leu Lys Phe Gly	
50 55 60	
ggt cag gcc tac agc gac gtg gaa cac act tca gtc cag tgc cat gcc	240
Gly Gln Ala Tyr Ser Asp Val Glu His Thr Ser Val Gln Cys His Ala	
65 70 75 80	
tta gat gga att gag tgt gcc agt cct agg acc ttt cta cga gaa aat	288
Leu Asp Gly Ile Glu Cys Ala Ser Pro Arg Thr Phe Leu Arg Glu Asn	
85 90 95	
aaa cct tgt ata aag tat acc gga cac tac ttc ata acc act tta ctc	336
Lys Pro Cys Ile Lys Tyr Thr Gly His Tyr Phe Ile Thr Thr Leu Leu	
100 105 110	
tac tcc ttc ttc ctg gga tgt ttt ggt gtg gat cga ttc tgt ttg gga	384
Tyr Ser Phe Phe Leu Gly Cys Phe Gly Val Asp Arg Phe Cys Leu Gly	
115 120 125	
cac act ggc act gca gta ggg aag ctg ttg acg ctt gga gga ctt ggg	432
His Thr Gly Thr Ala Val Gly Lys Leu Leu Thr Leu Gly Gly Leu Gly	
130 135 140	
att tgg tgg ttt gtt gac ctt att ttg cta att act gga ggg ctg atg	480
Ile Trp Trp Phe Val Asp Leu Ile Leu Leu Ile Thr Gly Gly Leu Met	
145 150 155 160	
cca agt gat ggc agc aac tgg tgc act gtt tac taa	516
Pro Ser Asp Gly Ser Asn Trp Cys Thr Val Tyr *	
165 170	

<210> 50

<211> 171

<212> PRT

80

<213> Homo sapiens

<400> 50

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Met Lys Lys Cys Leu Leu Pro Val Leu Ile Thr Cys Met Gln Thr Ala
 1           5           10           15
Ile Cys Lys Asp Arg Met Met Met Ile Met Ile Leu Leu Val Asn Tyr
      20           25           30
Leu Pro Asp Glu Phe Ile Glu Cys Glu Asp Pro Val Asp His Val Gly
      35           40           45
Asn Ala Thr Ala Ser Gln Glu Leu Gly Tyr Gly Cys Leu Lys Phe Gly
      50           55           60
Gly Gln Ala Tyr Ser Asp Val Glu His Thr Ser Val Gln Cys His Ala
      65           70           75           80
Leu Asp Gly Ile Glu Cys Ala Ser Pro Arg Thr Phe Leu Arg Glu Asn
      85           90           95
Lys Pro Cys Ile Lys Tyr Thr Gly His Tyr Phe Ile Thr Thr Leu Leu
      100          105          110
Tyr Ser Phe Phe Leu Gly Cys Phe Gly Val Asp Arg Phe Cys Leu Gly
      115          120          125
His Thr Gly Thr Ala Val Gly Lys Leu Leu Thr Leu Gly Gly Leu Gly
      130          135          140
Ile Trp Trp Phe Val Asp Leu Ile Leu Leu Ile Thr Gly Gly Leu Met
      145          150          155          160
Pro Ser Asp Gly Ser Asn Trp Cys Thr Val Tyr
      165          170

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<210> 51

<211> 870

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(870)

<400> 51

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atg ccc cta tta aaa ctt gta cat ggc tcc cca ttg gtt ttt gga gaa      48
Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
 1           5           10           15

aag ttc aag ctt ttt acc ttg gtg tct gcc tgt atc cca gtg ttc agg      96
Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
      20           25           30

```

81

ctg gct aga cgg cgg aag aag atc cta ttt tac tgt cac ttc cca gat	144
Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp	
35 40 45	
ctg ctt ctc acc aag aga gat tct ttt ctt aaa cga cta tac agg gcc	192
Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala	
50 55 60	
cca att gac tgg ata gag gaa tac acc aca ggc atg gca gac tgc atc	240
Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile	
65 70 75 80	
tta gtc aac agc cag ttc aca gct gct gtt ttt aag gaa aca ttc aag	288
Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys	
85 90 95	
tcc ctg tct cac ata gac cct gat gtc ctc tat cca tct cta aat gtc	336
Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val	
100 105 110	
acc agc ttt gac tca gtt gtt cct gaa aag ctg gat gac cta gtc ccc	384
Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro	
115 120 125	
aag ggg aaa aaa ttc ctg ctg ctc tcc atc aac aga tac gaa agg aag	432
Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys	
130 135 140	
aaa aat ctg act ttg gca ctg gaa gcc cta gta cag ctg cgt gga aga	480
Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg	
145 150 155 160	
ttg aca tcc caa gat tgg gag agg gtt cat ctg atc gtg gca ggt ggt	528
Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly	
165 170 175	
tat gac gag aga gtc ctg gag aat gtg gaa cat tat cag gaa ttg aag	576
Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys	
180 185 190	
aaa atg gtc caa cag tcc gac ctt ggc cag tat gtg acc ttc ttg agg	624
Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg	
195 200 205	

82

tct ttc tca gac aaa cag aaa atc tcc ctc ctc cac agc tgc acg tgt	672
Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys	
210 215 220	
gtg ctt tac aca cca agc aat gag cac ttt ggc att gtc cct ctg gaa	720
Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu	
225 230 235 240	
gcc atg tac atg cag tgc cca gtc att gct gtt aat tcg ggt gga ccc	768
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro	
245 250 255	
ttg gag tcc att gac cac agt gtc aca ggg ttt ctg tgt gag cct gac	816
Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp	
260 265 270	
ccg gtg cac ttc tca gaa gca ata gaa aag ttc atc cag aaa agt cat	864
Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Gln Lys Ser His	
275 280 285	
ccg tga	870
Pro *	

<210> 52
 <211> 289
 <212> PRT
 <213> Homo sapiens

<400> 52

Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu	
1 5 10 15	
Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg	
20 25 30	
Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp	
35 40 45	
Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala	
50 55 60	
Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile	
65 70 75 80	
Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys	
85 90 95	
Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val	

83

```

      100      105      110
Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro
      115      120      125
Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys
      130      135      140
Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg
145      150      155      160
Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly
      165      170      175
Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys
      180      185      190
Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg
      195      200      205
Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys
      210      215      220
Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
225      230      235      240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro
      245      250      255
Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp
      260      265      270
Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Gln Lys Ser His
      275      280      285
Pro

```

```

<210> 53
<211> 1041
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(1041)

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<221> misc_feature
<222> (1)...(1041)
<223> n = A,T,C or G

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<400> 53
atg cca cgg gtg ttt gtg ttt cgt gcc ctt ttg ttg gtc ctc atc ttt
Met Pro Arg Val Phe Val Phe Arg Ala Leu Leu Leu Val Leu Ile Phe
1          5          10          15

```

48

84

ctc tnt gtg gtt tcc tat tgg ctt ttt tac ggg gtc cgc att ttg gac	96
Leu Xaa Val Val Ser Tyr Trp Leu Phe Tyr Gly Val Arg Ile Leu Asp	
20 25 30	
tct cgg gac cgg aat tac cag ggc att gtg caa tat gca gtc tcc ctt	144
Ser Arg Asp Arg Asn Tyr Gln Gly Ile Val Gln Tyr Ala Val Ser Leu	
35 40 45	
gtg gat gcc ctc ctc ttc atc cat tac ctg gcc atc gtc ctg ctg gag	192
Val Asp Ala Leu Leu Phe Ile His Tyr Leu Ala Ile Val Leu Leu Glu	
50 55 60	
ctc agg cag ctg cag ccc atg ttc acg ctg cag gtg gtc cgc tcc acc	240
Leu Arg Gln Leu Gln Pro Met Phe Thr Leu Gln Val Val Arg Ser Thr	
65 70 75 80	
gat ggc gag tcc cgc ttc tac agc ctg gga cac ctg agt atc cag cga	288
Asp Gly Glu Ser Arg Phe Tyr Ser Leu Gly His Leu Ser Ile Gln Arg	
85 90 95	
gca gca ttg gtg gtc cta gaa aat tac tac aaa gat ttc acc atc tat	336
Ala Ala Leu Val Val Leu Glu Asn Tyr Tyr Lys Asp Phe Thr Ile Tyr	
100 105 110	
aac cca aac ctc cta aca gcc tcc aaa ttc cga gca gcc aag cat atg	384
Asn Pro Asn Leu Leu Thr Ala Ser Lys Phe Arg Ala Ala Lys His Met	
115 120 125	
gcc ggg ctg aaa gtc tac aat gta gat ggc ccc agt aac aat gcc act	432
Ala Gly Leu Lys Val Tyr Asn Val Asp Gly Pro Ser Asn Asn Ala Thr	
130 135 140	
ggc cag tcc cgg gcc atg att gct gca gct gct cgg cgc agg gac tca	480
Gly Gln Ser Arg Ala Met Ile Ala Ala Ala Arg Arg Arg Asp Ser	
145 150 155 160	
agc cac aac gag ttg tat tat gaa gag gcc gaa cat gaa cgg cga gta	528
Ser His Asn Glu Leu Tyr Tyr Glu Glu Ala Glu His Glu Arg Arg Val	
165 170 175	
aag aag cgg aaa gca agg ctg gtg gtt gca gtg gaa gag gcc ttc atc	576
Lys Lys Arg Lys Ala Arg Leu Val Val Ala Val Glu Glu Ala Phe Ile	
180 185 190	

85

cac att cag cgt ctc cag gct gag gag cag cag aaa gcc cca ggg gag	624
His Ile Gln Arg Leu Gln Ala Glu Glu Gln Gln Lys Ala Pro Gly Glu	
195 200 205	
gtg atg gac cct agg gag gcc gcc cag gcn att ttc ccc tcc atg gcc	672
Val Met Asp Pro Arg Glu Ala Ala Gln Xaa Ile Phe Pro Ser Met Ala	
210 215 220	
agg gct ctc cag aag tac ctg cgc atc acc cgg cag cag aac tac cac	720
Arg Ala Leu Gln Lys Tyr Leu Arg Ile Thr Arg Gln Gln Asn Tyr His	
225 230 235 240	
agc atg gag agc atc ctg cag cac ctg gcc ttc tgc atc acc aac ggc	768
Ser Met Glu Ser Ile Leu Gln His Leu Ala Phe Cys Ile Thr Asn Gly	
245 250 255	
atg acc ccc aag gcc ttc cta gaa cgg tac ctc agt gcg ggc ccc acc	816
Met Thr Pro Lys Ala Phe Leu Glu Arg Tyr Leu Ser Ala Gly Pro Thr	
260 265 270	
ctg caa tat gac aag gac cgc tgg ctc tct aca cag tgg agg ctt gtc	864
Leu Gln Tyr Asp Lys Asp Arg Trp Leu Ser Thr Gln Trp Arg Leu Val	
275 280 285	
agt gat gag gct gtg act aat gga tta cgg gat gga att gtg ttc gtc	912
Ser Asp Glu Ala Val Thr Asn Gly Leu Arg Asp Gly Ile Val Phe Val	
290 295 300	
ctt aag tgc ttg gac ttc agc ctc gta gtc aat gtg aag aaa att cca	960
Leu Lys Cys Leu Asp Phe Ser Leu Val Val Asn Val Lys Lys Ile Pro	
305 310 315 320	
ttc atc ata ctc tct gaa gag ttc ata gac ccc aaa tct cac aaa ttt	1008
Phe Ile Ile Leu Ser Glu Glu Phe Ile Asp Pro Lys Ser His Lys Phe	
325 330 335	
gtc ctt cgc tta cag tct gag aca tcc gtt taa	1041
Val Leu Arg Leu Gln Ser Glu Thr Ser Val *	
340 345	

<210> 54

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(346)

<223> Xaa = Any Amino Acid

<400> 54

Met	Pro	Arg	Val	Phe	Val	Phe	Arg	Ala	Leu	Leu	Leu	Val	Leu	Ile	Phe
1				5				10					15		
Leu	Xaa	Val	Val	Ser	Tyr	Trp	Leu	Phe	Tyr	Gly	Val	Arg	Ile	Leu	Asp
		20					25					30			
Ser	Arg	Asp	Arg	Asn	Tyr	Gln	Gly	Ile	Val	Gln	Tyr	Ala	Val	Ser	Leu
	35					40					45				
Val	Asp	Ala	Leu	Leu	Phe	Ile	His	Tyr	Leu	Ala	Ile	Val	Leu	Leu	Glu
	50				55					60					
Leu	Arg	Gln	Leu	Gln	Pro	Met	Phe	Thr	Leu	Gln	Val	Val	Arg	Ser	Thr
65				70					75					80	
Asp	Gly	Glu	Ser	Arg	Phe	Tyr	Ser	Leu	Gly	His	Leu	Ser	Ile	Gln	Arg
			85					90					95		
Ala	Ala	Leu	Val	Val	Leu	Glu	Asn	Tyr	Tyr	Lys	Asp	Phe	Thr	Ile	Tyr
	100						105					110			
Asn	Pro	Asn	Leu	Leu	Thr	Ala	Ser	Lys	Phe	Arg	Ala	Ala	Lys	His	Met
	115						120					125			
Ala	Gly	Leu	Lys	Val	Tyr	Asn	Val	Asp	Gly	Pro	Ser	Asn	Asn	Ala	Thr
	130				135					140					
Gly	Gln	Ser	Arg	Ala	Met	Ile	Ala	Ala	Ala	Ala	Arg	Arg	Arg	Asp	Ser
145				150					155					160	
Ser	His	Asn	Glu	Leu	Tyr	Tyr	Glu	Glu	Ala	Glu	His	Glu	Arg	Arg	Val
		165					170						175		
Lys	Lys	Arg	Lys	Ala	Arg	Leu	Val	Val	Ala	Val	Glu	Glu	Ala	Phe	Ile
	180						185						190		
His	Ile	Gln	Arg	Leu	Gln	Ala	Glu	Glu	Gln	Gln	Lys	Ala	Pro	Gly	Glu
	195				200							205			
Val	Met	Asp	Pro	Arg	Glu	Ala	Ala	Gln	Xaa	Ile	Phe	Pro	Ser	Met	Ala
	210				215						220				
Arg	Ala	Leu	Gln	Lys	Tyr	Leu	Arg	Ile	Thr	Arg	Gln	Gln	Asn	Tyr	His
225				230					235					240	
Ser	Met	Glu	Ser	Ile	Leu	Gln	His	Leu	Ala	Phe	Cys	Ile	Thr	Asn	Gly
		245						250					255		
Met	Thr	Pro	Lys	Ala	Phe	Leu	Glu	Arg	Tyr	Leu	Ser	Ala	Gly	Pro	Thr
	260						265					270			
Leu	Gln	Tyr	Asp	Lys	Asp	Arg	Trp	Leu	Ser	Thr	Gln	Trp	Arg	Leu	Val
	275						280					285			

87

Ser Asp Glu Ala Val Thr Asn Gly Leu Arg Asp Gly Ile Val Phe Val
 290 295 300
 Leu Lys Cys Leu Asp Phe Ser Leu Val Val Asn Val Lys Lys Ile Pro
 305 310 315 320
 Phe Ile Ile Leu Ser Glu Glu Phe Ile Asp Pro Lys Ser His Lys Phe
 325 330 335
 Val Leu Arg Leu Gln Ser Glu Thr Ser Val
 340 345

<210> 55
 <211> 195
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(195)

<400> 55
 atg gcc ttt ctc gcc aag aaa ggg tac cgg cat gac agc tca aca gca 48
 Met Ala Phe Leu Ala Lys Lys Gly Tyr Arg His Asp Ser Ser Thr Ala
 1 5 10 15
 gtg gcc ggc agc ccc cga ggc cat ggg cag agc cgc gag aca acc cag 96
 Val Ala Gly Ser Pro Arg Gly His Gly Gln Ser Arg Glu Thr Thr Gln
 20 25 30
 gaa cgc agg aag aag gaa gcc aac aag gcg aca aga gcc aac cac aac 144
 Glu Arg Arg Lys Lys Glu Ala Asn Lys Ala Thr Arg Ala Asn His Asn
 35 40 45
 cgg aga acc atg gcc gac cgc aag agg agc aaa ggc atg atc cca tcc 192
 Arg Arg Thr Met Ala Asp Arg Lys Arg Ser Lys Gly Met Ile Pro Ser
 50 55 60
 tga 195
 *

<210> 56
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 56

Met	Ala	Phe	Leu	Ala	Lys	Lys	Gly	Tyr	Arg	His	Asp	Ser	Ser	Thr	Ala
1				5				10						15	
Val	Ala	Gly	Ser	Pro	Arg	Gly	His	Gly	Gln	Ser	Arg	Glu	Thr	Thr	Gln
			20					25					30		
Glu	Arg	Arg	Lys	Lys	Glu	Ala	Asn	Lys	Ala	Thr	Arg	Ala	Asn	His	Asn
		35					40					45			
Arg	Arg	Thr	Met	Ala	Asp	Arg	Lys	Arg	Ser	Lys	Gly	Met	Ile	Pro	Ser
50						55					60				

<210> 57

<211> 1011

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1011)

<400> 57

atg	ggt	aca	tct	gat	tcc	cac	cac	gcg	ggg	ctc	agc	tta	gtt	agc	agg	48
Met	Gly	Thr	Ser	Asp	Ser	His	His	Ala	Gly	Leu	Ser	Leu	Val	Ser	Arg	
1				5				10					15			
aga	cct	tca	ggt	ggt	gct	gct	ggg	gaa	cgg	gag	ctg	gat	gag	gtt	gat	96
Arg	Pro	Ser	Gly	Gly	Ala	Ala	Gly	Glu	Arg	Glu	Leu	Asp	Glu	Val	Asp	
			20					25					30			
atg	tca	gat	ctc	tct	cca	gaa	gag	caa	tgg	agg	gtc	gag	cac	gca	cgc	144
Met	Ser	Asp	Leu	Ser	Pro	Glu	Glu	Gln	Trp	Arg	Val	Glu	His	Ala	Arg	
		35					40					45				
atg	cat	gcc	aag	cac	cgt	ggc	cat	gaa	gct	atg	cat	gct	gaa	atg	gtc	192
Met	His	Ala	Lys	His	Arg	Gly	His	Glu	Ala	Met	His	Ala	Glu	Met	Val	
	50					55				60						
ctc	atc	ctc	atc	gca	acc	ttg	gtg	gtg	gcc	cag	ctg	ctc	ctg	gtg	cag	240
Leu	Ile	Leu	Ile	Ala	Thr	Leu	Val	Val	Ala	Gln	Leu	Leu	Leu	Val	Gln	
	65				70				75						80	
tgg	aag	cag	agg	cac	cca	cgc	tcc	tac	aat	atg	gtg	acc	ctc	ttt	cag	288
Trp	Lys	Gln	Arg	His	Pro	Arg	Ser	Tyr	Asn	Met	Val	Thr	Leu	Phe	Gln	
			85					90							95	

atg tgg gtt gtt ccc ctc tat ttc aca gtg aag ctg cac tgg tgg agg	336
Met Trp Val Val Pro Leu Tyr Phe Thr Val Lys Leu His Trp Trp Arg	
100 105 110	
ttc cta gtg atc tgg atc ttg ttc tct gct gtc aca gcc ttt gtt acc	384
Phe Leu Val Ile Trp Ile Leu Phe Ser Ala Val Thr Ala Phe Val Thr	
115 120 125	
ttc cga gcc acc cga aaa cct cta gta cag aca acc cca agg ttg gtt	432
Phe Arg Ala Thr Arg Lys Pro Leu Val Gln Thr Thr Pro Arg Leu Val	
130 135 140	
tat aag tgg ttc ctg cta atc tat aaa atc agc tat gcc act ggc att	480
Tyr Lys Trp Phe Leu Leu Ile Tyr Lys Ile Ser Tyr Ala Thr Gly Ile	
145 150 155 160	
gtt ggc tac atg gct gtc atg ttt acc ctc ttt ggt ctt aac tta tta	528
Val Gly Tyr Met Ala Val Met Phe Thr Leu Phe Gly Leu Asn Leu Leu	
165 170 175	
ttc aag atc aaa cca gaa gat gcc atg gac ttt ggc atc tcc ctt ctc	576
Phe Lys Ile Lys Pro Glu Asp Ala Met Asp Phe Gly Ile Ser Leu Leu	
180 185 190	
ttc tat ggc ctc tac tat gga gtt ctg gaa cgg gac ttt gca gaa atg	624
Phe Tyr Gly Leu Tyr Tyr Gly Val Leu Glu Arg Asp Phe Ala Glu Met	
195 200 205	
tgt gca gac tac atg gca tct acc ata ggg ttc tac agc gag tcg ggc	672
Cys Ala Asp Tyr Met Ala Ser Thr Ile Gly Phe Tyr Ser Glu Ser Gly	
210 215 220	
atg cct acc aaa cat ctt tca gac agt gtg tgt gct gtg tgt ggg cag	720
Met Pro Thr Lys His Leu Ser Asp Ser Val Cys Ala Val Cys Gly Gln	
225 230 235 240	
cag atc ttt gtg gac gtc agt gaa gag ggg atc att gag aac acg tat	768
Gln Ile Phe Val Asp Val Ser Glu Glu Gly Ile Ile Glu Asn Thr Tyr	
245 250 255	
agg ctg tcc tgc aat cat gtc ttc cac gag ttc tgc atc cgt ggc tgg	816
Arg Leu Ser Cys Asn His Val Phe His Glu Phe Cys Ile Arg Gly Trp	
260 265 270	

90

tgc atc gtg gga aag aag caa acg tgt ccc tac tgc aaa gag aag gta	864
Cys Ile Val Gly Lys Lys Gln Thr Cys Pro Tyr Cys Lys Glu Lys Val	
275 280 285	
gac ctc aag agg atg ttc agc aat ccc tgg gag agg cct cac gtc atg	912
Asp Leu Lys Arg Met Phe Ser Asn Pro Trp Glu Arg Pro His Val Met	
290 295 300	
tat ggg caa ctg ctg gac tgg ctt cga tac ttg gta gcc tgg cag cct	960
Tyr Gly Gln Leu Leu Asp Trp Leu Arg Tyr Leu Val Ala Trp Gln Pro	
305 310 315 320	
gtc atc att ggt gta gtc caa ggc atc aac tac atc ctg ggc ctg gaa	1008
Val Ile Ile Gly Val Val Gln Gly Ile Asn Tyr Ile Leu Gly Leu Glu	
325 330 335	
tag	1011
*	

<210> 58
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 58

Met Gly Thr Ser Asp Ser His His Ala Gly Leu Ser Leu Val Ser Arg	
1 5 10 15	
Arg Pro Ser Gly Gly Ala Ala Gly Glu Arg Glu Leu Asp Glu Val Asp	
20 25 30	
Met Ser Asp Leu Ser Pro Glu Glu Gln Trp Arg Val Glu His Ala Arg	
35 40 45	
Met His Ala Lys His Arg Gly His Glu Ala Met His Ala Glu Met Val	
50 55 60	
Leu Ile Leu Ile Ala Thr Leu Val Val Ala Gln Leu Leu Leu Val Gln	
65 70 75 80	
Trp Lys Gln Arg His Pro Arg Ser Tyr Asn Met Val Thr Leu Phe Gln	
85 90 95	
Met Trp Val Val Pro Leu Tyr Phe Thr Val Lys Leu His Trp Trp Arg	
100 105 110	
Phe Leu Val Ile Trp Ile Leu Phe Ser Ala Val Thr Ala Phe Val Thr	
115 120 125	

91

Phe Arg Ala Thr Arg Lys Pro Leu Val Gln Thr Thr Pro Arg Leu Val
 130 135 140
 Tyr Lys Trp Phe Leu Leu Ile Tyr Lys Ile Ser Tyr Ala Thr Gly Ile
 145 150 155 160
 Val Gly Tyr Met Ala Val Met Phe Thr Leu Phe Gly Leu Asn Leu Leu
 165 170 175
 Phe Lys Ile Lys Pro Glu Asp Ala Met Asp Phe Gly Ile Ser Leu Leu
 180 185 190
 Phe Tyr Gly Leu Tyr Tyr Gly Val Leu Glu Arg Asp Phe Ala Glu Met
 195 200 205
 Cys Ala Asp Tyr Met Ala Ser Thr Ile Gly Phe Tyr Ser Glu Ser Gly
 210 215 220
 Met Pro Thr Lys His Leu Ser Asp Ser Val Cys Ala Val Cys Gly Gln
 225 230 235 240
 Gln Ile Phe Val Asp Val Ser Glu Glu Gly Ile Ile Glu Asn Thr Tyr
 245 250 255
 Arg Leu Ser Cys Asn His Val Phe His Glu Phe Cys Ile Arg Gly Trp
 260 265 270
 Cys Ile Val Gly Lys Lys Gln Thr Cys Pro Tyr Cys Lys Glu Lys Val
 275 280 285
 Asp Leu Lys Arg Met Phe Ser Asn Pro Trp Glu Arg Pro His Val Met
 290 295 300
 Tyr Gly Gln Leu Leu Asp Trp Leu Arg Tyr Leu Val Ala Trp Gln Pro
 305 310 315 320
 Val Ile Ile Gly Val Val Gln Gly Ile Asn Tyr Ile Leu Gly Leu Glu
 325 330 335

<210> 59
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(393)

<221> misc_feature
 <222> (1)...(393)
 <223> n = A,T,C or G

<400> 59

atg ctg gac ttg cag aag cag ctg ggc aga tnc cag ggn gcc ana ttt
 Met Leu Asp Leu Gln Lys Gln Leu Gly Arg Xaa Gln Xaa Ala Xaa Phe
 1 5 10 15

48

92

ccc ggc acc ttc gtg ggc acc aca gag ccc gcc tcc cca ccc ctg agc	96
Pro Gly Thr Phe Val Gly Thr Thr Glu Pro Ala Ser Pro Pro Leu Ser	
20 25 30	
agc acc tca ccc acc act gct gcg gcc act atg cct gtg gtg ccc tct	144
Ser Thr Ser Pro Thr Thr Ala Ala Ala Thr Met Pro Val Val Pro Ser	
35 40 45	
gtg gcc agc ctg gcc cct ccg ggg gag gcc tcg ctc tgc ctg gaa gag	192
Val Ala Ser Leu Ala Pro Pro Gly Glu Ala Ser Leu Cys Leu Glu Glu	
50 55 60	
gtg gcc ccc cct gcc agt ggg acc cgc aaa gct cgg gtg ctc tat gac	240
Val Ala Pro Pro Ala Ser Gly Thr Arg Lys Ala Arg Val Leu Tyr Asp	
65 70 75 80	
tac gag gca gcc gac agc agt gag ctg gcc ctg ctg gct gat gag ctc	288
Tyr Glu Ala Ala Asp Ser Ser Glu Leu Ala Leu Leu Ala Asp Glu Leu	
85 90 95	
atc act gtc tac agc ctg cct ggc atg gac cct gac tgg ctc att ggc	336
Ile Thr Val Tyr Ser Leu Pro Gly Met Asp Pro Asp Trp Leu Ile Gly	
100 105 110	
gag aga ggc aac aag aag ggc aag gtc cct gtc acc tac ttg gaa ctg	384
Glu Arg Gly Asn Lys Lys Gly Lys Val Pro Val Thr Tyr Leu Glu Leu	
115 120 125	
ctc agc tag	393
Leu Ser *	
130	

<210> 60

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(130)

<223> Xaa = Any Amino Acid

<400> 60

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Met Leu Asp Leu Gln Lys Gln Leu Gly Arg Xaa Gln Xaa Ala Xaa Phe
 1             5             10             15
Pro Gly Thr Phe Val Gly Thr Thr Glu Pro Ala Ser Pro Pro Leu Ser
          20             25             30
Ser Thr Ser Pro Thr Thr Ala Ala Ala Thr Met Pro Val Val Pro Ser
      35             40             45
Val Ala Ser Leu Ala Pro Pro Gly Glu Ala Ser Leu Cys Leu Glu Glu
      50             55             60
Val Ala Pro Pro Ala Ser Gly Thr Arg Lys Ala Arg Val Leu Tyr Asp
65             70             75             80
Tyr Glu Ala Ala Asp Ser Ser Glu Leu Ala Leu Leu Ala Asp Glu Leu
          85             90             95
Ile Thr Val Tyr Ser Leu Pro Gly Met Asp Pro Asp Trp Leu Ile Gly
      100             105             110
Glu Arg Gly Asn Lys Lys Gly Lys Val Pro Val Thr Tyr Leu Glu Leu
      115             120             125
Leu Ser
      130

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<210> 61

<211> 1383

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1383)

<221> misc_feature

<222> (1)...(1383)

<223> n = A,T,C or G

<400> 61

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atg gcc ccg ggt cgc gcg gtg gcc ggg ctc ctg ttg ctg gcg gcc gcc      48
Met Ala Pro Gly Arg Ala Val Ala Gly Leu Leu Leu Leu Ala Ala Ala
 1             5             10             15

gnc ctc gga gga gtg gcg gag ggg cca ggg cta gcc ttc agc gag gat      96
Xaa Leu Gly Gly Val Ala Glu Gly Pro Gly Leu Ala Phe Ser Glu Asp
          20             25             30

gtg ctg agc gtg ttc ggc gcg aat ctg agc ctg tcg gcg gcg cag ctc      144
Val Leu Ser Val Phe Gly Ala Asn Leu Ser Leu Ser Ala Ala Gln Leu

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35	40	45	
cag cac ttg ctg gag cag atg gga gcc gcc tcc cgc gtg ggc gtc ccg Gln His Leu Leu Glu Gln Met Gly Ala Ala Ser Arg Val Gly Val Pro 50 55 60			192
gag cct ggc cag ctg cac ttc aac cag tgt tta act gct gaa gag atc Glu Pro Gly Gln Leu His Phe Asn Gln Cys Leu Thr Ala Glu Glu Ile 65 70 75 80			240
ttt tcc ctt cat ggc ttt tca aat gct acc caa ata acc agc tcc aaa Phe Ser Leu His Gly Phe Ser Asn Ala Thr Gln Ile Thr Ser Ser Lys 85 90 95			288
ttc tct gtc atc tgt cca gca gtc tta cag caa ttg aac ttt cac cca Phe Ser Val Ile Cys Pro Ala Val Leu Gln Gln Leu Asn Phe His Pro 100 105 110			336
tgt gag gat cgg ccc aag cac aaa aca aga cca agt cat tca gaa gtt Cys Glu Asp Arg Pro Lys His Lys Thr Arg Pro Ser His Ser Glu Val 115 120 125			384
tgg gga tat gga ttc ctg tca gtg acg att att aat ctg gca tct ctc Trp Gly Tyr Gly Phe Leu Ser Val Thr Ile Ile Asn Leu Ala Ser Leu 130 135 140			432
ctc gga ttg att ttg act cca ctg ata aag aaa tct tat ttc cca aag Leu Gly Leu Ile Leu Thr Pro Leu Ile Lys Lys Ser Tyr Phe Pro Lys 145 150 155 160			480
att ttg acc ttt ttt gtg ggg ctg gct att ggg act ctt ttt tca aat Ile Leu Thr Phe Phe Val Gly Leu Ala Ile Gly Thr Leu Phe Ser Asn 165 170 175			528
gca att ttc caa ctt att cca gag gca ttt gga ttt gat ccc aaa gtc Ala Ile Phe Gln Leu Ile Pro Glu Ala Phe Gly Phe Asp Pro Lys Val 180 185 190			576
gac agt tat gtt gag aag gca gtt gct gtg ttt ggt gga ttt tac cta Asp Ser Tyr Val Glu Lys Ala Val Ala Val Phe Gly Gly Phe Tyr Leu 195 200 205			624
ctt ttc ttt ttt gaa aga atg cta aag atg tta tta aag aca tat ggt Leu Phe Phe Phe Glu Arg Met Leu Lys Met Leu Leu Lys Thr Tyr Gly			672

210	215	220	
cag aat ggt cat acc cac ttt gga aat gat aac ttt ggt cct caa gaa			720
Gln Asn Gly His Thr His Phe Gly Asn Asp Asn Phe Gly Pro Gln Glu			
225	230	235	240
aaa act cat caa cct aaa gca tta cct gcc atc aat ggt gtg aca tgc			768
Lys Thr His Gln Pro Lys Ala Leu Pro Ala Ile Asn Gly Val Thr Cys			
	245	250	255
tat gca aat cct gct gtc aca gaa gct aat gga cat atc cat ttt gat			816
Tyr Ala Asn Pro Ala Val Thr Glu Ala Asn Gly His Ile His Phe Asp			
	260	265	270
aat gtc agt gtg gta tct cta cag gat gga aaa aaa gag cca agt tca			864
Asn Val Ser Val Val Ser Leu Gln Asp Gly Lys Lys Glu Pro Ser Ser			
	275	280	285
tgt acc tgt ttg aag ggg ccc aaa ctg tca gaa ata ggg acg att gcc			912
Cys Thr Cys Leu Lys Gly Pro Lys Leu Ser Glu Ile Gly Thr Ile Ala			
	290	295	300
tgg atg ata acg ctc tgc gat gcc ctc cac aat ttc atc gat ggc ctg			960
Trp Met Ile Thr Leu Cys Asp Ala Leu His Asn Phe Ile Asp Gly Leu			
	305	310	315
gcg att ggg gct tcc tgc acc ttg tct ctc ctt cag gga ctc agt act			1008
Ala Ile Gly Ala Ser Cys Thr Leu Ser Leu Leu Gln Gly Leu Ser Thr			
	325	330	335
tcc ata gca atc cta tgt gag gag ttt ccc cac gag tta gga gac ttt			1056
Ser Ile Ala Ile Leu Cys Glu Glu Phe Pro His Glu Leu Gly Asp Phe			
	340	345	350
gtg atc cta ctc aat gca ggg atg agc act cga caa gcc ttg cta ttc			1104
Val Ile Leu Leu Asn Ala Gly Met Ser Thr Arg Gln Ala Leu Leu Phe			
	355	360	365
aac ttc ctt tct gca tgt tcc tgc tat gtt ggg cta gct ttt ggc att			1152
Asn Phe Leu Ser Ala Cys Ser Cys Tyr Val Gly Leu Ala Phe Gly Ile			
	370	375	380
ttg gtg ggc aac aat ttc gct cca aat att ata ttt gca ctt gct gga			1200
Leu Val Gly Asn Asn Phe Ala Pro Asn Ile Ile Phe Ala Leu Ala Gly			

96

385	390	395	400	
ggc atg ttc ctc tat att tct ctg gca gat atg ttt cca gag atg aat	1248			
Gly Met Phe Leu Tyr Ile Ser Leu Ala Asp Met Phe Pro Glu Met Asn				
405	410	415		
gat atg ctg aga gaa aag gta act gga aga aaa acc gat ttc acc ttc	1296			
Asp Met Leu Arg Glu Lys Val Thr Gly Arg Lys Thr Asp Phe Thr Phe				
420	425	430		
ttc atg att cag aat gct gga atg tta act gga ttc aca gcc att cta	1344			
Phe Met Ile Gln Asn Ala Gly Met Leu Thr Gly Phe Thr Ala Ile Leu				
435	440	445		
ctc att acc ttg tat gca gga gaa atc gaa ttg gag taa	1383			
Leu Ile Thr Leu Tyr Ala Gly Glu Ile Glu Leu Glu *				
450	455	460		

<210> 62
 <211> 460
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(460)
 <223> Xaa = Any Amino Acid

<400> 62

Met	Ala	Pro	Gly	Arg	Ala	Val	Ala	Gly	Leu	Leu	Leu	Leu	Ala	Ala	Ala
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Xaa	Leu	Gly	Gly	Val	Ala	Glu	Gly	Pro	Gly	Leu	Ala	Phe	Ser	Glu	Asp
		20						25					30		
Val	Leu	Ser	Val	Phe	Gly	Ala	Asn	Leu	Ser	Leu	Ser	Ala	Ala	Gln	Leu
	35						40					45			
Gln	His	Leu	Leu	Glu	Gln	Met	Gly	Ala	Ala	Ser	Arg	Val	Gly	Val	Pro
	50					55					60				
Glu	Pro	Gly	Gln	Leu	His	Phe	Asn	Gln	Cys	Leu	Thr	Ala	Glu	Glu	Ile
65				70					75					80	
Phe	Ser	Leu	His	Gly	Phe	Ser	Asn	Ala	Thr	Gln	Ile	Thr	Ser	Ser	Lys
			85					90					95		
Phe	Ser	Val	Ile	Cys	Pro	Ala	Val	Leu	Gln	Gln	Leu	Asn	Phe	His	Pro
		100						105					110		

Cys	Glu	Asp	Arg	Pro	Lys	His	Lys	Thr	Arg	Pro	Ser	His	Ser	Glu	Val
		115					120					125			
Trp	Gly	Tyr	Gly	Phe	Leu	Ser	Val	Thr	Ile	Ile	Asn	Leu	Ala	Ser	Leu
	130					135					140				
Leu	Gly	Leu	Ile	Leu	Thr	Pro	Leu	Ile	Lys	Lys	Ser	Tyr	Phe	Pro	Lys
145					150					155					160
Ile	Leu	Thr	Phe	Phe	Val	Gly	Leu	Ala	Ile	Gly	Thr	Leu	Phe	Ser	Asn
				165					170						175
Ala	Ile	Phe	Gln	Leu	Ile	Pro	Glu	Ala	Phe	Gly	Phe	Asp	Pro	Lys	Val
			180					185					190		
Asp	Ser	Tyr	Val	Glu	Lys	Ala	Val	Ala	Val	Phe	Gly	Gly	Phe	Tyr	Leu
		195					200					205			
Leu	Phe	Phe	Phe	Glu	Arg	Met	Leu	Lys	Met	Leu	Leu	Lys	Thr	Tyr	Gly
	210					215						220			
Gln	Asn	Gly	His	Thr	His	Phe	Gly	Asn	Asp	Asn	Phe	Gly	Pro	Gln	Glu
225					230					235					240
Lys	Thr	His	Gln	Pro	Lys	Ala	Leu	Pro	Ala	Ile	Asn	Gly	Val	Thr	Cys
				245					250					255	
Tyr	Ala	Asn	Pro	Ala	Val	Thr	Glu	Ala	Asn	Gly	His	Ile	His	Phe	Asp
			260					265					270		
Asn	Val	Ser	Val	Val	Ser	Leu	Gln	Asp	Gly	Lys	Lys	Glu	Pro	Ser	Ser
		275					280					285			
Cys	Thr	Cys	Leu	Lys	Gly	Pro	Lys	Leu	Ser	Glu	Ile	Gly	Thr	Ile	Ala
	290					295					300				
Trp	Met	Ile	Thr	Leu	Cys	Asp	Ala	Leu	His	Asn	Phe	Ile	Asp	Gly	Leu
305					310					315					320
Ala	Ile	Gly	Ala	Ser	Cys	Thr	Leu	Ser	Leu	Leu	Gln	Gly	Leu	Ser	Thr
				325					330					335	
Ser	Ile	Ala	Ile	Leu	Cys	Glu	Glu	Phe	Pro	His	Glu	Leu	Gly	Asp	Phe
			340					345					350		
Val	Ile	Leu	Leu	Asn	Ala	Gly	Met	Ser	Thr	Arg	Gln	Ala	Leu	Leu	Phe
	355						360				365				
Asn	Phe	Leu	Ser	Ala	Cys	Ser	Cys	Tyr	Val	Gly	Leu	Ala	Phe	Gly	Ile
	370					375					380				
Leu	Val	Gly	Asn	Asn	Phe	Ala	Pro	Asn	Ile	Ile	Phe	Ala	Leu	Ala	Gly
385					390					395					400
Gly	Met	Phe	Leu	Tyr	Ile	Ser	Leu	Ala	Asp	Met	Phe	Pro	Glu	Met	Asn
				405					410					415	
Asp	Met	Leu	Arg	Glu	Lys	Val	Thr	Gly	Arg	Lys	Thr	Asp	Phe	Thr	Phe
			420					425				430			
Phe	Met	Ile	Gln	Asn	Ala	Gly	Met	Leu	Thr	Gly	Phe	Thr	Ala	Ile	Leu
	435						440					445			
Leu	Ile	Thr	Leu	Tyr	Ala	Gly	Glu	Ile	Glu	Leu	Glu				
	450					455					460				

<210> 63
 <211> 378
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(378)

<400> 63
 atg ctg aca gaa gtc atg gag gtc tgg cat ggc tta gtg atc gcg gtg 48
 Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
 1 5 10 15

gtg tcc ctc ttc ctg cag gcc tgc ttc ctc acc gcc atc aac tac ctg 96
 Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
 20 25 30

ctc agc agg cac atg gcc cac aag agt gaa cag ata ctg aaa gcg gcc 144
 Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala
 35 40 45

agt ctc cag gtt ccc agg ccc agc cct ggc cac cat cat cca cct gct 192
 Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala
 50 55 60

gtc aaa gag atg aag gag act cag aca gag aga gac atc cca atg tct 240
 Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser
 65 70 75 80

gat tcc ctt tac agg cat gac agc gac aca ccc tca gat agc ttg gat 288
 Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp
 85 90 95

agc tcc tgc agt tcg cct cct gcc tgc cag gcc aca gag gat gtg gat 336
 Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp
 100 105 110

tac aca caa gtc gtc ttt tct gac cct gga gaa cta aaa tga 378
 Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys *
 115 120 125

99

<210> 64
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
 1 5 10 15
 Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
 20 25 30
 Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala
 35 40 45
 Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala
 50 55 60
 Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser
 65 70 75 80
 Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp
 85 90 95
 Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp
 100 105 110
 Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys
 115 120 125

<210> 65
 <211> 519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(519)

<400> 65
 atg ctg aca gaa gtc atg gag gtc tgg cat ggc tta gtg atc gcg gtg 48
 Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
 1 5 10 15
 gtg tcc ctc ttc ctg cag gcc tgc ttc ctc acc gcc atc aac tac ctg 96
 Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
 20 25 30
 ctc agc agg cac atg gcc cac aag agt gaa cag ata ctg aaa gcg gcc 144
 Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala
 35 40 45

100

agt ctc cag gtt ccc agg ccc agc cct ggc cac cat cat cca cct gct 192
 Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala
 50 55 60

gtc aaa gag atg aag gag act cag aca gag aga gac atc cca atg tct 240
 Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser
 65 70 75 80

gat tcc ctt tac agg cat gac agc gac aca ccc tca gat agc ttg gat 288
 Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp
 85 90 95

agc tcc tgc agt tcg cct cct gcc tgc cag gcc aca gag gat gtg gat 336
 Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp
 100 105 110

tac aca caa gtc gtc ttt tct gac cct gga gaa cta aaa aat gac tcc 384
 Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys Asn Asp Ser
 115 120 125

ccg ctg gac tat gag aac ata aag gaa atc aca gat tat gtc aat gtc 432
 Pro Leu Asp Tyr Glu Asn Ile Lys Glu Ile Thr Asp Tyr Val Asn Val
 130 135 140

aat cca gaa aga cac aag ccc agt ttc tgg tat ttt gtc aac cct gct 480
 Asn Pro Glu Arg His Lys Pro Ser Phe Trp Tyr Phe Val Asn Pro Ala
 145 150 155 160

ctg tct gag cca gcg gaa tat gat caa gtg gcc atg tga 519
 Leu Ser Glu Pro Ala Glu Tyr Asp Gln Val Ala Met *
 165 170

<210> 66

<211> 172

<212> PRT

<213> Homo sapiens

<400> 66

Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
 1 5 10 15
 Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
 20 25 30

101

Leu	Ser	Arg	His	Met	Ala	His	Lys	Ser	Glu	Gln	Ile	Leu	Lys	Ala	Ala
		35					40					45			
Ser	Leu	Gln	Val	Pro	Arg	Pro	Ser	Pro	Gly	His	His	His	Pro	Pro	Ala
	50					55					60				
Val	Lys	Glu	Met	Lys	Glu	Thr	Gln	Thr	Glu	Arg	Asp	Ile	Pro	Met	Ser
65					70					75					80
Asp	Ser	Leu	Tyr	Arg	His	Asp	Ser	Asp	Thr	Pro	Ser	Asp	Ser	Leu	Asp
				85					90					95	
Ser	Ser	Cys	Ser	Ser	Pro	Pro	Ala	Cys	Gln	Ala	Thr	Glu	Asp	Val	Asp
			100					105					110		
Tyr	Thr	Gln	Val	Val	Phe	Ser	Asp	Pro	Gly	Glu	Leu	Lys	Asn	Asp	Ser
		115					120					125			
Pro	Leu	Asp	Tyr	Glu	Asn	Ile	Lys	Glu	Ile	Thr	Asp	Tyr	Val	Asn	Val
		130				135					140				
Asn	Pro	Glu	Arg	His	Lys	Pro	Ser	Phe	Trp	Tyr	Phe	Val	Asn	Pro	Ala
145					150					155					160
Leu	Ser	Glu	Pro	Ala	Glu	Tyr	Asp	Gln	Val	Ala	Met				
				165				170							

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<210> 67
<211> 393
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(393)

<400> 67																
atg	caa	gca	gag	gct	ggg	gac	ctc	agc	aca	gcc	ctg	gag	agg	ttt	ggc	48
Met	Gln	Ala	Glu	Ala	Gly	Asp	Leu	Ser	Thr	Ala	Leu	Glu	Arg	Phe	Gly	
1		5				10				15						
caa	gcc	atc	tgc	ctg	ctg	cct	gag	agg	gct	tca	gcc	tac	aac	aac	cgt	96
Gln	Ala	Ile	Cys	Leu	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Tyr	Asn	Asn	Arg	
			20		25				30							
gcc	cag	gcc	cgg	cga	ctc	cag	gga	gac	gtg	gca	ggc	gcc	ctg	gag	gat	144
Ala	Gln	Ala	Arg	Arg	Leu	Gln	Gly	Asp	Val	Ala	Gly	Ala	Leu	Glu	Asp	
35			40				45									
ctg	gaa	cgc	gcg	gtg	gag	ctg	agc	ggc	ggc	cgg	ggc	cgc	gcc	gcc	cgc	192
Leu	Glu	Arg	Ala	Val	Glu	Leu	Ser	Gly	Gly	Arg	Gly	Arg	Ala	Ala	Arg	
50		55				60										

102

cag agc ttt gtg cag cgc gga ctc ctg gcg cgg ctg cag ggc cga gac 240
 Gln Ser Phe Val Gln Arg Gly Leu Leu Ala Arg Leu Gln Gly Arg Asp
 65 70 75 80

gac gac gcc cgc agg gac ttc gag agg gcg gca cgg ctg ggc agc ccc 288
 Asp Asp Ala Arg Arg Asp Phe Glu Arg Ala Ala Arg Leu Gly Ser Pro
 85 90 95

ttc gcg cgg cgc cag ctg gtg ctg ctc aac ccc tac gcc gcg ctg tgc 336
 Phe Ala Arg Arg Gln Leu Val Leu Leu Asn Pro Tyr Ala Ala Leu Cys
 100 105 110

aac cgc atg ctg gcc gac atg atg ggg cag ctg cgc cgc ccc cgt gac 384
 Asn Arg Met Leu Ala Asp Met Met Gly Gln Leu Arg Arg Pro Arg Asp
 115 120 125

agc cgc tga 393
 Ser Arg *
 130

<210> 68
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Gln Ala Glu Ala Gly Asp Leu Ser Thr Ala Leu Glu Arg Phe Gly
 1 5 10 15
 Gln Ala Ile Cys Leu Leu Pro Glu Arg Ala Ser Ala Tyr Asn Asn Arg
 20 25 30
 Ala Gln Ala Arg Arg Leu Gln Gly Asp Val Ala Gly Ala Leu Glu Asp
 35 40 45
 Leu Glu Arg Ala Val Glu Leu Ser Gly Gly Arg Gly Arg Ala Ala Arg
 50 55 60
 Gln Ser Phe Val Gln Arg Gly Leu Leu Ala Arg Leu Gln Gly Arg Asp
 65 70 75 80
 Asp Asp Ala Arg Arg Asp Phe Glu Arg Ala Ala Arg Leu Gly Ser Pro
 85 90 95
 Phe Ala Arg Arg Gln Leu Val Leu Leu Asn Pro Tyr Ala Ala Leu Cys
 100 105 110
 Asn Arg Met Leu Ala Asp Met Met Gly Gln Leu Arg Arg Pro Arg Asp
 115 120 125

103

Ser Arg
130

<210> 69
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(378)

<400> 69

atg agg cca cga tgc tgc atc ttg gct ctt gtc tgc tgg ata aca gtc 48
Met Arg Pro Arg Cys Cys Ile Leu Ala Leu Val Cys Trp Ile Thr Val
1 5 10 15

ttc ctc ctc cag tgt tca aaa gga act aca gac gct cct gtt ggc tca 96
Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val Gly Ser
20 25 30

gga ctg tgg ctg tgc cag ccg aca ccc agg tgt ggg aac aag atc tac 144
Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn Lys Ile Tyr
35 40 45

aac cct tca gag cag tgc tgt tat gat gat gcc atc tta tcc tta aag 192
Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile Leu Ser Leu Lys
50 55 60

gag acc cgc cgc tgt ggc tcc acc tgc acc ttc tgg ccc tgc ttt gag 240
Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe Trp Pro Cys Phe Glu
65 70 75 80

ctc tgc tgt ccc gag tct ttt ggc ccc cag cag aag ttt ctt gtg aag 288
Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln Gln Lys Phe Leu Val Lys
85 90 95

ttg agg gtt ctg ggt atg aag tct cag tgt cac tta tct ccc atc tcc 336
Leu Arg Val Leu Gly Met Lys Ser Gln Cys His Leu Ser Pro Ile Ser
100 105 110

cgg agc tgt acc agg aac agg agg cac gtc ctg tac cca taa 378
Arg Ser Cys Thr Arg Asn Arg Arg His Val Leu Tyr Pro *
115 120 125

104

<210> 70
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Arg Pro Arg Cys Cys Ile Leu Ala Leu Val Cys Trp Ile Thr Val
 1 5 10 15
 Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val Gly Ser
 20 25 30
 Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn Lys Ile Tyr
 35 40 45
 Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile Leu Ser Leu Lys
 50 55 60
 Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe Trp Pro Cys Phe Glu
 65 70 75 80
 Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln Gln Lys Phe Leu Val Lys
 85 90 95
 Leu Arg Val Leu Gly Met Lys Ser Gln Cys His Leu Ser Pro Ile Ser
 100 105 110
 Arg Ser Cys Thr Arg Asn Arg Arg His Val Leu Tyr Pro
 115 120 125

<210> 71
 <211> 657
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(657)

<400> 71
 atg gct caa gag aaa gat tgc caa gga atc atc gag gac gtc atc ctg 48
 Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile Leu
 1 5 10 15
 ctg ggt gcg cct gtg gag gga gaa gcc aag cat tgg gag cct ttc cgg 96
 Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe Arg
 20 25 30
 aag gtg gtg tcc ggg agg atc atc aac ggc tac tgc agg gga gac tgg 144

105

Lys	Val	Val	Ser	Gly	Arg	Ile	Ile	Asn	Gly	Tyr	Cys	Arg	Gly	Asp	Trp	
	35						40					45				
ctg	ctg	agt	ttc	gtg	tac	cgc	aca	tcc	tcg	gtg	cag	ctc	cac	gtc	gcc	192
Leu	Leu	Ser	Phe	Val	Tyr	Arg	Thr	Ser	Ser	Val	Gln	Leu	His	Val	Ala	
	50					55					60					
ggc	cta	cag	ccc	gtg	ctg	ctg	cag	gac	agg	agg	gtg	gag	aac	gtg	gac	240
Gly	Leu	Gln	Pro	Val	Leu	Leu	Gln	Asp	Arg	Arg	Val	Glu	Asn	Val	Asp	
	65				70				75						80	
ctg	acc	tct	gtg	gtc	agc	ggc	cac	ctg	gac	tat	gcc	aag	cag	atg	gat	288
Leu	Thr	Ser	Val	Val	Ser	Gly	His	Leu	Asp	Tyr	Ala	Lys	Gln	Met	Asp	
				85					90						95	
gcc	atc	ctg	aag	gcc	gtg	ggc	atc	cgc	acc	aag	cca	ggc	tgg	gac	gag	336
Ala	Ile	Leu	Lys	Ala	Val	Gly	Ile	Arg	Thr	Lys	Pro	Gly	Trp	Asp	Glu	
		100						105					110			
aag	ggg	ctc	ttg	ctg	gcc	cca	ggc	tgc	ctg	ccc	tcc	gag	gag	cct	cgc	384
Lys	Gly	Leu	Leu	Leu	Ala	Pro	Gly	Cys	Leu	Pro	Ser	Glu	Glu	Pro	Arg	
		115					120					125				
cag	gca	gca	gct	gcc	gcc	tca	tca	ggc	gag	acc	ccc	cac	cag	gtt	ggg	432
Gln	Ala	Ala	Ala	Ala	Ala	Ser	Ser	Gly	Glu	Thr	Pro	His	Gln	Val	Gly	
	130					135					140					
caa	acc	cag	ggt	ccc	ata	tcc	gga	gac	acc	tcc	aaa	ttg	gcc	atg	tcc	480
Gln	Thr	Gln	Gly	Pro	Ile	Ser	Gly	Asp	Thr	Ser	Lys	Leu	Ala	Met	Ser	
	145				150				155					160		
aca	gac	ccc	agc	caa	gcc	cag	gtg	cca	gta	ggg	ctg	gac	cag	tct	gaa	528
Thr	Asp	Pro	Ser	Gln	Ala	Gln	Val	Pro	Val	Gly	Leu	Asp	Gln	Ser	Glu	
			165					170						175		
ggg	gcc	tcc	ctt	cct	gct	gct	gcc	agc	cct	gaa	agg	ccc	ccc	atc	tgc	576
Gly	Ala	Ser	Leu	Pro	Ala	Ala	Ala	Ser	Pro	Glu	Arg	Pro	Pro	Ile	Cys	
		180						185						190		
agc	cat	ggc	atg	gac	ccc	aac	cca	ctg	ggc	tgc	ccc	gat	tgt	gcc	tgc	624
Ser	His	Gly	Met	Asp	Pro	Asn	Pro	Leu	Gly	Cys	Pro	Asp	Cys	Ala	Cys	
		195					200					205				
aag	acc	cag	ggc	ccc	agc	acg	ggg	ctg	gac	tga						657

106

Lys Thr Gln Gly Pro Ser Thr Gly Leu Asp *
 210 215

<210> 72

<211> 218

<212> PRT

<213> Homo sapiens

<400> 72

Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile Leu
 1 5 10 15
 Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe Arg
 20 25 30
 Lys Val Val Ser Gly Arg Ile Ile Asn Gly Tyr Cys Arg Gly Asp Trp
 35 40 45
 Leu Leu Ser Phe Val Tyr Arg Thr Ser Ser Val Gln Leu His Val Ala
 50 55 60
 Gly Leu Gln Pro Val Leu Leu Gln Asp Arg Arg Val Glu Asn Val Asp
 65 70 75 80
 Leu Thr Ser Val Val Ser Gly His Leu Asp Tyr Ala Lys Gln Met Asp
 85 90 95
 Ala Ile Leu Lys Ala Val Gly Ile Arg Thr Lys Pro Gly Trp Asp Glu
 100 105 110
 Lys Gly Leu Leu Leu Ala Pro Gly Cys Leu Pro Ser Glu Glu Pro Arg
 115 120 125
 Gln Ala Ala Ala Ala Ser Ser Gly Glu Thr Pro His Gln Val Gly
 130 135 140
 Gln Thr Gln Gly Pro Ile Ser Gly Asp Thr Ser Lys Leu Ala Met Ser
 145 150 155 160
 Thr Asp Pro Ser Gln Ala Gln Val Pro Val Gly Leu Asp Gln Ser Glu
 165 170 175
 Gly Ala Ser Leu Pro Ala Ala Ala Ser Pro Glu Arg Pro Pro Ile Cys
 180 185 190
 Ser His Gly Met Asp Pro Asn Pro Leu Gly Cys Pro Asp Cys Ala Cys
 195 200 205
 Lys Thr Gln Gly Pro Ser Thr Gly Leu Asp
 210 215

<210> 73

<211> 441

<212> DNA

<213> Homo sapiens

107

<220>

<221> CDS

<222> (1)...(441)

<400> 73

atg ttg ttg gcc ctg gtc tgt ctg ctc agc tgc ctg cta ccc tcc agt 48
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser Ser
1 5 10 15

gag gcc aag ctc tac ggt cgt tgt gaa ctg gcc aga gtg cta cat gac 96
Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu His Asp
20 25 30

ttc ggg ctg gac gga tac cgg gga tac agc ctg gct gac tgg gtc tgc 144
Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp Trp Val Cys
35 40 45

ctt gct tat ttc aca agc ggt ttc aac gca gct gct ttg gac tac gag 192
Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala Leu Asp Tyr Glu
50 55 60

gct gat ggg agc acc aac aac ggg atc ttc cag atc aac agc cgg agg 240
Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln Ile Asn Ser Arg Arg
65 70 75 80

tgg tgc agc aac ctc acc ccg aac gtc ccc aac gtg tgc cgg atg tac 288
Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn Val Cys Arg Met Tyr
85 90 95

tgc tca gat ttg ttg aat cct aat ctc aag gat acc gtt atc tgt gcc 336
Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp Thr Val Ile Cys Ala
100 105 110

atg aag ata acc caa gag cct cag ggt ctg ggt tac tgg gag gcc tgg 384
Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly Tyr Trp Glu Ala Trp
115 120 125

agg cat cac tgc cag gga aaa gac ctc act gaa tgg gtg gat ggc tgt 432
Arg His His Cys Gln Gly Lys Asp Leu Thr Glu Trp Val Asp Gly Cys
130 135 140

gac ttc tag 441
Asp Phe *
145

108

<210> 74
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 74
 Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser Ser
 1 5 10 15
 Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu His Asp
 20 25 30
 Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp Trp Val Cys
 35 40 45
 Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala Leu Asp Tyr Glu
 50 55 60
 Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln Ile Asn Ser Arg Arg
 65 70 75 80
 Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn Val Cys Arg Met Tyr
 85 90 95
 Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp Thr Val Ile Cys Ala
 100 105 110
 Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly Tyr Trp Glu Ala Trp
 115 120 125
 Arg His His Cys Gln Gly Lys Asp Leu Thr Glu Trp Val Asp Gly Cys
 130 135 140
 Asp Phe
 145

<210> 75
 <211> 345
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(345)

<400> 75
 atg ctg tgc ttc ctg agg gga atg gct ttc gtc ccc ttc ctc ttg gtg 48
 Met Leu Cys Phe Leu Arg Gly Met Ala Phe Val Pro Phe Leu Leu Val
 1 5 10 15
 acc tgg tcg tca gcc gcc ttc att atc tcc tac gtg gtc gcc gtg ctc 96

109

Thr	Trp	Ser	Ser	Ala	Ala	Phe	Ile	Ile	Ser	Tyr	Val	Val	Ala	Val	Leu	
			20					25					30			
tcc	ggg	cac	gtc	aac	ccc	ttc	ctc	ccg	tat	atc	agt	gat	acg	gga	aca	144
Ser	Gly	His	Val	Asn	Pro	Phe	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	
		35					40					45				
aca	cct	cca	gag	agt	ggc	att	ttt	gga	ttt	atg	ata	aac	ttc	tct	gca	192
Thr	Pro	Pro	Glu	Ser	Gly	Ile	Phe	Gly	Phe	Met	Ile	Asn	Phe	Ser	Ala	
		50				55				60						
ttt	ctt	ggc	gca	gcc	acg	atg	tat	aca	aga	tac	aaa	ata	gta	cag	aag	240
Phe	Leu	Gly	Ala	Ala	Thr	Met	Tyr	Thr	Arg	Tyr	Lys	Ile	Val	Gln	Lys	
	65				70				75					80		
caa	aat	caa	acc	tgc	tat	ttc	agc	act	cct	gtt	ttt	aac	ttg	gtg	tct	288
Gln	Asn	Gln	Thr	Cys	Tyr	Phe	Ser	Thr	Pro	Val	Phe	Asn	Leu	Val	Ser	
				85				90					95			
tta	gtg	ctt	gga	ttg	gtg	gga	tgt	ttc	gga	atg	ggc	att	gtc	gcc	aat	336
Leu	Val	Leu	Gly	Leu	Val	Gly	Cys	Phe	Gly	Met	Gly	Ile	Val	Ala	Asn	
		100				105						110				
ttt	cag	tga														345
Phe	Gln	*														

<210> 76

<211> 114

<212> PRT

<213> Homo sapiens

<400> 76

Met	Leu	Cys	Phe	Leu	Arg	Gly	Met	Ala	Phe	Val	Pro	Phe	Leu	Leu	Val	
1				5				10					15			
Thr	Trp	Ser	Ser	Ala	Ala	Phe	Ile	Ile	Ser	Tyr	Val	Val	Ala	Val	Leu	
		20					25					30				
Ser	Gly	His	Val	Asn	Pro	Phe	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	
		35					40					45				
Thr	Pro	Pro	Glu	Ser	Gly	Ile	Phe	Gly	Phe	Met	Ile	Asn	Phe	Ser	Ala	
	50					55				60						
Phe	Leu	Gly	Ala	Ala	Thr	Met	Tyr	Thr	Arg	Tyr	Lys	Ile	Val	Gln	Lys	
	65				70				75					80		

110

Gln Asn Gln Thr Cys Tyr Phe Ser Thr Pro Val Phe Asn Leu Val Ser
 85 90 95
 Leu Val Leu Gly Leu Val Gly Cys Phe Gly Met Gly Ile Val Ala Asn
 100 105 110
 Phe Gln

<210> 77
 <211> 972
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(972)

<400> 77

atg ccc cta tta aaa ctt gta cat ggc tcc cca ttg gtt ttt gga gaa 48
 Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
 1 5 10 15

aag ttc aag ctt ttt acc ttg gtg tct gcc tgt atc cca gtg ttc agg 96
 Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
 20 25 30

ctg gct aga cgg cgg aag aag atc cta ttt tac tgt cac ttc cca gat 144
 Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp
 35 40 45

ctg ctt ctc acc aag aga gat tct ttt ctt aaa cga cta tac agg gcc 192
 Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala
 50 55 60

cca att gac tgg ata gag gaa tac acc aca ggc atg gca gac tgc atc 240
 Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile
 65 70 75 80

tta gtc aac agc cag ttc aca gct gct gtt ttt aag gaa aca ttc aag 288
 Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys
 85 90 95

tcc ctg tct cac ata gac cct gat gtc ctc tat cca tct cta aat gtc 336
 Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val
 100 105 110

111

acc agc ttt gac tca gtt gtt cct gaa aag ctg gat gac cta gtc ccc	384
Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro	
115 120 125	
aag ggg aaa aaa ttc ctg ctg ctc tcc atc aac aga tac gaa agg aag	432
Lys Gly Lys Lys Phe Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys	
130 135 140	
aaa aat ctg act ttg gca ctg gaa gcc cta gta cag ctg cgt gga aga	480
Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg	
145 150 155 160	
ttg aca tcc caa gat tgg gag agg gtt cat ctg atc gtg gca ggt ggt	528
Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly	
165 170 175	
tat gac gag aga gtc ctg gag aat gtg gaa cat tat cag gaa ttg aag	576
Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys	
180 185 190	
aaa atg gtc caa cag tcc gac ctt ggc cag tat gtg acc ttc ttg agg	624
Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg	
195 200 205	
tct ttc tca gac aaa cag aaa atc tcc ctc ctc cac agc tgc acg tgt	672
Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys	
210 215 220	
gtg ctt tac aca cca agc aat gag cac ttt ggc att gtc cct ctg gaa	720
Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu	
225 230 235 240	
gcc atg tac atg cag tgc cca gtc att gct gtt aat tcg ggt gga ccc	768
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro	
245 250 255	
ttg gag tcc att gac cac agt gtc aca ggg ttt ctg tgt gag cct gac	816
Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp	
260 265 270	
ccg gtg cac ttc tca gaa gca ata gaa aag ttc atc cgt gaa cct tcc	864
Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg Glu Pro Ser	
275 280 285	

112

tta aaa gcc acc atg ggc ctg gct gga aga gcc aga gtg aag gaa aaa 912
 Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg Val Lys Glu Lys
 290 295 300

ttt tcc cct gaa gca ttt aca gaa cag ctc tac cga tat gtt acc aaa 960
 Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr Arg Tyr Val Thr Lys
 305 310 315 320

ctg ctg gta taa 972
 Leu Leu Val *

<210> 78
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 78
 Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
 1 5 10 15
 Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
 20 25 30
 Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp
 35 40 45
 Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala
 50 55 60
 Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile
 65 70 75 80
 Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys
 85 90 95
 Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val
 100 105 110
 Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro
 115 120 125
 Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys
 130 135 140
 Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg
 145 150 155 160
 Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly
 165 170 175
 Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys
 180 185 190

113

Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg
 195 200 205
 Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys
 210 215 220
 Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
 225 230 235 240
 Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro
 245 250 255
 Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp
 260 265 270
 Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg Glu Pro Ser
 275 280 285
 Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg Val Lys Glu Lys
 290 295 300
 Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr Arg Tyr Val Thr Lys
 305 310 315 320
 Leu Leu Val

<210> 79
 <211> 891
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(891)
 <223>

<221> misc_feature
 <222> (1)...(891)
 <223> n = A,T,C or G

<400> 79

atg cac ggg aag act gtg ctg atc acc ggg gcg aac agc ggc ctg ggc 48
 Met His Gly Lys Thr Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly
 1 5 10 15

cgn tcc acg gcc gcc gag cta ctg cgc ctg gga gcg cgg gtg atc atg 96
 Xaa Ser Thr Ala Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met

114

20	25	30	
ggc tgc cgg gac cgc gcg cgc gcc gag gag gcg gcg ggt cag ctc cgc			144
Gly Cys Arg Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg			
35	40	45	
cgc gag ctc cgc cag gcc gcg gag tgc ggc cca gag cct ggc gtc agc			192
Arg Glu Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser			
50	55	60	
ggg gtg ggc gag ctc ata gtc cgg gag ctg gac ctc gcc tcg ctg cgc			240
Gly Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg			
65	70	75	80
tcg gtg cgc gcc ttc tgc cag gaa atg ctc cag gaa gag cct agg ctg			288
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg Leu			
85	90	95	
gat gtc ttg atc aat aac gca ggg atc ttc cag tgc cct tac atg aag			336
Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr Met Lys			
100	105	110	
act gaa gat ggg ttt gag atg cag ttc gga gtg aac cat ctg ggg cac			384
Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His			
115	120	125	
ttt cta ctc acc aat ctt ctc ctt gga ctc ctc aaa agt tca gct ccc			432
Phe Leu Leu Thr Asn Leu Leu Gly Leu Leu Lys Ser Ser Ala Pro			
130	135	140	
agc agg att gtg gta gtt tct tcc aaa ctt tat aaa tac gga gac atc			480
Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr Lys Tyr Gly Asp Ile			
145	150	155	160
aat ttt gat gac ttg aac agt gaa caa agc tat aat aaa agc ttt tgt			528
Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser Tyr Asn Lys Ser Phe Cys			
165	170	175	
tat agc cgg agc aaa ctg gct aac att ctt ttt acc agg gaa cta gcc			576
Tyr Ser Arg Ser Lys Leu Ala Asn Ile Leu Phe Thr Arg Glu Leu Ala			
180	185	190	
cgc cgc tta gaa ggc aca aat gtc acc gtc aat gtg ttg cat cct ggt			624
Arg Arg Leu Glu Gly Thr Asn Val Thr Val Asn Val Leu His Pro Gly			

115

195	200	205	
att gta cgg aca aat ctg ggg agg cac ata cac att cca ctg ttg gtc			672
Ile Val Arg Thr Asn Leu Gly Arg His Ile His Ile Pro Leu Leu Val			
210	215	220	
aaa cca ctc ttc aat ttg gtg tca tgg gct ttt ttc aaa act cca gta			720
Lys Pro Leu Phe Asn Leu Val Ser Trp Ala Phe Phe Lys Thr Pro Val			
225	230	235	240
gaa ggt gcc cag act tcc att tat ttg gcc tct tca cct gag gta gaa			768
Glu Gly Ala Gln Thr Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu			
245	250	255	
gga gtg tca gga aga tac ttt ggg gat tgt aaa gag gaa gaa ctg ttg			816
Gly Val Ser Gly Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu			
260	265	270	
ccc aaa gct atg gat gaa tct gtt gca aga aaa ctc tgg gat atc agt			864
Pro Lys Ala Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser			
275	280	285	
gaa gtg atg gtt ggc ctg cta aaa tag			891
Glu Val Met Val Gly Leu Leu Lys *			
290	295		

<210> 80

<211> 296

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(296)

<223> Xaa = Any Amino Acid

<400> 80

Met His Gly Lys Thr Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly			
1	5	10	15
Xaa Ser Thr Ala Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met			
20	25	30	
Gly Cys Arg Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg			
35	40	45	

116

Arg Glu Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser
 50 55 60
 Gly Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg
 65 70 75 80
 Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg Leu
 85 90 95
 Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr Met Lys
 100 105 110
 Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 115 120 125
 Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys Ser Ser Ala Pro
 130 135 140
 Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr Lys Tyr Gly Asp Ile
 145 150 155 160
 Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser Tyr Asn Lys Ser Phe Cys
 165 170 175
 Tyr Ser Arg Ser Lys Leu Ala Asn Ile Leu Phe Thr Arg Glu Leu Ala
 180 185 190
 Arg Arg Leu Glu Gly Thr Asn Val Thr Val Asn Val Leu His Pro Gly
 195 200 205
 Ile Val Arg Thr Asn Leu Gly Arg His Ile His Ile Pro Leu Leu Val
 210 215 220
 Lys Pro Leu Phe Asn Leu Val Ser Trp Ala Phe Phe Lys Thr Pro Val
 225 230 235 240
 Glu Gly Ala Gln Thr Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu
 245 250 255
 Gly Val Ser Gly Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu
 260 265 270
 Pro Lys Ala Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser
 275 280 285
 Glu Val Met Val Gly Leu Leu Lys
 290 295

<210> 81
 <211> 1716
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1716)

<400> 81

atg gta gaa tca att aaa cac tgc att gtg ttg ctg cag att gcc aaa

48

117

Met	Val	Glu	Ser	Ile	Lys	His	Cys	Ile	Val	Leu	Leu	Gln	Ile	Ala	Lys	
1				5					10					15		
gac cag agt aat gcg gag aag cac gca gat gga atg ata agt act att																96
Asp Gln Ser Asn Ala Glu Lys His Ala Asp Gly Met Ile Ser Thr Ile																
				20				25					30			
aat ccc gta gat gca ata tat caa cct agt cct ttg gaa cct gtg atc																144
Asn Pro Val Asp Ala Ile Tyr Gln Pro Ser Pro Leu Glu Pro Val Ile																
				35				40					45			
agc aca atg cct tcc cag act gtg tta cct cca gaa cct gtt cag ttg																192
Ser Thr Met Pro Ser Gln Thr Val Leu Pro Pro Glu Pro Val Gln Leu																
				50				55				60				
tgt aag tca gag cag cgt cca tct tcc cta cca gtt gga cct gtg ttg																240
Cys Lys Ser Glu Gln Arg Pro Ser Ser Leu Pro Val Gly Pro Val Leu																
				65				70				75				80
gct acc ttg gga cat cat cag act cct aca cca aat agt aca ggc agt																288
Ala Thr Leu Gly His His Gln Thr Pro Thr Pro Asn Ser Thr Gly Ser																
								85				90				95
ggc cat tca cca ccg agt agc agt ctc act tct cca agc cac gtg aac																336
Gly His Ser Pro Pro Ser Ser Ser Leu Thr Ser Pro Ser His Val Asn																
								100				105				110
ttg tct cca aat aca gtc cca gag ttc tct tac tcc agc agt gaa gat																384
Leu Ser Pro Asn Thr Val Pro Glu Phe Ser Tyr Ser Ser Ser Glu Asp																
								115				120				125
gaa ttt tat gat gct gat gaa ttc cat caa agt ggc tca tcc cca aag																432
Glu Phe Tyr Asp Ala Asp Glu Phe His Gln Ser Gly Ser Ser Pro Lys																
								130				135				140
cgc tta ata gat tct tct gga tct gcc tca gtc ctg aca cac agc agc																480
Arg Leu Ile Asp Ser Ser Gly Ser Ala Ser Val Leu Thr His Ser Ser																
								145				150				160
tcg gga aat agt cta aaa cgc cca gat acc aca gaa tca ctt aat tct																528
Ser Gly Asn Ser Leu Lys Arg Pro Asp Thr Thr Glu Ser Leu Asn Ser																
								165				170				175
tcc ttg tcc aat gga aca agt gat gct gac ctg ttt gat tca cat gat																576

118

Ser	Leu	Ser	Asn	Gly	Thr	Ser	Asp	Ala	Asp	Leu	Phe	Asp	Ser	His	Asp		
			180					185					190				
gac	aga	gat	gat	gat	gcg	gag	gca	ggg	tct	gtg	gag	gag	cac	aag	agc	624	
Asp	Arg	Asp	Asp	Asp	Ala	Glu	Ala	Gly	Ser	Val	Glu	Glu	His	Lys	Ser		
			195				200					205					
ggt	atc	atg	cat	ctc	ttg	tcg	cag	gtt	aga	ctt	gga	atg	gat	ctt	act	672	
Val	Ile	Met	His	Leu	Leu	Ser	Gln	Val	Arg	Leu	Gly	Met	Asp	Leu	Thr		
	210						215				220						
aag	gta	gtt	ctt	cca	acg	ttt	att	ctt	gaa	aga	aga	tct	ctt	tta	gaa	720	
Lys	Val	Val	Leu	Pro	Thr	Phe	Ile	Leu	Glu	Arg	Arg	Ser	Leu	Leu	Glu		
225					230					235					240		
atg	tat	gca	gac	ttt	ttt	gca	cat	ccg	gac	ctg	ttt	gtg	agc	att	agt	768	
Met	Tyr	Ala	Asp	Phe	Phe	Ala	His	Pro	Asp	Leu	Phe	Val	Ser	Ile	Ser		
				245					250					255			
gac	cag	aag	gat	ccc	aag	gat	cga	atg	gtt	cag	gtt	gtg	aaa	tgg	tac	816	
Asp	Gln	Lys	Asp	Pro	Lys	Asp	Arg	Met	Val	Gln	Val	Val	Lys	Trp	Tyr		
			260					265					270				
ctc	tca	gcc	ttt	cat	gcg	gga	agg	aaa	gga	tca	gtt	gcc	aaa	aag	cca	864	
Leu	Ser	Ala	Phe	His	Ala	Gly	Arg	Lys	Gly	Ser	Val	Ala	Lys	Lys	Pro		
		275					280					285					
tac	aat	ccc	att	ttg	ggc	gag	att	ttt	cag	tgt	cat	tgg	aca	tta	cca	912	
Tyr	Asn	Pro	Ile	Leu	Gly	Glu	Ile	Phe	Gln	Cys	His	Trp	Thr	Leu	Pro		
	290					295					300						
aat	gat	act	gaa	gag	aac	aca	gaa	cta	gtt	tca	gaa	gga	cca	gtt	ccc	960	
Asn	Asp	Thr	Glu	Glu	Asn	Thr	Glu	Leu	Val	Ser	Glu	Gly	Pro	Val	Pro		
305					310					315					320		
tgg	gtt	tcc	aaa	aac	agt	gta	aca	ttt	gtg	gct	gag	cag	gtt	tcc	cat	1008	
Trp	Val	Ser	Lys	Asn	Ser	Val	Thr	Phe	Val	Ala	Glu	Gln	Val	Ser	His		
				325					330					335			
cat	cca	ccc	att	tca	gcc	ttt	tat	gct	gag	tgt	ttt	aac	aag	aag	ata	1056	
His	Pro	Pro	Ile	Ser	Ala	Phe	Tyr	Ala	Glu	Cys	Phe	Asn	Lys	Lys	Ile		
			340					345					350				
caa	ttc	aat	gct	cat	atc	tgg	acc	aaa	tca	aaa	ttc	ctt	ggg	atg	tca	1104	

119

Gln Phe Asn Ala His Ile Trp Thr Lys Ser Lys Phe Leu Gly Met Ser	
355 360 365	
att ggg gtg cac aac ata ggg cag ggc tgt gtc tca tgt cta gac tat	1152
Ile Gly Val His Asn Ile Gly Gln Gly Cys Val Ser Cys Leu Asp Tyr	
370 375 380	
gat gaa cat tac att ctc aca ttc ccc aat ggc tat gga agg tct atc	1200
Asp Glu His Tyr Ile Leu Thr Phe Pro Asn Gly Tyr Gly Arg Ser Ile	
385 390 395 400	
ctc aca gtg ccc tgg gtg gaa tta gga gga gaa tgc aat att aat tgt	1248
Leu Thr Val Pro Trp Val Glu Leu Gly Gly Glu Cys Asn Ile Asn Cys	
405 410 415	
tcc aaa aca ggc tat agt gca aat atc atc ttc cac act aaa ccc ttc	1296
Ser Lys Thr Gly Tyr Ser Ala Asn Ile Ile Phe His Thr Lys Pro Phe	
420 425 430	
tat ggg ggc aag aag cac aga att act gcc gag att ttt tct cca aat	1344
Tyr Gly Gly Lys Lys His Arg Ile Thr Ala Glu Ile Phe Ser Pro Asn	
435 440 445	
gac aag aag tct ttt tgc tca att gaa ggg gaa tgg aat ggt gtg atg	1392
Asp Lys Lys Ser Phe Cys Ser Ile Glu Gly Glu Trp Asn Gly Val Met	
450 455 460	
tat gca aaa tat gca aca ggg gaa aat aca gtc ttt gta gat acc aag	1440
Tyr Ala Lys Tyr Ala Thr Gly Glu Asn Thr Val Phe Val Asp Thr Lys	
465 470 475 480	
aag ttg cct ata atc aag aag aaa gtg agg aag ttg gaa gat cag aac	1488
Lys Leu Pro Ile Ile Lys Lys Lys Val Arg Lys Leu Glu Asp Gln Asn	
485 490 495	
gag tat gaa tcc cgc agc ctt tgg aag gat gtc act ttc aac tta aaa	1536
Glu Tyr Glu Ser Arg Ser Leu Trp Lys Asp Val Thr Phe Asn Leu Lys	
500 505 510	
atc aga gac att gat gca gca act gaa gca aag cac agg ctt gaa gaa	1584
Ile Arg Asp Ile Asp Ala Ala Thr Glu Ala Lys His Arg Leu Glu Glu	
515 520 525	
aga caa aga gca gaa gcc cga gaa agg aag gag aag gaa att cag tgg	1632

120

Arg Gln Arg Ala Glu Ala Arg Glu Arg Lys Glu Lys Glu Ile Gln Trp
 530 535 540

gag aca agg tta ttt cat gaa gat gga gaa tgc tgg gtt tat gat gaa 1680
 Glu Thr Arg Leu Phe His Glu Asp Gly Glu Cys Trp Val Tyr Asp Glu
 545 550 555 560

cca tta ctg aaa cgt ctt ggt gct gcc aag cat tag 1716
 Pro Leu Leu Lys Arg Leu Gly Ala Ala Lys His *
 565 570

<210> 82
 <211> 571
 <212> PRT
 <213> Homo sapiens

<400> 82
 Met Val Glu Ser Ile Lys His Cys Ile Val Leu Leu Gln Ile Ala Lys
 1 5 10 15
 Asp Gln Ser Asn Ala Glu Lys His Ala Asp Gly Met Ile Ser Thr Ile
 20 25 30
 Asn Pro Val Asp Ala Ile Tyr Gln Pro Ser Pro Leu Glu Pro Val Ile
 35 40 45
 Ser Thr Met Pro Ser Gln Thr Val Leu Pro Pro Glu Pro Val Gln Leu
 50 55 60
 Cys Lys Ser Glu Gln Arg Pro Ser Ser Leu Pro Val Gly Pro Val Leu
 65 70 75 80
 Ala Thr Leu Gly His His Gln Thr Pro Thr Pro Asn Ser Thr Gly Ser
 85 90 95
 Gly His Ser Pro Pro Ser Ser Ser Leu Thr Ser Pro Ser His Val Asn
 100 105 110
 Leu Ser Pro Asn Thr Val Pro Glu Phe Ser Tyr Ser Ser Ser Glu Asp
 115 120 125
 Glu Phe Tyr Asp Ala Asp Glu Phe His Gln Ser Gly Ser Ser Pro Lys
 130 135 140
 Arg Leu Ile Asp Ser Ser Gly Ser Ala Ser Val Leu Thr His Ser Ser
 145 150 155 160
 Ser Gly Asn Ser Leu Lys Arg Pro Asp Thr Thr Glu Ser Leu Asn Ser
 165 170 175
 Ser Leu Ser Asn Gly Thr Ser Asp Ala Asp Leu Phe Asp Ser His Asp
 180 185 190
 Asp Arg Asp Asp Asp Ala Glu Ala Gly Ser Val Glu Glu His Lys Ser
 195 200 205

121

Val	Ile	Met	His	Leu	Leu	Ser	Gln	Val	Arg	Leu	Gly	Met	Asp	Leu	Thr
210						215				220					
Lys	Val	Val	Leu	Pro	Thr	Phe	Ile	Leu	Glu	Arg	Arg	Ser	Leu	Leu	Glu
225					230					235					240
Met	Tyr	Ala	Asp	Phe	Phe	Ala	His	Pro	Asp	Leu	Phe	Val	Ser	Ile	Ser
			245						250					255	
Asp	Gln	Lys	Asp	Pro	Lys	Asp	Arg	Met	Val	Gln	Val	Val	Lys	Trp	Tyr
		260						265					270		
Leu	Ser	Ala	Phe	His	Ala	Gly	Arg	Lys	Gly	Ser	Val	Ala	Lys	Lys	Pro
		275					280					285			
Tyr	Asn	Pro	Ile	Leu	Gly	Glu	Ile	Phe	Gln	Cys	His	Trp	Thr	Leu	Pro
	290					295					300				
Asn	Asp	Thr	Glu	Glu	Asn	Thr	Glu	Leu	Val	Ser	Glu	Gly	Pro	Val	Pro
305					310					315					320
Trp	Val	Ser	Lys	Asn	Ser	Val	Thr	Phe	Val	Ala	Glu	Gln	Val	Ser	His
			325					330						335	
His	Pro	Pro	Ile	Ser	Ala	Phe	Tyr	Ala	Glu	Cys	Phe	Asn	Lys	Lys	Ile
		340						345					350		
Gln	Phe	Asn	Ala	His	Ile	Trp	Thr	Lys	Ser	Lys	Phe	Leu	Gly	Met	Ser
	355						360					365			
Ile	Gly	Val	His	Asn	Ile	Gly	Gln	Gly	Cys	Val	Ser	Cys	Leu	Asp	Tyr
	370					375					380				
Asp	Glu	His	Tyr	Ile	Leu	Thr	Phe	Pro	Asn	Gly	Tyr	Gly	Arg	Ser	Ile
385					390					395					400
Leu	Thr	Val	Pro	Trp	Val	Glu	Leu	Gly	Gly	Glu	Cys	Asn	Ile	Asn	Cys
			405					410						415	
Ser	Lys	Thr	Gly	Tyr	Ser	Ala	Asn	Ile	Ile	Phe	His	Thr	Lys	Pro	Phe
		420						425					430		
Tyr	Gly	Gly	Lys	Lys	His	Arg	Ile	Thr	Ala	Glu	Ile	Phe	Ser	Pro	Asn
	435						440					445			
Asp	Lys	Lys	Ser	Phe	Cys	Ser	Ile	Glu	Gly	Glu	Trp	Asn	Gly	Val	Met
	450					455					460				
Tyr	Ala	Lys	Tyr	Ala	Thr	Gly	Glu	Asn	Thr	Val	Phe	Val	Asp	Thr	Lys
465					470					475					480
Lys	Leu	Pro	Ile	Ile	Lys	Lys	Lys	Val	Arg	Lys	Leu	Glu	Asp	Gln	Asn
			485					490						495	
Glu	Tyr	Glu	Ser	Arg	Ser	Leu	Trp	Lys	Asp	Val	Thr	Phe	Asn	Leu	Lys
		500						505					510		
Ile	Arg	Asp	Ile	Asp	Ala	Ala	Thr	Glu	Ala	Lys	His	Arg	Leu	Glu	Glu
	515						520					525			
Arg	Gln	Arg	Ala	Glu	Ala	Arg	Glu	Arg	Lys	Glu	Lys	Glu	Ile	Gln	Trp
	530					535					540				
Glu	Thr	Arg	Leu	Phe	His	Glu	Asp	Gly	Glu	Cys	Trp	Val	Tyr	Asp	Glu
545					550					555					560

122

Pro Leu Leu Lys Arg Leu Gly Ala Ala Lys His
 565 570

<210> 83
 <211> 648
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(648)

<400> 83
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 Met Leu Leu Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr
 1 5 10 15

tcc tgc agc ctc ctc ttg cct cgg gct gcc cag atc ttg gcg gct gag 96
 Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu
 20 25 30

gct ggc tta cct tcg agc cgt tcc ttc atg gga ttt gct gct ccc ttc 144
 Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe
 35 40 45

acc aac aag cga aag gct tac tcg gag cgt aga atc atg ggg tac tca 192
 Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser
 50 55 60

atg cag gag atg tat gag gtg gtg tcc aac gtc cag gag tat cgt gag 240
 Met Gln Glu Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu
 65 70 75 80

ttt gtg ccc tgg tgt aag aag tct ctg gtg gta tcc agc cgt aag ggt 288
 Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly
 85 90 95

cat ttg aaa gcc cag ctg gag gtt ggc ttt cca cct gtc atg gaa cgt 336
 His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg
 100 105 110

tac acc tct gca gtt tcc atg gtc aaa cct cac atg gtc aag gct gtt 384
 Tyr Thr Ser Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val
 115 120 125

123

tgt act gat ggc aag ctc ttc aac cac tta gag act att tgg cga ttc 432
 Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe
 130 135 140

agc cct ggt att cct gcc tat cct cga acc tgc act gtg gac ttt tcg 480
 Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser
 145 150 155 160

att tcc ttt gaa ttt cgt tct ctg ctg cac tcc cag ctg gcc acc atg 528
 Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met
 165 170 175

ttt ttt gat gag gtt gtc aaa cag aat gtt gct gcc ttt gag cgt cgg 576
 Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg
 180 185 190

gca gcc acc aag ttt ggt cca gaa aca gcc atc ccc cgt gaa ctg atg 624
 Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met
 195 200 205

ttc cat gag gtg cac cag act tga 648
 Phe His Glu Val His Gln Thr *
 210 215

<210> 84

<211> 215

<212> PRT

<213> Homo sapiens

<400> 84

Met Leu Leu Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr
 1 5 10 15
 Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu
 20 25 30
 Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe
 35 40 45
 Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser
 50 55 60
 Met Gln Glu Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu
 65 70 75 80
 Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly
 85 90 95

124

His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg
 100 105 110
 Tyr Thr Ser Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val
 115 120 125
 Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe
 130 135 140
 Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser
 145 150 155 160
 Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met
 165 170 175
 Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg
 180 185 190
 Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met
 195 200 205
 Phe His Glu Val His Gln Thr
 210 215

<210> 85

<211> 615

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(615)

<400> 85

atg ggg ttt ctg acc tcc tgc agc ctc ctc ttg cct cgg gct gcc cag 48
 Met Gly Phe Leu Thr Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln
 1 5 10 15

atc ttg gcg gct gag gct ggc tta cct tcg agc cgt tcc ttc atg gga 96
 Ile Leu Ala Ala Glu Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly
 20 25 30

ttt gct gct ccc ttc acc aac aag cga aag gct tac tcg gag cgt aga 144
 Phe Ala Ala Pro Phe Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg
 35 40 45

atc atg ggg tac tca atg cag gag atg tat gag gtg gtg tcc aac gtc 192
 Ile Met Gly Tyr Ser Met Gln Glu Met Tyr Glu Val Val Ser Asn Val
 50 55 60

cag gag tat cgt gag ttt gtg ccc tgg tgt aag aag tct ctg gtg gta 240

125

Gln	Glu	Tyr	Arg	Glu	Phe	Val	Pro	Trp	Cys	Lys	Lys	Ser	Leu	Val	Val	
65					70					75					80	
tcc	agc	cgt	aag	ggt	cat	ttg	aaa	gcc	cag	ctg	gag	gtt	ggc	ttt	cca	288
Ser	Ser	Arg	Lys	Gly	His	Leu	Lys	Ala	Gln	Leu	Glu	Val	Gly	Phe	Pro	
				85					90					95		
cct	gtc	atg	gaa	cgt	tac	acc	tct	gca	gtt	tcc	atg	gtc	aaa	cct	cac	336
Pro	Val	Met	Glu	Arg	Tyr	Thr	Ser	Ala	Val	Ser	Met	Val	Lys	Pro	His	
			100					105					110			
atg	gtc	aag	gct	gtt	tgt	act	gat	ggc	aag	ctc	ttc	aac	cac	tta	gag	384
Met	Val	Lys	Ala	Val	Cys	Thr	Asp	Gly	Lys	Leu	Phe	Asn	His	Leu	Glu	
		115					120					125				
act	att	tgg	cga	ttc	agc	cct	ggt	att	cct	gcc	tat	cct	cga	acc	tgc	432
Thr	Ile	Trp	Arg	Phe	Ser	Pro	Gly	Ile	Pro	Ala	Tyr	Pro	Arg	Thr	Cys	
	130					135				140						
act	gtg	gac	ttt	tcg	att	tcc	ttt	gaa	ttt	cgt	tct	ctg	ctg	cac	tcc	480
Thr	Val	Asp	Phe	Ser	Ile	Ser	Phe	Glu	Phe	Arg	Ser	Leu	Leu	His	Ser	
145					150					155					160	
cag	ctg	gcc	acc	atg	ttt	ttt	gat	gag	gtt	gtc	aaa	cag	aat	gtt	gct	528
Gln	Leu	Ala	Thr	Met	Phe	Phe	Asp	Glu	Val	Val	Lys	Gln	Asn	Val	Ala	
				165					170					175		
gcc	ttt	gag	cgt	cgg	gca	gcc	acc	aag	ttt	ggt	cca	gaa	aca	gcc	atc	576
Ala	Phe	Glu	Arg	Arg	Ala	Ala	Thr	Lys	Phe	Gly	Pro	Glu	Thr	Ala	Ile	
			180					185					190			
ccc	cgt	gaa	ctg	atg	ttc	cat	gag	gtg	cac	cag	act	tga				615
Pro	Arg	Glu	Leu	Met	Phe	His	Glu	Val	His	Gln	Thr	*				
			195				200									

126

Ile Leu Ala Ala Glu Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly
 20 25 30
 Phe Ala Ala Pro Phe Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg
 35 40 45
 Ile Met Gly Tyr Ser Met Gln Glu Met Tyr Glu Val Val Ser Asn Val
 50 55 60
 Gln Glu Tyr Arg Glu Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val
 65 70 75 80
 Ser Ser Arg Lys Gly His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro
 85 90 95
 Pro Val Met Glu Arg Tyr Thr Ser Ala Val Ser Met Val Lys Pro His
 100 105 110
 Met Val Lys Ala Val Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu
 115 120 125
 Thr Ile Trp Arg Phe Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys
 130 135 140
 Thr Val Asp Phe Ser Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser
 145 150 155 160
 Gln Leu Ala Thr Met Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala
 165 170 175
 Ala Phe Glu Arg Arg Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile
 180 185 190
 Pro Arg Glu Leu Met Phe His Glu Val His Gln Thr
 195 200

<210> 87
 <211> 570
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(570)

<400> 87

atg gcc ctg ctc tcg cgc ccc gcg ctc acc ctc ctg ctc ctc ctc atg 48
 Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Leu Met
 1 5 10 15

gcc gct gtt gtc agg tgc cag gag cag gcc cag acc acc gac tgg aga 96
 Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg
 20 25 30

gcc acc ctg aag acc atc cgg aac ggc gtt cat aag ata gac acg tac 144

127

Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr	
35 40 45	
ctg aac gcc gcc ttg gac ctc ctg gga ggc gag gac ggt ctc tgc cag	192
Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu Cys Gln	
50 55 60	
tat aaa tgc agt gac gga tct aag cct ttc cca cgt tat ggt tat aaa	240
Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys	
65 70 75 80	
ccc tcc cca ccg aat gga tgt ggc tct cca ctg ttt ggt gtt cat ctt	288
Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu	
85 90 95	
aac att ggt atc cct tcc ctg aca aag tgt tgc aac caa cac gac agg	336
Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg	
100 105 110	
tgc tat gaa acc tgt ggc aaa agc aag aat gac tgt gat gaa gaa ttc	384
Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe	
115 120 125	
cag tat tgc ctc tcc aag atc tgc cga gat gta cag aaa aca cta gga	432
Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly	
130 135 140	
cta act cag cat gtt cag gca tgt gaa aca aca gtg gag ctc ttg ttt	480
Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe	
145 150 155 160	
gac agt gtt ata cat tta ggt tgt aaa cca tat ctg gac agc caa cga	528
Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg	
165 170 175	
gcc gca tgc agg tgt cat tat gaa gaa aaa act gat ctt taa	570
Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu *	
180 185	

<210> 88

<211> 189

<212> PRT

<213> Homo sapiens

128

<400> 88

Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Leu Met
 1 5 10 15
 Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg
 20 25 30
 Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr
 35 40 45
 Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu Cys Gln
 50 55 60
 Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys
 65 70 75 80
 Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu
 85 90 95
 Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg
 100 105 110
 Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe
 115 120 125
 Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly
 130 135 140
 Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe
 145 150 155 160
 Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg
 165 170 175
 Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu
 180 185

<210> 89

<211> 696

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(696)

<400> 89

atg ttt ctg gtg ggc ctg aca ggg ggc att gcc tca ggc aag agc tca 48
 Met Phe Leu Val Gly Leu Thr Gly Gly Ile Ala Ser Gly Lys Ser Ser
 1 5 10 15
 gtg atc cag gtg ttc cag cag ctg ggc tgt gcg gtg att gac gtg gac 96
 Val Ile Gln Val Phe Gln Gln Leu Gly Cys Ala Val Ile Asp Val Asp
 20 25 30

129

gtg atg gcc cgg cac gtc gtg cag cca gga tac cct gcc cac cgg cgc Val Met Ala Arg His Val Val Gln Pro Gly Tyr Pro Ala His Arg Arg 35 40 45	144
atc gta gag gtc ttc ggc act gag gtc ttg ctg gag aac ggc gac ata Ile Val Glu Val Phe Gly Thr Glu Val Leu Leu Glu Asn Gly Asp Ile 50 55 60	192
aat cgc aag gtc ctg ggg gac ctg atc ttt aac cag cct gac cgg cgg Asn Arg Lys Val Leu Gly Asp Leu Ile Phe Asn Gln Pro Asp Arg Arg 65 70 75 80	240
cag ctg ctc aac gcc atc acc cac ccc gag att cgc aag gag atg atg Gln Leu Leu Asn Ala Ile Thr His Pro Glu Ile Arg Lys Glu Met Met 85 90 95	288
aag gag acg ttc aag tac ttc ctc cgg gga tac cgc tac gtg att ctg Lys Glu Thr Phe Lys Tyr Phe Leu Arg Gly Tyr Arg Tyr Val Ile Leu 100 105 110	336
gat atc ccc ctg ctg ttt gag acc aag aag ttg ctc aag tac atg aag Asp Ile Pro Leu Leu Phe Glu Thr Lys Lys Leu Leu Lys Tyr Met Lys 115 120 125	384
cac acc gtg gta gta tac tgc gac cgg gac aca cag ctg gca cgg ctg His Thr Val Val Val Tyr Cys Asp Arg Asp Thr Gln Leu Ala Arg Leu 130 135 140	432
atg cgg cgg aac agc ctg aac cgc aag gac gca gag gcc cgc atc aat Met Arg Arg Asn Ser Leu Asn Arg Lys Asp Ala Glu Ala Arg Ile Asn 145 150 155 160	480
gcc cag ctg ccc ctg aca gac aag gcc cgc atg gcc cgc cat gtc cta Ala Gln Leu Pro Leu Thr Asp Lys Ala Arg Met Ala Arg His Val Leu 165 170 175	528
gac aac tcg ggc gag tgg agt gtc acc aaa cgc cag gtc atc ctc ttg Asp Asn Ser Gly Glu Trp Ser Val Thr Lys Arg Gln Val Ile Leu Leu 180 185 190	576
cac act gag ctg gag cgc tcc ctg gag tac ctg ccg ctg agg ttt ggg His Thr Glu Leu Glu Arg Ser Leu Glu Tyr Leu Pro Leu Arg Phe Gly 195 200 205	624

130

gtc ctc aca ggg ctc gct gcc att gcc agc ctc ctc tac ctg ctc acc 672
 Val Leu Thr Gly Leu Ala Ala Ile Ala Ser Leu Leu Tyr Leu Leu Thr
 210 215 220

cac tac ctt ctg cct tac gcc tag 696
 His Tyr Leu Leu Pro Tyr Ala *
 225 230

<210> 90
 <211> 231
 <212> PRT
 <213> Homo sapiens

<400> 90
 Met Phe Leu Val Gly Leu Thr Gly Gly Ile Ala Ser Gly Lys Ser Ser
 1 5 10 15
 Val Ile Gln Val Phe Gln Gln Leu Gly Cys Ala Val Ile Asp Val Asp
 20 25 30
 Val Met Ala Arg His Val Val Gln Pro Gly Tyr Pro Ala His Arg Arg
 35 40 45
 Ile Val Glu Val Phe Gly Thr Glu Val Leu Leu Glu Asn Gly Asp Ile
 50 55 60
 Asn Arg Lys Val Leu Gly Asp Leu Ile Phe Asn Gln Pro Asp Arg Arg
 65 70 75 80
 Gln Leu Leu Asn Ala Ile Thr His Pro Glu Ile Arg Lys Glu Met Met
 85 90 95
 Lys Glu Thr Phe Lys Tyr Phe Leu Arg Gly Tyr Arg Tyr Val Ile Leu
 100 105 110
 Asp Ile Pro Leu Leu Phe Glu Thr Lys Lys Leu Leu Lys Tyr Met Lys
 115 120 125
 His Thr Val Val Val Tyr Cys Asp Arg Asp Thr Gln Leu Ala Arg Leu
 130 135 140
 Met Arg Arg Asn Ser Leu Asn Arg Lys Asp Ala Glu Ala Arg Ile Asn
 145 150 155 160
 Ala Gln Leu Pro Leu Thr Asp Lys Ala Arg Met Ala Arg His Val Leu
 165 170 175
 Asp Asn Ser Gly Glu Trp Ser Val Thr Lys Arg Gln Val Ile Leu Leu
 180 185 190
 His Thr Glu Leu Glu Arg Ser Leu Glu Tyr Leu Pro Leu Arg Phe Gly
 195 200 205
 Val Leu Thr Gly Leu Ala Ala Ile Ala Ser Leu Leu Tyr Leu Leu Thr
 210 215 220

131

His Tyr Leu Leu Pro Tyr Ala
225 230

<210> 91
<211> 198
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(198)

<221> misc_feature
<222> (1)...(198)
<223> n = A,T,C or G

<400> 91
atg gac gca ctg gcg ctg ctt ggg gga ctg gta aat nta gcc cgt ctg 48
Met Asp Ala Leu Ala Leu Leu Gly Gly Leu Val Asn Xaa Ala Arg Leu
1 5 10 15
ccc gag cgc tgg gga cct ggc cgc ttt gac tac tgg ggc aac tcc cac 96
Pro Glu Arg Trp Gly Pro Gly Arg Phe Asp Tyr Trp Gly Asn Ser His
20 25 30
cag atc atg cac ctg ctg agc gtg ggc tcc atc ctg cag ctg cac gcc 144
Gln Ile Met His Leu Leu Ser Val Gly Ser Ile Leu Gln Leu His Ala
35 40 45
ggc gtc gtg ccc gac ctg ctc tgg gct gcc cac cac gcc tgt ccc cgg 192
Gly Val Val Pro Asp Leu Leu Trp Ala Ala His His Ala Cys Pro Arg
50 55 60
gac tga 198
Asp *
65

<210> 92
<211> 65
<212> PRT
<213> Homo sapiens

<220>

132

<221> VARIANT

<222> (1)...(65)

<223> Xaa = Any Amino Acid

<400> 92

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Met Asp Ala Leu Ala Leu Leu Gly Gly Leu Val Asn Xaa Ala Arg Leu
 1           5           10           15
Pro Glu Arg Trp Gly Pro Gly Arg Phe Asp Tyr Trp Gly Asn Ser His
           20           25           30
Gln Ile Met His Leu Leu Ser Val Gly Ser Ile Leu Gln Leu His Ala
           35           40           45
Gly Val Val Pro Asp Leu Leu Trp Ala Ala His His Ala Cys Pro Arg
           50           55           60
Asp
65

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<210> 93

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(498)

<400> 93

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atg gtg tct aca gtg ttc tcg act tcg tcg ctg atg ctt gct ctg tca      48
Met Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu Ser
 1           5           10           15

agg cac agc cta ttg tct cct ttg ctc agt gtg aca tca ttc aga cgc      96
Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg Arg
           20           25           30

ttc tac aga ggt gac agc cca aca gat tcc caa aag gac atg att gaa      144
Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile Glu
           35           40           45

atc cct ttg cct cca tgg cag gag aga act gat gaa tcc ata gaa acc      192
Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu Thr
           50           55           60

aaa aga gcc cgc ctg ctc tat gag agc aga aag agg gga atg ttg gaa      240
Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu Glu

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133

65	70	75	80	
aac tgc att ctt ctt agt ctt ttt gct aaa gaa cat ctg cag cac atg				288
Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His Met				
	85	90	95	
aca gaa aag cag ctg aac ctc tat gac cgc ctg att aac gag cct agt				336
Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro Ser				
	100	105	110	
aat gac tgg gat att tac tac tgg gcc aca gaa gct aaa cca gcc cca				384
Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala Pro				
	115	120	125	
gaa ata ttt gaa aat gaa gtc atg gcc ctg ctg aga gac ttt gct aaa				432
Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala Lys				
	130	135	140	
aac aaa aac aaa gag cag aga ctg cgt gcc cca gat ctt gag tac ctc				480
Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr Leu				
	145	150	155	160
ttt gaa aag cca cgt tga				498
Phe Glu Lys Pro Arg *				
	165			

<210> 94

<211> 165

<212> PRT

<213> Homo sapiens

<400> 94

Met Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu Ser				
1	5	10	15	
Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg Arg				
	20	25	30	
Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile Glu				
	35	40	45	
Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu Thr				
	50	55	60	
Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu Glu				
65	70	75	80	
Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His Met				

134

[illegible]

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<210> 95
<211> 501
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(501)
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<400> 95																
atg	gcg	gtg	tct	aca	gtg	ttc	tcg	act	tcg	tcg	ctg	atg	ctt	gct	ctg	48
Met	Ala	Val	Ser	Thr	Val	Phe	Ser	Thr	Ser	Ser	Leu	Met	Leu	Ala	Leu	
1		5			10					15						
tca	agg	cac	agc	cta	ttg	tct	cct	ttg	ctc	agt	gtg	aca	tca	ttc	aga	96
Ser	Arg	His	Ser	Leu	Leu	Ser	Pro	Leu	Leu	Ser	Val	Thr	Ser	Phe	Arg	
			20		25					30						
cgc	ttc	tac	aga	ggc	gac	agc	cca	aca	gat	tcc	caa	aag	gac	atg	att	144
Arg	Phe	Tyr	Arg	Gly	Asp	Ser	Pro	Thr	Asp	Ser	Gln	Lys	Asp	Met	Ile	
			35		40					45						
gaa	atc	cct	ttg	cct	cca	tgg	cag	gag	aga	act	gat	gaa	tcc	ata	gaa	192
Glu	Ile	Pro	Leu	Pro	Pro	Trp	Gln	Glu	Arg	Thr	Asp	Glu	Ser	Ile	Glu	
50		55					60									
acc	aaa	aga	gcc	cgc	ctg	ctc	tat	gag	agc	aga	aag	agg	gga	atg	ttg	240
Thr	Lys	Arg	Ala	Arg	Leu	Leu	Tyr	Glu	Ser	Arg	Lys	Arg	Gly	Met	Leu	
65		70					75					80				
gaa	aac	tgc	att	ctt	ctt	agt	ctt	ttt	gct	aaa	gaa	cat	ctg	cag	cac	288
Glu	Asn	Cys	Ile	Leu	Leu	Ser	Leu	Phe	Ala	Lys	Glu	His	Leu	Gln	His	

135

	85	90	95	
atg aca gaa aag cag ctg aac ctc tat gac cgc ctg att aac gag cct				336
Met Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro				
	100	105	110	
agt aat gac tgg gat att tac tac tgg gcc aca gaa gct aaa cca gcc				384
Ser Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala				
	115	120	125	
cca gaa ata ttt gaa aat gaa gtc atg gcc ctg ctg aga gac ttt gct				432
Pro Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala				
	130	135	140	
aaa aac aaa aac aaa gag cag aga ctg cgt gcc cca gat ctt gag tac				480
Lys Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr				
	145	150	155	160
ctc ttt gaa aag cca cgt tga				501
Leu Phe Glu Lys Pro Arg *				
	165			

<210> 96

<211> 166

<212> PRT

<213> Homo sapiens

<400> 96

Met Ala Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu				
1	5	10	15	
Ser Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg				
20	25	30		
Arg Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile				
35	40	45		
Glu Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu				
50	55	60		
Thr Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu				
65	70	75	80	
Glu Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His				
85	90	95		
Met Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro				
100	105	110		
Ser Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala				

136

115 120 125
 Pro Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala
 130 135 140
 Lys Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr
 145 150 155 160
 Leu Phe Glu Lys Pro Arg
 165

<210> 97
 <211> 492
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(492)

<400> 97
 atg gct ggc ttc tat gga ttg tat acc tgg ctg act cat act atg ttt 48
 Met Ala Gly Phe Tyr Gly Leu Tyr Thr Trp Leu Thr His Thr Met Phe
 1 5 10 15

 ggc atc aat att gtc ttc ata cca tca gca tta gca gca atc ctt gga 96
 Gly Ile Asn Ile Val Phe Ile Pro Ser Ala Leu Ala Ala Ile Leu Gly
 20 25 30

 gca gtg cca ttc ctg ggg aca tac tgg gca gca gta cct gca gtt ctt 144
 Ala Val Pro Phe Leu Gly Thr Tyr Trp Ala Ala Val Pro Ala Val Leu
 35 40 45

 gac ctg tgg ctg aca caa ggg tta gga tgc aag gcc att tta ctg ttg 192
 Asp Leu Trp Leu Thr Gln Gly Leu Gly Cys Lys Ala Ile Leu Leu Leu
 50 55 60

 att ttt cat ctc ttg cca aca tac ttt gta gat act gca atc tac tct 240
 Ile Phe His Leu Leu Pro Thr Tyr Phe Val Asp Thr Ala Ile Tyr Ser
 65 70 75 80

 gac ata tca gga ggt ggc cat cct tac ctg aca ggc ttg gca gtg gcc 288
 Asp Ile Ser Gly Gly Gly His Pro Tyr Leu Thr Gly Leu Ala Val Ala
 85 90 95

 ggt gga gca tac tac cta ggc ctg gaa gga gca atc atc ggt cct att 336
 Gly Gly Ala Tyr Tyr Leu Gly Leu Glu Gly Ala Ile Ile Gly Pro Ile

137

100	105	110	
ctt ctc tgc ata ctt gtg gtt gct tcc aat atc tat agt gcc atg cta			384
Leu Leu Cys Ile Leu Val Val Ala Ser Asn Ile Tyr Ser Ala Met Leu			
115	120	125	
gtg agt ccc acg aat tca gtt ccc acg cca aac cag acc cca tgg cct			432
Val Ser Pro Thr Asn Ser Val Pro Thr Pro Asn Gln Thr Pro Trp Pro			
130	135	140	
gct cag cct cag cgg act ttc cgt gac att tct gaa gat ctg aaa tct			480
Ala Gln Pro Gln Arg Thr Phe Arg Asp Ile Ser Glu Asp Leu Lys Ser			
145	150	155	160
tca gta ggt tga			492
Ser Val Gly *			

<210> 98
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 98

Met	Ala	Gly	Phe	Tyr	Gly	Leu	Tyr	Thr	Trp	Leu	Thr	His	Thr	Met	Phe
1				5					10					15	
Gly	Ile	Asn	Ile	Val	Phe	Ile	Pro	Ser	Ala	Leu	Ala	Ala	Ile	Leu	Gly
		20					25					30			
Ala	Val	Pro	Phe	Leu	Gly	Thr	Tyr	Trp	Ala	Ala	Val	Pro	Ala	Val	Leu
	35					40					45				
Asp	Leu	Trp	Leu	Thr	Gln	Gly	Leu	Gly	Cys	Lys	Ala	Ile	Leu	Leu	Leu
50					55				60						
Ile	Phe	His	Leu	Leu	Pro	Thr	Tyr	Phe	Val	Asp	Thr	Ala	Ile	Tyr	Ser
65			70					75				80			
Asp	Ile	Ser	Gly	Gly	Gly	His	Pro	Tyr	Leu	Thr	Gly	Leu	Ala	Val	Ala
		85				90						95			
Gly	Gly	Ala	Tyr	Tyr	Leu	Gly	Leu	Glu	Gly	Ala	Ile	Ile	Gly	Pro	Ile
	100					105					110				
Leu	Leu	Cys	Ile	Leu	Val	Val	Ala	Ser	Asn	Ile	Tyr	Ser	Ala	Met	Leu
	115					120					125				
Val	Ser	Pro	Thr	Asn	Ser	Val	Pro	Thr	Pro	Asn	Gln	Thr	Pro	Trp	Pro
	130					135				140					
Ala	Gln	Pro	Gln	Arg	Thr	Phe	Arg	Asp	Ile	Ser	Glu	Asp	Leu	Lys	Ser

138

145 150 155 160
 Ser Val Gly

<210> 99
 <211> 1464
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1464)

<221> misc_feature
 <222> (1)...(1464)
 <223> n = A,T,C or G

<400> 99

atg tgg gga cct aac tcc tat gca tgg gtg ctc atg cag ttg gcc acc 48
 Met Trp Gly Pro Asn Ser Tyr Ala Trp Val Leu Met Gln Leu Ala Thr
 1 5 10 15

gcc cag gcg ggc atc att ctg gtg tct gtg aac cca gcc tac cag gct 96
 Ala Gln Ala Gly Ile Ile Leu Val Ser Val Asn Pro Ala Tyr Gln Ala
 20 25 30

atg gaa ctg gag tac gtc ctc aag aag gtg ggc tgc aag gcc ctt gtg 144
 Met Glu Leu Glu Tyr Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val
 35 40 45

ttc ccc aag caa ttc aag acc cag caa tac tac aac gtc ctg aag cag 192
 Phe Pro Lys Gln Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln
 50 55 60

atc tgt cca gaa gtg gag aat gcc cag cca ggg gcc ttg aag agt cag 240
 Ile Cys Pro Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln
 65 70 75 80

agg ctc cca gat ctg acc aca gtc atc tcg gtg gat gcc cct ttg ccg 288
 Arg Leu Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro
 85 90 95

ggg acc ctg ctc ctg gat gaa gtg gtg gcg gct ggc agc aca cgg cag 336
 Gly Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln

139

100	105	110	
cat ctg gac cag ctc caa tac aac cag cag ttc ctg tcc tgc cat gac			384
His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His Asp			
115	120	125	
ccc atc aac atc cag ttc acc tcg ggg aca aca ggc agc ccc aag ggg			432
Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro Lys Gly			
130	135	140	
gcc acc ctc tcc cac tac aac att gtc aac aac tcc aac att tta gga			480
Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn Ile Leu Gly			
145	150	155	160
gag cgc ctg aaa ctg cat gag aag aca cca gag cag ttg cgg atg atc			528
Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln Leu Arg Met Ile			
165	170	175	
ctg ccc aac ccc ctg tac cat tgc ctg ggt tcc gtg gca ggc aca atg			576
Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser Val Ala Gly Thr Met			
180	185	190	
atg tgt ctg atg tac ggt gcc acc ctc atc ctg gcc tct ccc atc ttc			624
Met Cys Leu Met Tyr Gly Ala Thr Leu Ile Leu Ala Ser Pro Ile Phe			
195	200	205	
aat ggc aag aag gca ctg gag gcc atc agc aga gag aga ggc acc ttc			672
Asn Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg Glu Arg Gly Thr Phe			
210	215	220	
ctg tat ggt acc ccc acg atg ttc gtg gac att ctg aac cag cca gac			720
Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile Leu Asn Gln Pro Asp			
225	230	235	240
ttc tcc agt tat gac atc tcg acc atg tgt gga ggt gtc att gct ggg			768
Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly Gly Val Ile Ala Gly			
245	250	255	
tcc cct gca cct cca gag ttg atc cga gcc atc atc aac aag ata aat			816
Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn			
260	265	270	
atg aag gac ctg gtg gtt gct tat gga acc aca gag aac agt ccc gtg			864
Met Lys Asp Leu Val Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val			

140

275	280	285	
aca ttc gcg cac ttc cct gag gac act gtg gag cag aag gca gaa agc			912
Thr Phe Ala His Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser			
290	295	300	
gtg ggc aga att atg cct cac acg gag gcc cgg atc atg aac atg gag			960
Val Gly Arg Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu			
305	310	315	320
gca ggg acg ctg gca aag ctg aac acg ccc ggg gag ctg tgc atc cga			1008
Ala Gly Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg			
325	330	335	
ggg tac tgc gtc atg ctg ggc tac tgg ggt gag cct cag aag aca gag			1056
Gly Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu			
340	345	350	
gaa gca gtg gat cag gac aag tgg tat tgg aca gga gat gtc gcc aca			1104
Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala Thr			
355	360	365	
atg aat gag cag ggc ttc tgc aag atc gtg ggc cgc tct aag gat atg			1152
Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys Asp Met			
370	375	380	
atc atc cgg ggt ggt gag aac atc tac ccc gca gag ctc gag gac ttc			1200
Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu Glu Asp Phe			
385	390	395	400
ttt cac aca cac ccg aag ntg cag gaa gtg cag gtg gtg gga gtg aag			1248
Phe His Thr His Pro Lys Xaa Gln Glu Val Gln Val Val Gly Val Lys			
405	410	415	
gac gat cgg atg ggg gaa gag att tgt gcc tgc att cgg ctg aag gac			1296
Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys Ile Arg Leu Lys Asp			
420	425	430	
ggg gag gag acc acg gtg gag gag ata aaa gct ttc tgc aaa ggg aag			1344
Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala Phe Cys Lys Gly Lys			
435	440	445	
atc tct cac ttc aag att ccg aag tac atc gtg ttt gtc aca aac tac			1392
Ile Ser His Phe Lys Ile Pro Lys Tyr Ile Val Phe Val Thr Asn Tyr			

141

450 455 460
 ccc ctc acc att tca gga aag atc cag aaa ttc aaa ctt cga gag cag 1440
 Pro Leu Thr Ile Ser Gly Lys Ile Gln Lys Phe Lys Leu Arg Glu Gln
 465 470 475 480
 atg gaa cga cat cta aat ctg tga 1464
 Met Glu Arg His Leu Asn Leu *
 485

<210> 100

<211> 487

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(487)

<223> Xaa = Any Amino Acid

<400> 100

Met Trp Gly Pro Asn Ser Tyr Ala Trp Val Leu Met Gln Leu Ala Thr
 1 5 10 15
 Ala Gln Ala Gly Ile Ile Leu Val Ser Val Asn Pro Ala Tyr Gln Ala
 20 25 30
 Met Glu Leu Glu Tyr Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val
 35 40 45
 Phe Pro Lys Gln Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln
 50 55 60
 Ile Cys Pro Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln
 65 70 75 80
 Arg Leu Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro
 85 90 95
 Gly Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln
 100 105 110
 His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His Asp
 115 120 125
 Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro Lys Gly
 130 135 140
 Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn Ile Leu Gly
 145 150 155 160
 Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln Leu Arg Met Ile
 165 170 175

142

Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser Val Ala Gly Thr Met
 180 185 190
 Met Cys Leu Met Tyr Gly Ala Thr Leu Ile Leu Ala Ser Pro Ile Phe
 195 200 205
 Asn Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg Glu Arg Gly Thr Phe
 210 215 220
 Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile Leu Asn Gln Pro Asp
 225 230 235 240
 Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly Gly Val Ile Ala Gly
 245 250 255
 Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn
 260 265 270
 Met Lys Asp Leu Val Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val
 275 280 285
 Thr Phe Ala His Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser
 290 295 300
 Val Gly Arg Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu
 305 310 315 320
 Ala Gly Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg
 325 330 335
 Gly Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu
 340 345 350
 Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala Thr
 355 360 365
 Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys Asp Met
 370 375 380
 Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu Glu Asp Phe
 385 390 395 400
 Phe His Thr His Pro Lys Xaa Gln Glu Val Gln Val Val Gly Val Lys
 405 410 415
 Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys Ile Arg Leu Lys Asp
 420 425 430
 Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala Phe Cys Lys Gly Lys
 435 440 445
 Ile Ser His Phe Lys Ile Pro Lys Tyr Ile Val Phe Val Thr Asn Tyr
 450 455 460
 Pro Leu Thr Ile Ser Gly Lys Ile Gln Lys Phe Lys Leu Arg Glu Gln
 465 470 475 480
 Met Glu Arg His Leu Asn Leu
 485

<210> 101

<211> 348

<212> DNA

143

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(348)

<400> 101

atg ggg atc acc ttc ctg gct gct ggg acc agc gtg cct gac tgc atg	48
Met Gly Ile Thr Phe Leu Ala Ala Gly Thr Ser Val Pro Asp Cys Met	
1 5 10 15	
gcc agc ctc att gtg gcc aga caa ggg atg ggg gac atg gct gtg tcc	96
Ala Ser Leu Ile Val Ala Arg Gln Gly Met Gly Asp Met Ala Val Ser	
20 25 30	
aac tcc att ggg agc aac gtg ttt gac atc ctg att ggc ctc ggt ctc	144
Asn Ser Ile Gly Ser Asn Val Phe Asp Ile Leu Ile Gly Leu Gly Leu	
35 40 45	
ccc tgg gct ctg cag acc ctg gct gtg gat tac gga tcc tac atc cgg	192
Pro Trp Ala Leu Gln Thr Leu Ala Val Asp Tyr Gly Ser Tyr Ile Arg	
50 55 60	
ctg aat agc agg ggg ctg atc tac tcc gta ggc ttg ctc ctg gcc tct	240
Leu Asn Ser Arg Gly Leu Ile Tyr Ser Val Gly Leu Leu Leu Ala Ser	
65 70 75 80	
gtt ttt gtc acg gtg ttc ggc gtc cac ctg aac aag tgg cag ctg gac	288
Val Phe Val Thr Val Phe Gly Val His Leu Asn Lys Trp Gln Leu Asp	
85 90 95	
aag aag ctg ggc tgt ggg tgc ctc ctc ctg tat ggg tgt tcc tgt gct	336
Lys Lys Leu Gly Cys Gly Cys Leu Leu Leu Tyr Gly Cys Ser Cys Ala	
100 105 110	
tct cca tca tga	348
Ser Pro Ser *	
115	

<210> 102

<211> 115

<212> PRT

<213> Homo sapiens

144

<400> 102

Met Gly Ile Thr Phe Leu Ala Ala Gly Thr Ser Val Pro Asp Cys Met
 1 5 10 15
 Ala Ser Leu Ile Val Ala Arg Gln Gly Met Gly Asp Met Ala Val Ser
 20 25 30
 Asn Ser Ile Gly Ser Asn Val Phe Asp Ile Leu Ile Gly Leu Gly Leu
 35 40 45
 Pro Trp Ala Leu Gln Thr Leu Ala Val Asp Tyr Gly Ser Tyr Ile Arg
 50 55 60
 Leu Asn Ser Arg Gly Leu Ile Tyr Ser Val Gly Leu Leu Leu Ala Ser
 65 70 75 80
 Val Phe Val Thr Val Phe Gly Val His Leu Asn Lys Trp Gln Leu Asp
 85 90 95
 Lys Lys Leu Gly Cys Gly Cys Leu Leu Leu Tyr Gly Cys Ser Cys Ala
 100 105 110
 Ser Pro Ser
 115

<210> 103

<211> 1239

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1239)

<400> 103

atg gcg ggc tct gtg gga ctg gcg ttg tgc ggg cag acg ttg gtg gtg 48
 Met Ala Gly Ser Val Gly Leu Ala Leu Cys Gly Gln Thr Leu Val Val
 1 5 10 15
 cgg ggc ggc agc cga ttc ctg gcc acc tcc ata gca agc agt gat gat 96
 Arg Gly Gly Ser Arg Phe Leu Ala Thr Ser Ile Ala Ser Ser Asp Asp
 20 25 30
 gac agc ctc ttc atc tat gac tgc agt gct gca gaa aag aag tca caa 144
 Asp Ser Leu Phe Ile Tyr Asp Cys Ser Ala Ala Glu Lys Lys Ser Gln
 35 40 45
 gaa aat aaa ggg gag gac gcg ccc ttg gac cag ggg agc ggt gcg att 192
 Glu Asn Lys Gly Glu Asp Ala Pro Leu Asp Gln Gly Ser Gly Ala Ile
 50 55 60

145

ctg gcg tcc acc ttc tcc aag tct ggc agc tat ttt gct tta acc gat	240
Leu Ala Ser Thr Phe Ser Lys Ser Gly Ser Tyr Phe Ala Leu Thr Asp	
65 70 75 80	
gac agt aag cgt ctg att ctt ttc cgt aca aaa cca tgg caa tgt ctg	288
Asp Ser Lys Arg Leu Ile Leu Phe Arg Thr Lys Pro Trp Gln Cys Leu	
85 90 95	
agt gtc agg acc gtg gca agg agg tgt aca gcc ctg act ttc ata gcc	336
Ser Val Arg Thr Val Ala Arg Arg Cys Thr Ala Leu Thr Phe Ile Ala	
100 105 110	
tcg gag gag aag gtc ttg gtg gcc gac aag tct gga gac gtc tac tcc	384
Ser Glu Glu Lys Val Leu Val Ala Asp Lys Ser Gly Asp Val Tyr Ser	
115 120 125	
ttt tcg gtg ctg gag cca cac ggg tgt ggc cgt cta gag ctg ggg cac	432
Phe Ser Val Leu Glu Pro His Gly Cys Gly Arg Leu Glu Leu Gly His	
130 135 140	
ctg tct atg ctg tta gat gtg gct gtg agt cct gat gac cgc ttc atc	480
Leu Ser Met Leu Leu Asp Val Ala Val Ser Pro Asp Asp Arg Phe Ile	
145 150 155 160	
ctc act gcc gac cgg gac gag aag atc cga gtc agc tgg gcc gcg gcg	528
Leu Thr Ala Asp Arg Asp Glu Lys Ile Arg Val Ser Trp Ala Ala Ala	
165 170 175	
ccc cat agc atc gag tcc ttc tgc ttg ggg cac aca gag ttt gtg agc	576
Pro His Ser Ile Glu Ser Phe Cys Leu Gly His Thr Glu Phe Val Ser	
180 185 190	
cgt atc tcc gtg gtg cca act cag ccc ggg ctg ctt ctg tcc tcc tct	624
Arg Ile Ser Val Val Pro Thr Gln Pro Gly Leu Leu Leu Ser Ser Ser	
195 200 205	
ggg gac ggc acc ctg agg ctc tgg gag tac agg agc ggc cgc cag ctg	672
Gly Asp Gly Thr Leu Arg Leu Trp Glu Tyr Arg Ser Gly Arg Gln Leu	
210 215 220	
cac tgc tgt cac ctg gcc agt ctg cag gag ctg gtg gac ccc cag gcc	720
His Cys Cys His Leu Ala Ser Leu Gln Glu Leu Val Asp Pro Gln Ala	
225 230 235 240	

146

ccc cag aag ttt gcc gcg tcc agg att gca ttc tgg tgc cag gag aac	768
Pro Gln Lys Phe Ala Ala Ser Arg Ile Ala Phe Trp Cys Gln Glu Asn	
245 250 255	
tgc gtg gcg ctc ctg tgc gac ggc act cct gtg gtc tac atc ttc cag	816
Cys Val Ala Leu Leu Cys Asp Gly Thr Pro Val Val Tyr Ile Phe Gln	
260 265 270	
ctg gac gcc cgc aga cag cag ttg gtg tac agg cag cag ctg gcg ttc	864
Leu Asp Ala Arg Arg Gln Gln Leu Val Tyr Arg Gln Gln Leu Ala Phe	
275 280 285	
cag cac caa gtg tgg gac gtg gct ttc gag gag acc cag ggg ctg tgg	912
Gln His Gln Val Trp Asp Val Ala Phe Glu Glu Thr Gln Gly Leu Trp	
290 295 300	
gtg ctc cag gac tgc cag gaa gcc ccc ctg gtg ctc tac agg cct gtg	960
Val Leu Gln Asp Cys Gln Glu Ala Pro Leu Val Leu Tyr Arg Pro Val	
305 310 315 320	
ggc gac cag tgg cag tct gtt cct gag agc acc gtg tta aag aaa gtc	1008
Gly Asp Gln Trp Gln Ser Val Pro Glu Ser Thr Val Leu Lys Lys Val	
325 330 335	
tct ggt gtt ctt cgt ggg aac tgg gcc atg ctg gaa ggc tct gcc ggc	1056
Ser Gly Val Leu Arg Gly Asn Trp Ala Met Leu Glu Gly Ser Ala Gly	
340 345 350	
gca gac gcc agc ttc agc agt ctc tac aag gcc acg ttc gac aac gtg	1104
Ala Asp Ala Ser Phe Ser Ser Leu Tyr Lys Ala Thr Phe Asp Asn Val	
355 360 365	
acc tcc tac ctg aag aag aaa gag gag aga ctg cag cag cag cta gag	1152
Thr Ser Tyr Leu Lys Lys Lys Glu Glu Arg Leu Gln Gln Gln Leu Glu	
370 375 380	
aag aag cag cgg cgc cgg agt ccc ccg cct ggg ccc gac ggg cat gcc	1200
Lys Lys Gln Arg Arg Arg Ser Pro Pro Pro Gly Pro Asp Gly His Ala	
385 390 395 400	
aag aag atg aga ccg ggg gag gcg acg cta agt tgc tga	1239
Lys Lys Met Arg Pro Gly Glu Ala Thr Leu Ser Cys *	
405 410	

147

<210> 104
 <211> 412
 <212> PRT
 <213> Homo sapiens

<400> 104

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Met Ala Gly Ser Val Gly Leu Ala Leu Cys Gly Gln Thr Leu Val Val
 1           5           10           15
Arg Gly Gly Ser Arg Phe Leu Ala Thr Ser Ile Ala Ser Ser Asp Asp
      20           25           30
Asp Ser Leu Phe Ile Tyr Asp Cys Ser Ala Ala Glu Lys Lys Ser Gln
      35           40           45
Glu Asn Lys Gly Glu Asp Ala Pro Leu Asp Gln Gly Ser Gly Ala Ile
      50           55           60
Leu Ala Ser Thr Phe Ser Lys Ser Gly Ser Tyr Phe Ala Leu Thr Asp
65           70           75           80
Asp Ser Lys Arg Leu Ile Leu Phe Arg Thr Lys Pro Trp Gln Cys Leu
      85           90           95
Ser Val Arg Thr Val Ala Arg Arg Cys Thr Ala Leu Thr Phe Ile Ala
      100          105          110
Ser Glu Glu Lys Val Leu Val Ala Asp Lys Ser Gly Asp Val Tyr Ser
      115          120          125
Phe Ser Val Leu Glu Pro His Gly Cys Gly Arg Leu Glu Leu Gly His
      130          135          140
Leu Ser Met Leu Leu Asp Val Ala Val Ser Pro Asp Asp Arg Phe Ile
145          150          155          160
Leu Thr Ala Asp Arg Asp Glu Lys Ile Arg Val Ser Trp Ala Ala Ala
      165          170          175
Pro His Ser Ile Glu Ser Phe Cys Leu Gly His Thr Glu Phe Val Ser
      180          185          190
Arg Ile Ser Val Val Pro Thr Gln Pro Gly Leu Leu Leu Ser Ser Ser
      195          200          205
Gly Asp Gly Thr Leu Arg Leu Trp Glu Tyr Arg Ser Gly Arg Gln Leu
      210          215          220
His Cys Cys His Leu Ala Ser Leu Gln Glu Leu Val Asp Pro Gln Ala
225          230          235          240
Pro Gln Lys Phe Ala Ala Ser Arg Ile Ala Phe Trp Cys Gln Glu Asn
      245          250          255
Cys Val Ala Leu Leu Cys Asp Gly Thr Pro Val Val Tyr Ile Phe Gln
      260          265          270
Leu Asp Ala Arg Arg Gln Gln Leu Val Tyr Arg Gln Gln Leu Ala Phe
      275          280          285

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148

Gln His Gln Val Trp Asp Val Ala Phe Glu Glu Thr Gln Gly Leu Trp
 290 295 300
 Val Leu Gln Asp Cys Gln Glu Ala Pro Leu Val Leu Tyr Arg Pro Val
 305 310 315 320
 Gly Asp Gln Trp Gln Ser Val Pro Glu Ser Thr Val Leu Lys Lys Val
 325 330 335
 Ser Gly Val Leu Arg Gly Asn Trp Ala Met Leu Glu Gly Ser Ala Gly
 340 345 350
 Ala Asp Ala Ser Phe Ser Ser Leu Tyr Lys Ala Thr Phe Asp Asn Val
 355 360 365
 Thr Ser Tyr Leu Lys Lys Lys Glu Glu Arg Leu Gln Gln Gln Leu Glu
 370 375 380
 Lys Lys Gln Arg Arg Arg Ser Pro Pro Pro Gly Pro Asp Gly His Ala
 385 390 395 400
 Lys Lys Met Arg Pro Gly Glu Ala Thr Leu Ser Cys
 405 410

<210> 105

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(645)

<400> 105

atg agt gat ttg gaa gat gat gag aca ccc cag ctt tct gcc cat gcc	48
Met Ser Asp Leu Glu Asp Asp Glu Thr Pro Gln Leu Ser Ala His Ala	
1 5 10 15	
tta gca gct ctc cag gaa ttt tat gct gag caa aag caa caa att gag	96
Leu Ala Ala Leu Gln Glu Phe Tyr Ala Glu Gln Lys Gln Gln Ile Glu	
20 25 30	
cca ggc gag gat gat aaa tat aac att gga ata ata gaa gag aat tgg	144
Pro Gly Glu Asp Asp Lys Tyr Asn Ile Gly Ile Ile Glu Glu Asn Trp	
35 40 45	
caa ctg agc cag ttt tgg tat agt cag gaa act gct ctg cag ctg gca	192
Gln Leu Ser Gln Phe Trp Tyr Ser Gln Glu Thr Ala Leu Gln Leu Ala	
50 55 60	
cag gag gca att gca gct gta gga gaa ggt ggc aga atc gca tgt gtg	240

149

Gln	Glu	Ala	Ile	Ala	Ala	Val	Gly	Glu	Gly	Gly	Arg	Ile	Ala	Cys	Val	
65					70					75					80	
agt gcc cct agt gtt tac cag aaa ctc aga gag ctg tgc aga gaa aac																288
Ser Ala Pro Ser Val Tyr Gln Lys Leu Arg Glu Leu Cys Arg Glu Asn																
				85					90						95	
ttt tcg ata tac atc ttt gaa tat gac aaa aga ttt gcc atg tat gga																336
Phe Ser Ile Tyr Ile Phe Glu Tyr Asp Lys Arg Phe Ala Met Tyr Gly																
			100					105					110			
gag gag ttt att ttc tat gat tac aat aat cca ttg gac tta ccc gaa																384
Glu Glu Phe Ile Phe Tyr Asp Tyr Asn Asn Pro Leu Asp Leu Pro Glu																
		115					120					125				
aga att gct gca cat agt ttt gac atc gta ata gca gat cct ccc tat																432
Arg Ile Ala Ala His Ser Phe Asp Ile Val Ile Ala Asp Pro Pro Tyr																
		130				135				140						
ctt tcg gag gaa tgt ctc aga aaa aca tcg gaa acc gtc aag tac ctg																480
Leu Ser Glu Glu Cys Leu Arg Lys Thr Ser Glu Thr Val Lys Tyr Leu																
145					150				155						160	
acg cgg ggc aag att ctg ctg tgc aca ggt gcc atc atg gaa gaa cag																528
Thr Arg Gly Lys Ile Leu Leu Cys Thr Gly Ala Ile Met Glu Glu Gln																
			165					170					175			
gca gca gaa ctc ctt gga gtg aag atg tgc acg ttt gtt cca aga cac																576
Ala Ala Glu Leu Leu Gly Val Lys Met Cys Thr Phe Val Pro Arg His																
		180					185					190				
acc cgg aac ttg gca aat gag ttt cgc tgt tat gtg aat tat gat tct																624
Thr Arg Asn Leu Ala Asn Glu Phe Arg Cys Tyr Val Asn Tyr Asp Ser																
		195				200					205					
ggg ctg gac tgt ggg atc tga																645
Gly Leu Asp Cys Gly Ile *																
210																

<210> 106

<211> 214

<212> PRT

<213> Homo sapiens

150

<400> 106

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Met Ser Asp Leu Glu Asp Asp Glu Thr Pro Gln Leu Ser Ala His Ala
 1           5           10           15
Leu Ala Ala Leu Gln Glu Phe Tyr Ala Glu Gln Lys Gln Gln Ile Glu
      20           25           30
Pro Gly Glu Asp Asp Lys Tyr Asn Ile Gly Ile Ile Glu Glu Asn Trp
      35           40           45
Gln Leu Ser Gln Phe Trp Tyr Ser Gln Glu Thr Ala Leu Gln Leu Ala
      50           55           60
Gln Glu Ala Ile Ala Ala Val Gly Glu Gly Gly Arg Ile Ala Cys Val
65           70           75           80
Ser Ala Pro Ser Val Tyr Gln Lys Leu Arg Glu Leu Cys Arg Glu Asn
      85           90           95
Phe Ser Ile Tyr Ile Phe Glu Tyr Asp Lys Arg Phe Ala Met Tyr Gly
      100          105          110
Glu Glu Phe Ile Phe Tyr Asp Tyr Asn Asn Pro Leu Asp Leu Pro Glu
      115          120          125
Arg Ile Ala Ala His Ser Phe Asp Ile Val Ile Ala Asp Pro Pro Tyr
      130          135          140
Leu Ser Glu Glu Cys Leu Arg Lys Thr Ser Glu Thr Val Lys Tyr Leu
145          150          155          160
Thr Arg Gly Lys Ile Leu Leu Cys Thr Gly Ala Ile Met Glu Glu Gln
      165          170          175
Ala Ala Glu Leu Leu Gly Val Lys Met Cys Thr Phe Val Pro Arg His
      180          185          190
Thr Arg Asn Leu Ala Asn Glu Phe Arg Cys Tyr Val Asn Tyr Asp Ser
      195          200          205
Gly Leu Asp Cys Gly Ile
210

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<210> 107

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(264)

<400> 107

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atg aag agc agc act ctg ttg acg atc cta gtt ctc cag gcc ctt ctg
Met Lys Ser Ser Thr Leu Leu Thr Ile Leu Val Leu Gln Ala Leu Leu
 1           5           10           15

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48

151

gtc tct acg gcc gtg ccc aaa gga cct gca ggc ccg aag aag cag tgc 96
 Val Ser Thr Ala Val Pro Lys Gly Pro Ala Gly Pro Lys Lys Gln Cys
 20 25 30

tgg tgc ggc gag tgc acc agc tgg tcg ggc gtg tgg acc tgc gac gac 144
 Trp Cys Gly Glu Cys Thr Ser Trp Ser Gly Val Trp Thr Cys Asp Asp
 35 40 45

ctc ctc acc aag tgc gcc gcc acc tgc aag aac tgc gtc ccc gtc tcc 192
 Leu Leu Thr Lys Cys Ala Ala Thr Cys Lys Asn Cys Val Pro Val Ser
 50 55 60

acg gac aag ggc gcc acc aag tac aga tgc cgc gac ttc ctc ccc gaa 240
 Thr Asp Lys Gly Ala Thr Lys Tyr Arg Cys Arg Asp Phe Leu Pro Glu
 65 70 75 80

aac tgc ggc tgc aag atc cac tag 264
 Asn Cys Gly Cys Lys Ile His *
 85

<210> 108

<211> 87

<212> PRT

<213> Homo sapiens

<400> 108

Met Lys Ser Ser Thr Leu Leu Thr Ile Leu Val Leu Gln Ala Leu Leu
 1 5 10 15
 Val Ser Thr Ala Val Pro Lys Gly Pro Ala Gly Pro Lys Lys Gln Cys
 20 25 30
 Trp Cys Gly Glu Cys Thr Ser Trp Ser Gly Val Trp Thr Cys Asp Asp
 35 40 45
 Leu Leu Thr Lys Cys Ala Ala Thr Cys Lys Asn Cys Val Pro Val Ser
 50 55 60
 Thr Asp Lys Gly Ala Thr Lys Tyr Arg Cys Arg Asp Phe Leu Pro Glu
 65 70 75 80
 Asn Cys Gly Cys Lys Ile His
 85

<210> 109

<211> 378

<212> DNA

152

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(378)

<400> 109

atg aag gaa gaa gga aaa ctc cta ttt tat gcg aca agc cgt gcc tat	48
Met Lys Glu Glu Gly Lys Leu Leu Phe Tyr Ala Thr Ser Arg Ala Tyr	
1 5 10 15	
gtg gaa tct atc tgt tcg aat aat ttt gac agt ttc cta cat gaa act	96
Val Glu Ser Ile Cys Ser Asn Asn Phe Asp Ser Phe Leu His Glu Thr	
20 25 30	
cat gaa aac aaa tac gga aaa gga att tac ttt gca aaa gat gcc atc	144
His Glu Asn Lys Tyr Gly Lys Gly Ile Tyr Phe Ala Lys Asp Ala Ile	
35 40 45	
tat tcc cac aaa aat tgc ccg tat gat gcc aaa aac gtc gtt atg ttt	192
Tyr Ser His Lys Asn Cys Pro Tyr Asp Ala Lys Asn Val Val Met Phe	
50 55 60	
gta gcc caa gtt ctg gtt gga aag ttt act gaa gga aat ata acg tac	240
Val Ala Gln Val Leu Val Gly Lys Phe Thr Glu Gly Asn Ile Thr Tyr	
65 70 75 80	
acg agc cct cct cca cag ttc gac agc tgt gtg gat acc aga tcg aat	288
Thr Ser Pro Pro Pro Gln Phe Asp Ser Cys Val Asp Thr Arg Ser Asn	
85 90 95	
ccc tcc gtt ttt gtc atc ttt cag aaa gat cag gtt tac cca caa tat	336
Pro Ser Val Phe Val Ile Phe Gln Lys Asp Gln Val Tyr Pro Gln Tyr	
100 105 110	
gtg att gaa tat act gaa gac aaa gcc tgc gtg att agt tag	378
Val Ile Glu Tyr Thr Glu Asp Lys Ala Cys Val Ile Ser *	
115 120 125	

<210> 110

<211> 125

<212> PRT

<213> Homo sapiens

153

<400> 110
 Met Lys Glu Glu Gly Lys Leu Leu Phe Tyr Ala Thr Ser Arg Ala Tyr
 1 5 10 15
 Val Glu Ser Ile Cys Ser Asn Asn Phe Asp Ser Phe Leu His Glu Thr
 20 25 30
 His Glu Asn Lys Tyr Gly Lys Gly Ile Tyr Phe Ala Lys Asp Ala Ile
 35 40 45
 Tyr Ser His Lys Asn Cys Pro Tyr Asp Ala Lys Asn Val Val Met Phe
 50 55 60
 Val Ala Gln Val Leu Val Gly Lys Phe Thr Glu Gly Asn Ile Thr Tyr
 65 70 75 80
 Thr Ser Pro Pro Pro Gln Phe Asp Ser Cys Val Asp Thr Arg Ser Asn
 85 90 95
 Pro Ser Val Phe Val Ile Phe Gln Lys Asp Gln Val Tyr Pro Gln Tyr
 100 105 110
 Val Ile Glu Tyr Thr Glu Asp Lys Ala Cys Val Ile Ser
 115 120 125

<210> 111
 <211> 1965
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1965)

<400> 111
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 Met Ala Ala Ala Ala Leu Gly Ser Ser Ser Gly Ser Ala Ser Pro Ala
 1 5 10 15
 gtg gct gag ctc tgc cag aac acc ccg gag acc ttt ttg gag gcc tcc 96
 Val Ala Glu Leu Cys Gln Asn Thr Pro Glu Thr Phe Leu Glu Ala Ser
 20 25 30
 aag ctg ctg ctc acc tat gct gac aac atc ctc aga aac cct aat gat 144
 Lys Leu Leu Leu Thr Tyr Ala Asp Asn Ile Leu Arg Asn Pro Asn Asp
 35 40 45
 gaa aaa tat aga tcc atc cgg att gga aac aca gcc ttt tct act aga 192
 Glu Lys Tyr Arg Ser Ile Arg Ile Gly Asn Thr Ala Phe Ser Thr Arg
 50 55 60

154

ctc ttg cct gtc aga gga gct gtt gaa tgt tta ttt gaa atg ggc ttt	240
Leu Leu Pro Val Arg Gly Ala Val Glu Cys Leu Phe Glu Met Gly Phe	
65 70 75 80	
gaa gag gga gaa aca cat ctc atc ttt cct aaa aaa gct tca gtg gag	288
Glu Glu Gly Glu Thr His Leu Ile Phe Pro Lys Lys Ala Ser Val Glu	
85 90 95	
cag ctg caa aaa att cgt gac ctg att gcc ata gag aga agt agc aga	336
Gln Leu Gln Lys Ile Arg Asp Leu Ile Ala Ile Glu Arg Ser Ser Arg	
100 105 110	
ctg gat ggc tca aat aag agc cac aaa gta aag tca tct cag caa cct	384
Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro	
115 120 125	
gca gcc agt acc cag ctt cct aca aca cca tct tca aat ccc agt ggg	432
Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly	
130 135 140	
tta aac cag cac aca agg aac cgt caa ggg cag tca tca gat cca cca	480
Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro	
145 150 155 160	
tct gct tca acg gtt gct gct gac tca gcc att cta gaa gtt ctt cag	528
Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln	
165 170 175	
tcc aac att cag cat gtg ctg gtc tat gaa aat cct gct ctt cag gag	576
Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu	
180 185 190	
aaa gcg ttg gct tgt att ccg gtc caa gaa cta aaa agg aaa tca caa	624
Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln	
195 200 205	
gaa aag tta tcg aga gct aga aaa ttg gat aaa ggt atc aat ata agt	672
Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser	
210 215 220	
gat gag gat ttt ctt ttg ctg gag ctt ttg cac tgg ttt aag gaa gaa	720
Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu	
225 230 235 240	

155

ttt ttt cac tgg gtg aat aac gtt ttg tgc agc aaa tgt ggt gga cag	768
Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln	
245 250 255	
act agg tct aga gat aga tca tta ctg ccc agt gat gat gag ctg aag	816
Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys	
260 265 270	
tgg ggt gca aag gaa gtg gaa gat cat tac tgt gat gcc tgc cag ttc	864
Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe	
275 280 285	
agc aat cga ttc cca aga tat aat aac cct gag aaa ctt ttg gaa aca	912
Ser Asn Arg Phe Pro Arg Tyr Asn Asn Pro Glu Lys Leu Leu Glu Thr	
290 295 300	
aga tgt gga cgg tgt ggc gag tgg gcc aat tgt ttt aca ctg tgc tgc	960
Arg Cys Gly Arg Cys Gly Glu Trp Ala Asn Cys Phe Thr Leu Cys Cys	
305 310 315 320	
cga gct gta ggg ttt gaa gct cgc tat gtt tgg gat tac aca gac cat	1008
Arg Ala Val Gly Phe Glu Ala Arg Tyr Val Trp Asp Tyr Thr Asp His	
325 330 335	
gtc tgg aca gaa gtc tat tct cct tct cag cag cgg tgg ctg cac tgt	1056
Val Trp Thr Glu Val Tyr Ser Pro Ser Gln Gln Arg Trp Leu His Cys	
340 345 350	
gat gca tgt gaa gat gtc tgt gac aag cca ctc ctt tat gaa ata gga	1104
Asp Ala Cys Glu Asp Val Cys Asp Lys Pro Leu Leu Tyr Glu Ile Gly	
355 360 365	
tgg ggc aag aag ctt tcc tat gtc ata gca ttt tca aaa gat gag gta	1152
Trp Gly Lys Lys Leu Ser Tyr Val Ile Ala Phe Ser Lys Asp Glu Val	
370 375 380	
gtt gat gtc act tgg cga tat tcc tgc aaa cat gaa gag gtg att gcc	1200
Val Asp Val Thr Trp Arg Tyr Ser Cys Lys His Glu Glu Val Ile Ala	
385 390 395 400	
aga aga act aag gtt aaa gaa gca tta ctt cga gac act att aat ggg	1248
Arg Arg Thr Lys Val Lys Glu Ala Leu Leu Arg Asp Thr Ile Asn Gly	
405 410 415	

156

ctt aat aag cag agg caa ctg ttt ttg tca gaa aac aga agg aaa gaa Leu Asn Lys Gln Arg Gln Leu Phe Leu Ser Glu Asn Arg Arg Lys Glu 420 425 430	1296
ctt ctc cag agg ata att gtg gag ctt gtt gaa ttt ata tct ccc aaa Leu Leu Gln Arg Ile Ile Val Glu Leu Val Glu Phe Ile Ser Pro Lys 435 440 445	1344
acc cct aaa cct gga gaa ctt ggg gga aga ata tct ggg tca gtg gct Thr Pro Lys Pro Gly Glu Leu Gly Gly Arg Ile Ser Gly Ser Val Ala 450 455 460	1392
tgg aga gta gcc cga ggt gaa atg ggt cta cag aga aaa gaa acc ttg Trp Arg Val Ala Arg Gly Glu Met Gly Leu Gln Arg Lys Glu Thr Leu 465 470 475 480	1440
ttt att ccc tgt gaa aat gag aag att tct aaa cag ctc cac ctt tgt Phe Ile Pro Cys Glu Asn Glu Lys Ile Ser Lys Gln Leu His Leu Cys 485 490 495	1488
tac aat att gtg aaa gat cgt tat gtt cga gtt tca aat aac aat caa Tyr Asn Ile Val Lys Asp Arg Tyr Val Arg Val Ser Asn Asn Asn Gln 500 505 510	1536
acc att tct gga tgg gag aat ggc gtg tgg aaa atg gaa tct ata ttc Thr Ile Ser Gly Trp Glu Asn Gly Val Trp Lys Met Glu Ser Ile Phe 515 520 525	1584
aga aaa gtt gaa aca gac tgg cac atg gta tat ttg gcc cga aag gaa Arg Lys Val Glu Thr Asp Trp His Met Val Tyr Leu Ala Arg Lys Glu 530 535 540	1632
gga tca tct ttt gct tat att tcc tgg aag ttt gag tgt ggg tca gtt Gly Ser Ser Phe Ala Tyr Ile Ser Trp Lys Phe Glu Cys Gly Ser Val 545 550 555 560	1680
ggc cta aaa gta gat agc att tct att aga aca agt agt caa act ttt Gly Leu Lys Val Asp Ser Ile Ser Ile Arg Thr Ser Ser Gln Thr Phe 565 570 575	1728
cag act gga aca gta gaa tgg aaa ttg cga tct gat aca gca caa gta Gln Thr Gly Thr Val Glu Trp Lys Leu Arg Ser Asp Thr Ala Gln Val 580 585 590	1776

157

gaa ctg aca ggc gat aac agt ctt cac tcc tat gct gat ttt tct ggt 1824
Glu Leu Thr Gly Asp Asn Ser Leu His Ser Tyr Ala Asp Phe Ser Gly
595 600 605

gcc act gaa gtt att ttg gaa gca gaa tta agc aga gga gat ggt gat 1872
Ala Thr Glu Val Ile Leu Glu Ala Glu Leu Ser Arg Gly Asp Gly Asp
610 615 620

gtc gct tgg caa cac acc cag ctg ttt aga caa agc tta aat gac cat 1920
Val Ala Trp Gln His Thr Gln Leu Phe Arg Gln Ser Leu Asn Asp His
625 630 635 640

gaa gaa aat tgt ttg gag ata att ata aaa ttc agt gac ctt tga 1965
Glu Glu Asn Cys Leu Glu Ile Ile Ile Lys Phe Ser Asp Leu *
645 650

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<210> 112
<211> 654
<212> PRT
<213> Homo sapiens
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<400> 112																
Met	Ala	Ala	Ala	Ala	Leu	Gly	Ser	Ser	Ser	Gly	Ser	Ala	Ser	Pro	Ala	
1				5					10					15		
Val	Ala	Glu	Leu	Cys	Gln	Asn	Thr	Pro	Glu	Thr	Phe	Leu	Glu	Ala	Ser	
			20					25					30			
Lys	Leu	Leu	Leu	Thr	Tyr	Ala	Asp	Asn	Ile	Leu	Arg	Asn	Pro	Asn	Asp	
		35					40					45				
Glu	Lys	Tyr	Arg	Ser	Ile	Arg	Ile	Gly	Asn	Thr	Ala	Phe	Ser	Thr	Arg	
	50					55					60					
Leu	Leu	Pro	Val	Arg	Gly	Ala	Val	Glu	Cys	Leu	Phe	Glu	Met	Gly	Phe	
65					70					75				80		
Glu	Glu	Gly	Glu	Thr	His	Leu	Ile	Phe	Pro	Lys	Lys	Ala	Ser	Val	Glu	
				85					90					95		
Gln	Leu	Gln	Lys	Ile	Arg	Asp	Leu	Ile	Ala	Ile	Glu	Arg	Ser	Ser	Arg	
			100					105					110			
Leu	Asp	Gly	Ser	Asn	Lys	Ser	His	Lys	Val	Lys	Ser	Ser	Gln	Gln	Pro	
	115					120					125					
Ala	Ala	Ser	Thr	Gln	Leu	Pro	Thr	Thr	Pro	Ser	Ser	Asn	Pro	Ser	Gly	
	130					135				140						
Leu	Asn	Gln	His	Thr	Arg	Asn	Arg	Gln	Gly	Gln	Ser	Ser	Asp	Pro	Pro	
145					150					155					160	

158

Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln
 165 170 175
 Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu
 180 185 190
 Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln
 195 200 205
 Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser
 210 215 220
 Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu
 225 230 235 240
 Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln
 245 250 255
 Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys
 260 265 270
 Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe
 275 280 285
 Ser Asn Arg Phe Pro Arg Tyr Asn Asn Pro Glu Lys Leu Leu Glu Thr
 290 295 300
 Arg Cys Gly Arg Cys Gly Glu Trp Ala Asn Cys Phe Thr Leu Cys Cys
 305 310 315 320
 Arg Ala Val Gly Phe Glu Ala Arg Tyr Val Trp Asp Tyr Thr Asp His
 325 330 335
 Val Trp Thr Glu Val Tyr Ser Pro Ser Gln Gln Arg Trp Leu His Cys
 340 345 350
 Asp Ala Cys Glu Asp Val Cys Asp Lys Pro Leu Leu Tyr Glu Ile Gly
 355 360 365
 Trp Gly Lys Lys Leu Ser Tyr Val Ile Ala Phe Ser Lys Asp Glu Val
 370 375 380
 Val Asp Val Thr Trp Arg Tyr Ser Cys Lys His Glu Glu Val Ile Ala
 385 390 395 400
 Arg Arg Thr Lys Val Lys Glu Ala Leu Leu Arg Asp Thr Ile Asn Gly
 405 410 415
 Leu Asn Lys Gln Arg Gln Leu Phe Leu Ser Glu Asn Arg Arg Lys Glu
 420 425 430
 Leu Leu Gln Arg Ile Ile Val Glu Leu Val Glu Phe Ile Ser Pro Lys
 435 440 445
 Thr Pro Lys Pro Gly Glu Leu Gly Gly Arg Ile Ser Gly Ser Val Ala
 450 455 460
 Trp Arg Val Ala Arg Gly Glu Met Gly Leu Gln Arg Lys Glu Thr Leu
 465 470 475 480
 Phe Ile Pro Cys Glu Asn Glu Lys Ile Ser Lys Gln Leu His Leu Cys
 485 490 495
 Tyr Asn Ile Val Lys Asp Arg Tyr Val Arg Val Ser Asn Asn Asn Gln
 500 505 510

159

Thr	Ile	Ser	Gly	Trp	Glu	Asn	Gly	Val	Trp	Lys	Met	Glu	Ser	Ile	Phe
515						520						525			
Arg	Lys	Val	Glu	Thr	Asp	Trp	His	Met	Val	Tyr	Leu	Ala	Arg	Lys	Glu
530						535						540			
Gly	Ser	Ser	Phe	Ala	Tyr	Ile	Ser	Trp	Lys	Phe	Glu	Cys	Gly	Ser	Val
545						550						555			
Gly	Leu	Lys	Val	Asp	Ser	Ile	Ser	Ile	Arg	Thr	Ser	Ser	Gln	Thr	Phe
			565						570			575			
Gln	Thr	Gly	Thr	Val	Glu	Trp	Lys	Leu	Arg	Ser	Asp	Thr	Ala	Gln	Val
			580						585			590			
Glu	Leu	Thr	Gly	Asp	Asn	Ser	Leu	His	Ser	Tyr	Ala	Asp	Phe	Ser	Gly
595						600						605			
Ala	Thr	Glu	Val	Ile	Leu	Glu	Ala	Glu	Leu	Ser	Arg	Gly	Asp	Gly	Asp
610						615						620			
Val	Ala	Trp	Gln	His	Thr	Gln	Leu	Phe	Arg	Gln	Ser	Leu	Asn	Asp	His
625						630						635			
Glu	Glu	Asn	Cys	Leu	Glu	Ile	Ile	Ile	Lys	Phe	Ser	Asp	Leu		
			645						650						

<210> 113
<211> 585
<212> DNA
<213> Homo sapiens

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<220>  
<221> CDS  
<222> (1)...(585)
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<400> 113																
atg	tct	gca	ttg	tgg	ctg	ctg	ctg	ggc	ctc	ctt	gcc	ctg	atg	gac	ttg	48
Met	Ser	Ala	Leu	Trp	Leu	Leu	Leu	Gly	Leu	Leu	Ala	Leu	Met	Asp	Leu	
1			5			10			15							
tct	gaa	agc	agc	aac	tgg	gga	tgc	tat	gga	aac	atc	caa	agc	ctg	gac	96
Ser	Glu	Ser	Ser	Asn	Trp	Gly	Cys	Tyr	Gly	Asn	Ile	Gln	Ser	Leu	Asp	
			20			25			30							
acc	cct	gga	gca	tct	tgt	ggg	att	gga	aga	cgt	cac	ggc	ctg	aac	tac	144
Thr	Pro	Gly	Ala	Ser	Cys	Gly	Ile	Gly	Arg	Arg	His	Gly	Leu	Asn	Tyr	
35			40			45										
tgt	gga	gtt	cgt	gct	tct	gaa	agg	ctg	gct	gaa	ata	gac	atg	cca	tac	192
Cys	Gly	Val	Arg	Ala	Ser	Glu	Arg	Leu	Ala	Glu	Ile	Asp	Met	Pro	Tyr	
50			55			60										

160

ctc ctg aaa tat caa ccc atg atg caa acc att ggc caa aag tac tgc	240
Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys	
65 70 75 80	
atg gat cct gcc gtg atc gct ggt gtc ttg tcc agg aag tct ccc ggt	288
Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly	
85 90 95	
gac aaa att ctg gtc aac atg ggc gat agg act agc atg gtg cag gac	336
Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp	
100 105 110	
cct ggc tct caa gct ccc aca tcc tgg att agt gag tct cag gtt tcc	384
Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser	
115 120 125	
cag aca act gaa gtt ctg act act aga atc aaa gaa atc cag agg agg	432
Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg	
130 135 140	
ttt cca acc tgg acc cct gac cag tac ctg aga ggt gga ctc tgt gcc	480
Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala	
145 150 155 160	
tac agt ggg ggt gct ggc tat gtc cga agc agc cag gac ctg agc tgt	528
Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys	
165 170 175	
gac ttc tgc aat gat gtc ctt gca cga gcc aag tac ctc aag aga cat	576
Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His	
180 185 190	
ggc ttc taa	585
Gly Phe *	

<210> 114

<211> 194

<212> PRT

<213> Homo sapiens

<400> 114

161

Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp Leu
 1 5 10 15
 Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser Leu Asp
 20 25 30
 Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu Asn Tyr
 35 40 45
 Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met Pro Tyr
 50 55 60
 Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys
 65 70 75 80
 Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly
 85 90 95
 Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp
 100 105 110
 Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser
 115 120 125
 Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg
 130 135 140
 Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala
 145 150 155 160
 Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys
 165 170 175
 Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His
 180 185 190
 Gly Phe

<210> 115

<211> 933

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(933)

<221> misc_feature

<222> (1)...(933)

<223> n = A,T,C or G

<400> 115

atg ctg gtg gtg gag gtg gcg aac ggc cgc tcc ctg gtg tgg gga gcc
 Met Leu Val Val Glu Val Ala Asn Gly Arg Ser Leu Val Trp Gly Ala
 1 5 10 15

48

162

gag gcg gtg cag gcc ctc cgg gag cgc ctg ggt gtg ggg ggc cgc acg Glu Ala Val Gln Ala Leu Arg Glu Arg Leu Gly Val Gly Gly Arg Thr 20 25 30	96
gta ggc gcc ctg ccc cgc ggg ccc cgc cag aac tcg cgc ctg ggc ctc Val Gly Ala Leu Pro Arg Gly Pro Arg Gln Asn Ser Arg Leu Gly Leu 35 40 45	144
ccg ctg ctg ctg atg ccc gaa gag gcg cgg ctc ttg gcc gag atc ggc Pro Leu Leu Leu Met Pro Glu Glu Ala Arg Leu Leu Ala Glu Ile Gly 50 55 60	192
gcc gtg act ctg gtc agc gcc ccg cgt cca gac tct cgg cac cac agc Ala Val Thr Leu Val Ser Ala Pro Arg Pro Asp Ser Arg His His Ser 65 70 75 80	240
ctg gcc ctg aca tcc ttc aag cgc can caa gag gag agc ttc cag gag Leu Ala Leu Thr Ser Phe Lys Arg Xaa Gln Glu Glu Ser Phe Gln Glu 85 90 95	288
cag agc gcc ttg gca gct gag gcc cgg gag acc cgt cgt cag gag ctc Gln Ser Ala Leu Ala Ala Glu Ala Arg Glu Thr Arg Arg Gln Glu Leu 100 105 110	336
ctg gag aag att acg gag ggc cag gct gct aag aag cag aaa cta gaa Leu Glu Lys Ile Thr Glu Gly Gln Ala Ala Lys Lys Gln Lys Leu Glu 115 120 125	384
cag gct tca ggg gcc agc tca agc cag gag gcc ggc tcg agc cag gct Gln Ala Ser Gly Ala Ser Ser Ser Gln Glu Ala Gly Ser Ser Gln Ala 130 135 140	432
gcc aaa gag gat gag acc agt gat ggc cag gct tcg gga gag cag gag Ala Lys Glu Asp Glu Thr Ser Asp Gly Gln Ala Ser Gly Glu Gln Glu 145 150 155 160	480
gaa gct ggc ccc tcg tct tcc caa gca gga ccc tca aat ggg gta gcc Glu Ala Gly Pro Ser Ser Ser Gln Ala Gly Pro Ser Asn Gly Val Ala 165 170 175	528
ccc ttg ccc aga tct gct ctc ctt gtc cag ctg gcc act gcc agg cct Pro Leu Pro Arg Ser Ala Leu Leu Val Gln Leu Ala Thr Ala Arg Pro 180 185 190	576

163

cga ccg gtc aag gcc agg ccc ctg gac tgg cgt gtc cag tct aaa gac	624
Arg Pro Val Lys Ala Arg Pro Leu Asp Trp Arg Val Gln Ser Lys Asp	
195 200 205	
tgg ccc cac gcc ggc cgc cct gcc cac gag ctg cgc tac agt atc tac	672
Trp Pro His Ala Gly Arg Pro Ala His Glu Leu Arg Tyr Ser Ile Tyr	
210 215 220	
aga gac ctg tgg gag cga ggc ttc ttc ctc agt gcg gct ggc aag ttc	720
Arg Asp Leu Trp Glu Arg Gly Phe Phe Leu Ser Ala Ala Gly Lys Phe	
225 230 235 240	
gga ggt gac ttc ctg gtc tat cct ggt gac ccc ctc cgc ttc cac gcc	768
Gly Gly Asp Phe Leu Val Tyr Pro Gly Asp Pro Leu Arg Phe His Ala	
245 250 255	
cat tat atc gct cag tgc tgg gcc cct gag gac acc atc cca ctc caa	816
His Tyr Ile Ala Gln Cys Trp Ala Pro Glu Asp Thr Ile Pro Leu Gln	
260 265 270	
gac ctg gtt gct gct ggg cgc ctt gga acc agc gtc aga aag acc ctg	864
Asp Leu Val Ala Ala Gly Arg Leu Gly Thr Ser Val Arg Lys Thr Leu	
275 280 285	
ctc ctc tgt tct ccg cag cct gat ggt aag gtg gtc tac acc tcc ctg	912
Leu Leu Cys Ser Pro Gln Pro Asp Gly Lys Val Val Tyr Thr Ser Leu	
290 295 300	
caa tgg gcc agc ctg cag tga	933
Gln Trp Ala Ser Leu Gln *	
305 310	

<210> 116

<211> 310

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

164

<400> 116

Met Leu Val Val Glu Val Ala Asn Gly Arg Ser Leu Val Trp Gly Ala
 1 5 10 15
 Glu Ala Val Gln Ala Leu Arg Glu Arg Leu Gly Val Gly Gly Arg Thr
 20 25 30
 Val Gly Ala Leu Pro Arg Gly Pro Arg Gln Asn Ser Arg Leu Gly Leu
 35 40 45
 Pro Leu Leu Leu Met Pro Glu Glu Ala Arg Leu Leu Ala Glu Ile Gly
 50 55 60
 Ala Val Thr Leu Val Ser Ala Pro Arg Pro Asp Ser Arg His His Ser
 65 70 75 80
 Leu Ala Leu Thr Ser Phe Lys Arg Xaa Gln Glu Glu Ser Phe Gln Glu
 85 90 95
 Gln Ser Ala Leu Ala Ala Glu Ala Arg Glu Thr Arg Arg Gln Glu Leu
 100 105 110
 Leu Glu Lys Ile Thr Glu Gly Gln Ala Ala Lys Lys Gln Lys Leu Glu
 115 120 125
 Gln Ala Ser Gly Ala Ser Ser Ser Gln Glu Ala Gly Ser Ser Gln Ala
 130 135 140
 Ala Lys Glu Asp Glu Thr Ser Asp Gly Gln Ala Ser Gly Glu Gln Glu
 145 150 155 160
 Glu Ala Gly Pro Ser Ser Ser Gln Ala Gly Pro Ser Asn Gly Val Ala
 165 170 175
 Pro Leu Pro Arg Ser Ala Leu Leu Val Gln Leu Ala Thr Ala Arg Pro
 180 185 190
 Arg Pro Val Lys Ala Arg Pro Leu Asp Trp Arg Val Gln Ser Lys Asp
 195 200 205
 Trp Pro His Ala Gly Arg Pro Ala His Glu Leu Arg Tyr Ser Ile Tyr
 210 215 220
 Arg Asp Leu Trp Glu Arg Gly Phe Phe Leu Ser Ala Ala Gly Lys Phe
 225 230 235 240
 Gly Gly Asp Phe Leu Val Tyr Pro Gly Asp Pro Leu Arg Phe His Ala
 245 250 255
 His Tyr Ile Ala Gln Cys Trp Ala Pro Glu Asp Thr Ile Pro Leu Gln
 260 265 270
 Asp Leu Val Ala Ala Gly Arg Leu Gly Thr Ser Val Arg Lys Thr Leu
 275 280 285
 Leu Leu Cys Ser Pro Gln Pro Asp Gly Lys Val Val Tyr Thr Ser Leu
 290 295 300
 Gln Trp Ala Ser Leu Gln
 305 310

<210> 117

<211> 828

165

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(828)

<400> 117

atg gca aat ttc aag ggc cac gcg ctt cca ggg agt ttc ttc ctg atc	48
Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile	
1 5 10 15	
att ggg ctg tgt tgg tca gtg aag tac ccg ctg aag tac ttt agc cac	96
Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His	
20 25 30	
acg cgg aag aac agc cca cta cat tac tat cag cgt ctc gag atc gtc	144
Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val	
35 40 45	
gaa gcc gca att agg act ttg ttt tcc gtc act ggg atc ctg gca gag	192
Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu	
50 55 60	
cag ttt gtt ccg gat ggg ccc cac ctg cac ctc tac cat gag aac cac	240
Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His	
65 70 75 80	
tgg ata aag tta atg aat tgg cag cac agc acc atg tac cta ttc ttt	288
Trp Ile Lys Leu Met Asn Trp Gln His Ser Thr Met Tyr Leu Phe Phe	
85 90 95	
gca gtc tca gga att gtt gac atg ctc acc tat ctg gtc agc cac gtt	336
Ala Val Ser Gly Ile Val Asp Met Leu Thr Tyr Leu Val Ser His Val	
100 105 110	
ccc ttg ggg gtg gac aga ctg gtt atg gct gtg gca gta ttc atg gaa	384
Pro Leu Gly Val Asp Arg Leu Val Met Ala Val Ala Val Phe Met Glu	
115 120 125	
ggt ttc ctc ttc tac tac cac gtc cac aac cgg cct ccg ctg gac cag	432
Gly Phe Leu Phe Tyr Tyr His Val His Asn Arg Pro Pro Leu Asp Gln	
130 135 140	

166

cac atc cac tca ctc ctg ctg tat gct ctg ttc gga ggg tgt gtt agt 480
 His Ile His Ser Leu Leu Tyr Ala Leu Phe Gly Gly Cys Val Ser
 145 150 155 160

atc tcc cta gag gtg atc ttc cgg gac cac att gtg ctg gaa ctt ttc 528
 Ile Ser Leu Glu Val Ile Phe Arg Asp His Ile Val Leu Glu Leu Phe
 165 170 175

cga acc agt ctc atc att ctt cag gga acc tgg ttc tgg cag att ggg 576
 Arg Thr Ser Leu Ile Ile Leu Gln Gly Thr Trp Phe Trp Gln Ile Gly
 180 185 190

ttt gtg ctg ttc cca cct ttt gga aca ccc gaa tgg gac cag aag gat 624
 Phe Val Leu Phe Pro Pro Phe Gly Thr Pro Glu Trp Asp Gln Lys Asp
 195 200 205

gat gcc aac ctc atg ttc atc acc atg tgc ttc tgc tgg cac tac ctg 672
 Asp Ala Asn Leu Met Phe Ile Thr Met Cys Phe Cys Trp His Tyr Leu
 210 215 220

gct gcc ctc agc att gtg gcc gtc aac tat tct ctt gtt tac tgc ctt 720
 Ala Ala Leu Ser Ile Val Ala Val Asn Tyr Ser Leu Val Tyr Cys Leu
 225 230 235 240

ttg act cgg atg aag aga cac gga agg gga gaa atc att gga att cag 768
 Leu Thr Arg Met Lys Arg His Gly Arg Gly Glu Ile Ile Gly Ile Gln
 245 250 255

aag ctg aat tca gat gac act tac cag acc gcc ctc ttg agt ggc tca 816
 Lys Leu Asn Ser Asp Asp Thr Tyr Gln Thr Ala Leu Leu Ser Gly Ser
 260 265 270

gat gag gaa tga 828
 Asp Glu Glu *
 275

<210> 118

<211> 275

<212> PRT

<213> Homo sapiens

<400> 118

Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile

167

1	5	10	15
Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His			
	20	25	30
Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val			
	35	40	45
Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu			
	50	55	60
Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His			
65	70	75	80
Trp Ile Lys Leu Met Asn Trp Gln His Ser Thr Met Tyr Leu Phe Phe			
	85	90	95
Ala Val Ser Gly Ile Val Asp Met Leu Thr Tyr Leu Val Ser His Val			
	100	105	110
Pro Leu Gly Val Asp Arg Leu Val Met Ala Val Ala Val Phe Met Glu			
	115	120	125
Gly Phe Leu Phe Tyr Tyr His Val His Asn Arg Pro Pro Leu Asp Gln			
	130	135	140
His Ile His Ser Leu Leu Leu Tyr Ala Leu Phe Gly Gly Cys Val Ser			
145	150	155	160
Ile Ser Leu Glu Val Ile Phe Arg Asp His Ile Val Leu Glu Leu Phe			
	165	170	175
Arg Thr Ser Leu Ile Ile Leu Gln Gly Thr Trp Phe Trp Gln Ile Gly			
	180	185	190
Phe Val Leu Phe Pro Pro Phe Gly Thr Pro Glu Trp Asp Gln Lys Asp			
	195	200	205
Asp Ala Asn Leu Met Phe Ile Thr Met Cys Phe Cys Trp His Tyr Leu			
	210	215	220
Ala Ala Leu Ser Ile Val Ala Val Asn Tyr Ser Leu Val Tyr Cys Leu			
225	230	235	240
Leu Thr Arg Met Lys Arg His Gly Arg Gly Glu Ile Ile Gly Ile Gln			
	245	250	255
Lys Leu Asn Ser Asp Asp Thr Tyr Gln Thr Ala Leu Leu Ser Gly Ser			
	260	265	270
Asp Glu Glu			
275			

<210> 119

<211> 867

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(867)

<400> 119

atg ggg cgc ctg acg gaa gcg gcg gca gcg ggc agc ggc tct cgg gct	48
Met Gly Arg Leu Thr Glu Ala Ala Ala Ala Gly Ser Gly Ser Arg Ala	
1 5 10 15	
gca ggc tgg gca ggg tcc cct ccc acg ctc ctg ccg ctg tct ccc acg	96
Ala Gly Trp Ala Gly Ser Pro Pro Thr Leu Leu Pro Leu Ser Pro Thr	
20 25 30	
tcc ccc agg tgc gcg gcc acc atg gcg tcc agc gac gag gac ggc acc	144
Ser Pro Arg Cys Ala Ala Thr Met Ala Ser Ser Asp Glu Asp Gly Thr	
35 40 45	
aac ggc ggc gcc tcg gag gcc ggc gag gac cgg gag gct ccc ggc aag	192
Asn Gly Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro Gly Lys	
50 55 60	
cgg agg cgc ctg ggg ttc ttg gcc acc gcc tgg ctc acc ttc tac gac	240
Arg Arg Arg Leu Gly Phe Leu Ala Thr Ala Trp Leu Thr Phe Tyr Asp	
65 70 75 80	
atc gcc atg acc gcg ggg tgg ttg gtt cta gct att gcc atg gta cgt	288
Ile Ala Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met Val Arg	
85 90 95	
ttt tat atg gaa aaa gga aca cac aga ggt tta tat aaa agt att cag	336
Phe Tyr Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser Ile Gln	
100 105 110	
aag aca ctt aaa ttt ttc cag aca ttt gcc ttg ctt gag ata gtt cac	384
Lys Thr Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile Val His	
115 120 125	
tgt tta att gga att gta cct act tct gtg att gtg act ggg gtc caa	432
Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly Val Gln	
130 135 140	
gtg agt tca aga atc ttt atg gtg tgg ctc att act cac agt ata aaa	480
Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser Ile Lys	
145 150 155 160	
cca atc cag aat gaa gag agt gtg gtg ctt ttt ctg gtc gcg tgg act	528
Pro Ile Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala Trp Thr	

169

165	170	175	
gtg aca gag atc act cgc tat tcc ttc tac aca ttc agc ctt ctt gac			576
Val Thr Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asp			
180	185	190	
cac ttg cca tac ttc att aaa tgg gcc aga tat aat ttt ttt atc atc			624
His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe Ile Ile			
195	200	205	
tta tat cct gtt gga gtt gct ggt gaa ctt ctt aca ata tac gct gcc			672
Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr Ala Ala			
210	215	220	
ttg ccg cat gtg aag aaa aca gga atg ttt tca ata aga ctt cct aac			720
Leu Pro His Val Lys Lys Thr Gly Met Phe Ser Ile Arg Leu Pro Asn			
225	230	235	240
aaa tac aat gtc tct ttt gac tac tat tat ttt ctt ctt ata acc atg			768
Lys Tyr Asn Val Ser Phe Asp Tyr Tyr Tyr Phe Leu Leu Ile Thr Met			
245	250	255	
gca tca tat ata cct ttg ttt cca caa ctc tat ttt cat atg tta cgt			816
Ala Ser Tyr Ile Pro Leu Phe Pro Gln Leu Tyr Phe His Met Leu Arg			
260	265	270	
caa aga aga aag gtg ctt cat gga gag gtg att gta gaa aag gat gat			864
Gln Arg Arg Lys Val Leu His Gly Glu Val Ile Val Glu Lys Asp Asp			
275	280	285	
taa			867
*			

<210> 120

<211> 288

<212> PRT

<213> Homo sapiens

<400> 120

Met Gly Arg Leu Thr Glu Ala Ala Ala Ala Gly Ser Gly Ser Arg Ala			
1	5	10	15
Ala Gly Trp Ala Gly Ser Pro Pro Thr Leu Leu Pro Leu Ser Pro Thr			

170

				20				25				30			
Ser	Pro	Arg	Cys	Ala	Ala	Thr	Met	Ala	Ser	Ser	Asp	Glu	Asp	Gly	Thr
35				40				45							
Asn	Gly	Gly	Ala	Ser	Glu	Ala	Gly	Glu	Asp	Arg	Glu	Ala	Pro	Gly	Lys
50				55				60							
Arg	Arg	Arg	Leu	Gly	Phe	Leu	Ala	Thr	Ala	Trp	Leu	Thr	Phe	Tyr	Asp
65				70				75				80			
Ile	Ala	Met	Thr	Ala	Gly	Trp	Leu	Val	Leu	Ala	Ile	Ala	Met	Val	Arg
85				90				95							
Phe	Tyr	Met	Glu	Lys	Gly	Thr	His	Arg	Gly	Leu	Tyr	Lys	Ser	Ile	Gln
100				105				110							
Lys	Thr	Leu	Lys	Phe	Phe	Gln	Thr	Phe	Ala	Leu	Leu	Glu	Ile	Val	His
115				120				125							
Cys	Leu	Ile	Gly	Ile	Val	Pro	Thr	Ser	Val	Ile	Val	Thr	Gly	Val	Gln
130				135				140							
Val	Ser	Ser	Arg	Ile	Phe	Met	Val	Trp	Leu	Ile	Thr	His	Ser	Ile	Lys
145				150				155				160			
Pro	Ile	Gln	Asn	Glu	Glu	Ser	Val	Val	Leu	Phe	Leu	Val	Ala	Trp	Thr
165				170				175							
Val	Thr	Glu	Ile	Thr	Arg	Tyr	Ser	Phe	Tyr	Thr	Phe	Ser	Leu	Leu	Asp
180				185				190							
His	Leu	Pro	Tyr	Phe	Ile	Lys	Trp	Ala	Arg	Tyr	Asn	Phe	Phe	Ile	Ile
195				200				205							
Leu	Tyr	Pro	Val	Gly	Val	Ala	Gly	Glu	Leu	Leu	Thr	Ile	Tyr	Ala	Ala
210				215				220							
Leu	Pro	His	Val	Lys	Lys	Thr	Gly	Met	Phe	Ser	Ile	Arg	Leu	Pro	Asn
225				230				235				240			
Lys	Tyr	Asn	Val	Ser	Phe	Asp	Tyr	Tyr	Tyr	Phe	Leu	Leu	Ile	Thr	Met
245				250				255							
Ala	Ser	Tyr	Ile	Pro	Leu	Phe	Pro	Gln	Leu	Tyr	Phe	His	Met	Leu	Arg
260				265				270							
Gln	Arg	Arg	Lys	Val	Leu	His	Gly	Glu	Val	Ile	Val	Glu	Lys	Asp	Asp
275				280				285							

<210> 121

<211> 177

<212> DNA

<213> Homo sapiens

$\langle 220 \rangle$

<221> CDS

<222> (1)...(177)

<400> 121

171

atg gcc gcc acc ttc gac gac tgc ctg tat gcc ttg tgc gtg gtg gac 48
 Met Ala Ala Thr Phe Asp Asp Cys Leu Tyr Ala Leu Cys Val Val Asp
 1 5 10 15

acc atc aag agg tcc agc cag acg ggc gag tgg cag aac att gcc atc 96
 Thr Ile Lys Arg Ser Ser Gln Thr Gly Glu Trp Gln Asn Ile Ala Ile
 20 25 30

atg acc gag gag ccg gag ctg agc ccc gcc tac ctg atc agc gag gcc 144
 Met Thr Glu Glu Pro Glu Leu Ser Pro Ala Tyr Leu Ile Ser Glu Ala
 35 40 45

atg cgc cgc agc agg atg tcc ctc tac tgt tag 177
 Met Arg Arg Ser Arg Met Ser Leu Tyr Cys *
 50 55

<210> 122

<211> 58

<212> PRT

<213> Homo sapiens

<400> 122

Met Ala Ala Thr Phe Asp Asp Cys Leu Tyr Ala Leu Cys Val Val Asp
 1 5 10 15
 Thr Ile Lys Arg Ser Ser Gln Thr Gly Glu Trp Gln Asn Ile Ala Ile
 20 25 30
 Met Thr Glu Glu Pro Glu Leu Ser Pro Ala Tyr Leu Ile Ser Glu Ala
 35 40 45
 Met Arg Arg Ser Arg Met Ser Leu Tyr Cys
 50 55

<210> 123

<211> 1158

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1158)

<400> 123

atg cag tac cac gcg ctg tcg ttg gcc atg cac ggc ttc tcg gtg acc 48
 Met Gln Tyr His Ala Leu Ser Leu Ala Met His Gly Phe Ser Val Thr

172

1	5	10	15	
ctc ctg ggg ttc tgc aac tcc aaa ccc cat gat gag ctc ttg cag aac				96
Leu Leu Gly Phe Cys Asn Ser Lys Pro His Asp Glu Leu Leu Gln Asn				
	20	25	30	
aac aga att cag att gtg ggg ttg aca gaa ctt cag agt ctt gca gtt				144
Asn Arg Ile Gln Ile Val Gly Leu Thr Glu Leu Gln Ser Leu Ala Val				
	35	40	45	
ggg ccc cga gtt ttc cag tac gga gtc aaa gtt gta ctt cag gct atg				192
Gly Pro Arg Val Phe Gln Tyr Gly Val Lys Val Val Leu Gln Ala Met				
	50	55	60	
tac ttg ctg tgg aag ttg atg tgg agg gag cca ggt gcc tat atc ttt				240
Tyr Leu Leu Trp Lys Leu Met Trp Arg Glu Pro Gly Ala Tyr Ile Phe				
	65	70	75	80
ctc cag aac ccc cca ggt ctg cct agc att gct gtc tgc tgg ttc gtg				288
Leu Gln Asn Pro Pro Gly Leu Pro Ser Ile Ala Val Cys Trp Phe Val				
	85	90	95	
ggc tgc ctt tgt gga agc aag ctc gtc att gac tgg cac aac tat ggc				336
Gly Cys Leu Cys Gly Ser Lys Leu Val Ile Asp Trp His Asn Tyr Gly				
	100	105	110	
tac tcc atc atg ggt ctg gtg cat ggc ccc aac cat ccc ctc gtt ctg				384
Tyr Ser Ile Met Gly Leu Val His Gly Pro Asn His Pro Leu Val Leu				
	115	120	125	
ctg gcc aag tgg tac gag aag ttc ttt ggg cgc ctg tcc cac ctg aac				432
Leu Ala Lys Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn				
	130	135	140	
ctg tgt gtt acc aat gct atg cga gaa gac ctg gcg gat aac tgg cac				480
Leu Cys Val Thr Asn Ala Met Arg Glu Asp Leu Ala Asp Asn Trp His				
	145	150	155	160
atc agg gct gtg acc gtc tac gac aag ccc gca tct ttc ttt aaa gag				528
Ile Arg Ala Val Thr Val Tyr Asp Lys Pro Ala Ser Phe Phe Lys Glu				
	165	170	175	
aca cct ctg gac ctg cag cac cgg ctc ttc atg aag ctg ggc agc atg				576
Thr Pro Leu Asp Leu Gln His Arg Leu Phe Met Lys Leu Gly Ser Met				

173

180	185	190	
cac tct ccg ttc agg gcc cgc tca gaa cct gag gac cca gtc acg gag			624
His Ser Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu			
195	200	205	
cgg tcg gcc ttc acg gag cgg gat gct ggg agc ggg ctg gtg acg cgt			672
Arg Ser Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg			
210	215	220	
ctc cgt gag cgg cca gcc ctg ctg gtc agc agc acg agc tgg aca gag			720
Leu Arg Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu			
225	230	235	240
gac gaa gac ttc tcc atc ctg ctg gca gct tta gaa aag ttt gaa caa			768
Asp Glu Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln			
245	250	255	
ctg act ctt gat gga cac aac ctt cct tct ctc gtc tgt gtg ata aca			816
Leu Thr Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr			
260	265	270	
ggc aaa ggg cct ctg agg gag tat tat agc cgc ctc atc cac cag aag			864
Gly Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys			
275	280	285	
cac ttc cag cac atc cag gtc tgc acc ccc tgg ctg gag gcc gag gac			912
His Phe Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp			
290	295	300	
tac ccc ctg ctt cta ggg tcg gcg gac ctg ggt gtc tgt ctg cac acg			960
Tyr Pro Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr			
305	310	315	320
tcc tcc agt ggc ctg gac ctg ccc atg aag gtg gtg gac atg ttc ggg			1008
Ser Ser Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly			
325	330	335	
tgc tgt ttg cct gtg tgt gct gtg aac ttc aag tgt tta cat gag ctg			1056
Cys Cys Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu			
340	345	350	
gtg aaa cat gaa gaa aat ggc ctg gtc ttt gag gac tca gag gaa ctg			1104
Val Lys His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu			

174

355	360	365	
gca gct cag ctg cag atg ctt ttc tca aac ttt cct gat ctg cgg gca			1152
Ala Ala Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Leu Arg Ala			
370	375	380	
agc taa			1158
Ser *			
385			

<210> 124
 <211> 385
 <212> PRT
 <213> Homo sapiens

<400> 124

Met	Gln	Tyr	His	Ala	Leu	Ser	Leu	Ala	Met	His	Gly	Phe	Ser	Val	Thr
1				5				10						15	
Leu	Leu	Gly	Phe	Cys	Asn	Ser	Lys	Pro	His	Asp	Glu	Leu	Leu	Gln	Asn
		20					25					30			
Asn	Arg	Ile	Gln	Ile	Val	Gly	Leu	Thr	Glu	Leu	Gln	Ser	Leu	Ala	Val
	35					40					45				
Gly	Pro	Arg	Val	Phe	Gln	Tyr	Gly	Val	Lys	Val	Val	Leu	Gln	Ala	Met
50					55			60							
Tyr	Leu	Leu	Trp	Lys	Leu	Met	Trp	Arg	Glu	Pro	Gly	Ala	Tyr	Ile	Phe
65				70				75						80	
Leu	Gln	Asn	Pro	Pro	Gly	Leu	Pro	Ser	Ile	Ala	Val	Cys	Trp	Phe	Val
			85					90						95	
Gly	Cys	Leu	Cys	Gly	Ser	Lys	Leu	Val	Ile	Asp	Trp	His	Asn	Tyr	Gly
	100						105					110			
Tyr	Ser	Ile	Met	Gly	Leu	Val	His	Gly	Pro	Asn	His	Pro	Leu	Val	Leu
	115					120						125			
Leu	Ala	Lys	Trp	Tyr	Glu	Lys	Phe	Phe	Gly	Arg	Leu	Ser	His	Leu	Asn
	130					135					140				
Leu	Cys	Val	Thr	Asn	Ala	Met	Arg	Glu	Asp	Leu	Ala	Asp	Asn	Trp	His
145				150					155					160	
Ile	Arg	Ala	Val	Thr	Val	Tyr	Asp	Lys	Pro	Ala	Ser	Phe	Phe	Lys	Glu
			165					170						175	
Thr	Pro	Leu	Asp	Leu	Gln	His	Arg	Leu	Phe	Met	Lys	Leu	Gly	Ser	Met
		180					185					190			
His	Ser	Pro	Phe	Arg	Ala	Arg	Ser	Glu	Pro	Glu	Asp	Pro	Val	Thr	Glu
	195						200					205			
Arg	Ser	Ala	Phe	Thr	Glu	Arg	Asp	Ala	Gly	Ser	Gly	Leu	Val	Thr	Arg

175

210 215 220
 Leu Arg Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu
 225 230 235 240
 Asp Glu Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln
 245 250 255
 Leu Thr Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr
 260 265 270
 Gly Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys
 275 280 285
 His Phe Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp
 290 295 300
 Tyr Pro Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr
 305 310 315 320
 Ser Ser Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly
 325 330 335
 Cys Cys Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu
 340 345 350
 Val Lys His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu
 355 360 365
 Ala Ala Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Leu Arg Ala
 370 375 380
 Ser
 385

<210> 125
 <211> 1002
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1002)

<221> misc_feature
 <222> (1)...(1002)
 <223> n = A,T,C or G

<400> 125
 atg gcg gcc gcc gca ggn nga ncg ctc ctg ctg ctc ctc tcc tct cgg 48
 Met Ala Ala Ala Ala Xaa Xaa Xaa Leu Leu Leu Leu Leu Ser Ser Arg
 1 5 10 15
 ggc ggc ggc ggc ggg ggc gcc ggc ggc tgc ggg gcg ctg act gcc ggc 96
 Gly Gly Gly Gly Gly Gly Ala Gly Gly Cys Gly Ala Leu Thr Ala Gly

176

20	25	30	
tgc ttc cct ggg ctg ggc gtc agc cgc cac cgg cag cag cag cac cac			144
Cys Phe Pro Gly Leu Gly Val Ser Arg His Arg Gln Gln Gln His His			
35	40	45	
cgg acg gta cac cag agg atc gct tcc tgg cag aat ttg gga gct gtt			192
Arg Thr Val His Gln Arg Ile Ala Ser Trp Gln Asn Leu Gly Ala Val			
50	55	60	
tat tgc agc act gtt gtg ccc tct gat gat gtt aca gtg gtt tat caa			240
Tyr Cys Ser Thr Val Val Pro Ser Asp Asp Val Thr Val Val Tyr Gln			
65	70	75	80
aat ggg tta cct gtg ata tct gtg agg cta cca tcc cgg cgt gaa cgc			288
Asn Gly Leu Pro Val Ile Ser Val Arg Leu Pro Ser Arg Arg Glu Arg			
85	90	95	
tgt cag ttc aca ctc aag cct atc tct gac tct gtt ggt gta ttt tta			336
Cys Gln Phe Thr Leu Lys Pro Ile Ser Asp Ser Val Gly Val Phe Leu			
100	105	110	
cga caa ctg caa gaa gag gat cgg gga att gac aga gtt gct atc tat			384
Arg Gln Leu Gln Glu Glu Asp Arg Gly Ile Asp Arg Val Ala Ile Tyr			
115	120	125	
tca cca gat ggt gtt cgc gtt gct gct tca aca gga ata gac ctc ctc			432
Ser Pro Asp Gly Val Arg Val Ala Ala Ser Thr Gly Ile Asp Leu Leu			
130	135	140	
ctc ctt gat gac ttt aag ctg gtc att aat gac tta aca tac cac gta			480
Leu Leu Asp Asp Phe Lys Leu Val Ile Asn Asp Leu Thr Tyr His Val			
145	150	155	160
cga cca cca aaa aga gac ctc tta agt cat gaa aat gca gca acg ctg			528
Arg Pro Pro Lys Arg Asp Leu Leu Ser His Glu Asn Ala Ala Thr Leu			
165	170	175	
aat gat gta aag aca ttg gtc cag caa cta tac acc aca ctg tgc att			576
Asn Asp Val Lys Thr Leu Val Gln Gln Leu Tyr Thr Thr Leu Cys Ile			
180	185	190	
gag cag cac cag tta aac aag gaa agg gag ctt att gaa aga cta gag			624
Glu Gln His Gln Leu Asn Lys Glu Arg Glu Leu Ile Glu Arg Leu Glu			

177

195	200	205	
gat ctc aaa gag cag ctg gct ccc ctg gaa aag gta cga att gag att			672
Asp Leu Lys Glu Gln Leu Ala Pro Leu Glu Lys Val Arg Ile Glu Ile			
210	215	220	
agc aga aaa gct gag aag agg acc act ttg gtg cta tgg ggt ggc ctt			720
Ser Arg Lys Ala Glu Lys Arg Thr Thr Leu Val Leu Trp Gly Gly Leu			
225	230	235	240
gcc tac atg gcc aca cag ttt ggc att ttg gcc cgg ctt acc tgg tgg			768
Ala Tyr Met Ala Thr Gln Phe Gly Ile Leu Ala Arg Leu Thr Trp Trp			
245	250	255	
gaa tat tcc tgg gac atc atg gag cca gta aca tac ttc atc act tat			816
Glu Tyr Ser Trp Asp Ile Met Glu Pro Val Thr Tyr Phe Ile Thr Tyr			
260	265	270	
gga agt gcc atg gca atg tat gca tat ttt gta atg aca cgc cag gaa			864
Gly Ser Ala Met Ala Met Tyr Ala Tyr Phe Val Met Thr Arg Gln Glu			
275	280	285	
tat gtt tat cca gaa gcc aga gac aga caa tac tta cta ttt ttc cat			912
Tyr Val Tyr Pro Glu Ala Arg Asp Arg Gln Tyr Leu Leu Phe Phe His			
290	295	300	
aaa gga gcc aaa aag tca cgt ttt gac cta gag aaa tac aat caa ctc			960
Lys Gly Ala Lys Lys Ser Arg Phe Asp Leu Glu Lys Tyr Asn Gln Leu			
305	310	315	320
aag gat gca att gct cag cag aaa tgg acc tta aga gac tga			1002
Lys Asp Ala Ile Ala Gln Gln Lys Trp Thr Leu Arg Asp *			
325	330		

<210> 126

<211> 333

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

178

<400> 126

Met Ala Ala Ala Ala Xaa Xaa Xaa Leu Leu Leu Leu Ser Ser Arg
 1 5 10 15
 Gly Gly Gly Gly Gly Gly Ala Gly Gly Cys Gly Ala Leu Thr Ala Gly
 20 25 30
 Cys Phe Pro Gly Leu Gly Val Ser Arg His Arg Gln Gln Gln His His
 35 40 45
 Arg Thr Val His Gln Arg Ile Ala Ser Trp Gln Asn Leu Gly Ala Val
 50 55 60
 Tyr Cys Ser Thr Val Val Pro Ser Asp Asp Val Thr Val Val Tyr Gln
 65 70 75 80
 Asn Gly Leu Pro Val Ile Ser Val Arg Leu Pro Ser Arg Arg Glu Arg
 85 90 95
 Cys Gln Phe Thr Leu Lys Pro Ile Ser Asp Ser Val Gly Val Phe Leu
 100 105 110
 Arg Gln Leu Gln Glu Glu Asp Arg Gly Ile Asp Arg Val Ala Ile Tyr
 115 120 125
 Ser Pro Asp Gly Val Arg Val Ala Ala Ser Thr Gly Ile Asp Leu Leu
 130 135 140
 Leu Leu Asp Asp Phe Lys Leu Val Ile Asn Asp Leu Thr Tyr His Val
 145 150 155 160
 Arg Pro Pro Lys Arg Asp Leu Leu Ser His Glu Asn Ala Ala Thr Leu
 165 170 175
 Asn Asp Val Lys Thr Leu Val Gln Gln Leu Tyr Thr Thr Leu Cys Ile
 180 185 190
 Glu Gln His Gln Leu Asn Lys Glu Arg Glu Leu Ile Glu Arg Leu Glu
 195 200 205
 Asp Leu Lys Glu Gln Leu Ala Pro Leu Glu Lys Val Arg Ile Glu Ile
 210 215 220
 Ser Arg Lys Ala Glu Lys Arg Thr Thr Leu Val Leu Trp Gly Gly Leu
 225 230 235 240
 Ala Tyr Met Ala Thr Gln Phe Gly Ile Leu Ala Arg Leu Thr Trp Trp
 245 250 255
 Glu Tyr Ser Trp Asp Ile Met Glu Pro Val Thr Tyr Phe Ile Thr Tyr
 260 265 270
 Gly Ser Ala Met Ala Met Tyr Ala Tyr Phe Val Met Thr Arg Gln Glu
 275 280 285
 Tyr Val Tyr Pro Glu Ala Arg Asp Arg Gln Tyr Leu Leu Phe Phe His
 290 295 300
 Lys Gly Ala Lys Lys Ser Arg Phe Asp Leu Glu Lys Tyr Asn Gln Leu
 305 310 315 320
 Lys Asp Ala Ile Ala Gln Gln Lys Trp Thr Leu Arg Asp
 325 330

179

<210> 127
 <211> 1164
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1164)

<221> misc_feature
 <222> (1)...(1164)
 <223> n = A,T,C or G

<400> 127
 atg gtc ata ccc act ttg gcc tcc ctg gct tct cca act aca cta cag 48
 Met Val Ile Pro Thr Leu Ala Ser Leu Ala Ser Pro Thr Thr Leu Gln
 1 5 10 15
 tcc cag atg ctt ggg ggc cta gga cag gat gtt ttg tta aat aat tca 96
 Ser Gln Met Leu Gly Gly Leu Gly Gln Asp Val Leu Leu Asn Asn Ser
 20 25 30
 ctc act cct aaa tat ctt ggc tgt aag caa gac aac agc tct tcc cct 144
 Leu Thr Pro Lys Tyr Leu Gly Cys Lys Gln Asp Asn Ser Ser Ser Pro
 35 40 45
 aag ccc agc tcc gtg ttc aga aat gga ttc tct ggc att aag aag cct 192
 Lys Pro Ser Ser Val Phe Arg Asn Gly Phe Ser Gly Ile Lys Lys Pro
 50 55 60
 tgg cac aga tgt cac gtc tgc aac cac cac ttc cag ttc aaa cag cac 240
 Trp His Arg Cys His Val Cys Asn His His Phe Gln Phe Lys Gln His
 65 70 75 80
 ctt cga gac cac atg aat aca cac acc aac aga cgc cct tac agt tgt 288
 Leu Arg Asp His Met Asn Thr His Thr Asn Arg Arg Pro Tyr Ser Cys
 85 90 95
 cgg att tgt cgc aag tcc tat gta cgt cct ggc agc ctg agc aca cac 336
 Arg Ile Cys Arg Lys Ser Tyr Val Arg Pro Gly Ser Leu Ser Thr His
 100 105 110
 atg aaa ctt cat cat ggt gag aac cgt ctg aag aaa ctc atg tgt tgt 384

180

Met	Lys	Leu	His	His	Gly	Glu	Asn	Arg	Leu	Lys	Lys	Leu	Met	Cys	Cys	
	115						120					125				
gag ttt tgt gca aaa gtg ttt ggc cac atc cga gtc tat ttt ggc cat 432																
Glu	Phe	Cys	Ala	Lys	Val	Phe	Gly	His	Ile	Arg	Val	Tyr	Phe	Gly	His	
	130					135					140					
ctg aaa gaa gtg cat agg gtt gtg atc agc act gag cct gcg ccc agt 480																
Leu	Lys	Glu	Val	His	Arg	Val	Val	Ile	Ser	Thr	Glu	Pro	Ala	Pro	Ser	
	145				150					155				160		
gaa ctg cag cca gga gac ata cca aag aac aga gac atg agt gtg cga 528																
Glu	Leu	Gln	Pro	Gly	Asp	Ile	Pro	Lys	Asn	Arg	Asp	Met	Ser	Val	Arg	
				165					170					175		
ggc atg gag gga tca ttg gag agg gaa aac aag tcc aac ctg gaa gaa 576																
Gly	Met	Glu	Gly	Ser	Leu	Glu	Arg	Glu	Asn	Lys	Ser	Asn	Leu	Glu	Glu	
			180				185						190			
gac ttc ctt cta aac cag gca gac gaa gtc aaa tta caa atc aaa tgt 624																
Asp	Phe	Leu	Leu	Asn	Gln	Ala	Asp	Glu	Val	Lys	Leu	Gln	Ile	Lys	Cys	
		195					200					205				
ggt cnt tgt cag att act gct cag tct ttt gcg gaa ata aaa ttt cat 672																
Gly	Xaa	Cys	Gln	Ile	Thr	Ala	Gln	Ser	Phe	Ala	Glu	Ile	Lys	Phe	His	
	210					215					220					
tta ctt gat gtt cat gga gag gaa att gag ggc agg cta caa gaa ggg 720																
Leu	Leu	Asp	Val	His	Gly	Glu	Glu	Ile	Glu	Gly	Arg	Leu	Gln	Glu	Gly	
	225				230					235				240		
acc ttc cca gga agc aag ggg act cag gaa gag ttg gtg cag cac gct 768																
Thr	Phe	Pro	Gly	Ser	Lys	Gly	Thr	Gln	Glu	Glu	Leu	Val	Gln	His	Ala	
			245						250				255			
agc ccc gac tgg aaa agg cat cct gag aga ggg aag ccg gag aag gtt 816																
Ser	Pro	Asp	Trp	Lys	Arg	His	Pro	Glu	Arg	Gly	Lys	Pro	Glu	Lys	Val	
			260					265					270			
cat tcc tcc tcc gag gaa tca cat gca tgt cca aga ctg aaa agg cag 864																
His	Ser	Ser	Ser	Glu	Glu	Ser	His	Ala	Cys	Pro	Arg	Leu	Lys	Arg	Gln	
		275					280					285				
ctc cac ctt cat cag aat ggc gtg gaa atg ctc atg gaa aat gaa gga 912																

181

Leu His Leu His Gln Asn Gly Val Glu Met Leu Met Glu Asn Glu Gly
 290 295 300
 ccc cag tca gga acc aac aag cca agg gaa acc tgc cag ggc cct gag 960
 Pro Gln Ser Gly Thr Asn Lys Pro Arg Glu Thr Cys Gln Gly Pro Glu
 305 310 315 320
 tgt cct ggc ctc cac acg ttt ctc ttg tgg tcc cat tca ggc ttt aac 1008
 Cys Pro Gly Leu His Thr Phe Leu Leu Trp Ser His Ser Gly Phe Asn
 325 330 335
 tgc ctg ctt tgt gca gag atg ctg gga cgg aaa gag gac ctc ctc cac 1056
 Cys Leu Leu Cys Ala Glu Met Leu Gly Arg Lys Glu Asp Leu Leu His
 340 345 350
 cac tgg aag cac cag cat aac tgt gag gac cct tcc aaa ctg tgg gct 1104
 His Trp Lys His Gln His Asn Cys Glu Asp Pro Ser Lys Leu Trp Ala
 355 360 365
 att tta aat acg gtc tcc aac cag gga gtg atc gaa ctt tcc agt gaa 1152
 Ile Leu Asn Thr Val Ser Asn Gln Gly Val Ile Glu Leu Ser Ser Glu
 370 375 380
 gct gag aaa tga 1164
 Ala Glu Lys *
 385

<210> 128

<211> 387

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(387)

<223> Xaa = Any Amino Acid

<400> 128

Met Val Ile Pro Thr Leu Ala Ser Leu Ala Ser Pro Thr Thr Leu Gln
 1 5 10 15
 Ser Gln Met Leu Gly Gly Leu Gly Gln Asp Val Leu Leu Asn Asn Ser
 20 25 30
 Leu Thr Pro Lys Tyr Leu Gly Cys Lys Gln Asp Asn Ser Ser Ser Pro

[illegible]

183

385

<210> 129
 <211> 2022
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(2022)

<221> misc_feature
 <222> (1)...(2022)
 <223> n = A,T,C or G

<400> 129

atg	aag	aag	gac	tgc	agt	ctt	cct	ctt	act	gtc	ctt	acc	tgt	gct	aaa	48
Met	Lys	Lys	Asp	Cys	Ser	Leu	Pro	Leu	Thr	Val	Leu	Thr	Cys	Ala	Lys	
1				5					10					15		

gca	tgt	cca	cac	atg	gct	act	tgt	gga	aat	gtt	ctg	ttt	gag	gga	aga	96
Ala	Cys	Pro	His	Met	Ala	Thr	Cys	Gly	Asn	Val	Leu	Phe	Glu	Gly	Arg	
			20					25					30			

aca	gtt	cag	cta	ggg	aag	ctt	tgc	tgc	act	gga	gtt	gaa	act	gaa	gat	144
Thr	Val	Gln	Leu	Gly	Lys	Leu	Cys	Cys	Thr	Gly	Val	Glu	Thr	Glu	Asp	
		35					40					45				

gat	gaa	gat	act	gag	tca	aat	tca	tcg	gta	gaa	caa	gca	tcg	gtt	gaa	192
Asp	Glu	Asp	Thr	Glu	Ser	Asn	Ser	Ser	Val	Glu	Gln	Ala	Ser	Val	Glu	
	50					55					60					

gta	cct	gat	gga	cca	aca	ctc	cat	gac	cca	gac	ctc	tat	att	gag	att	240
Val	Pro	Asp	Gly	Pro	Thr	Leu	His	Asp	Pro	Asp	Leu	Tyr	Ile	Glu	Ile	
65					70				75					80		

gtg	aaa	aat	acg	aag	tct	gtc	cca	gaa	tat	tca	gag	gtg	gct	tat	ccc	288
Val	Lys	Asn	Thr	Lys	Ser	Val	Pro	Glu	Tyr	Ser	Glu	Val	Ala	Tyr	Pro	
				85					90					95		

gat	tat	ttt	ggt	cac	att	ccg	cct	cca	ttc	aaa	gag	cct	att	tta	gaa	336
Asp	Tyr	Phe	Gly	His	Ile	Pro	Pro	Pro	Phe	Lys	Glu	Pro	Ile	Leu	Glu	
			100					105						110		

184

agg cct tat ggt gta caa agg aca aaa att gct caa gat att gaa agg Arg Pro Tyr Gly Val Gln Arg Thr Lys Ile Ala Gln Asp Ile Glu Arg 115 120 125	384
cta ata cat cag agt gat atc ata gat cgt gtg gta tat gac ttg gat Leu Ile His Gln Ser Asp Ile Ile Asp Arg Val Val Tyr Asp Leu Asp 130 135 140	432
aac cca aat tac acc att cca gaa gag gga gat att ttg aaa ttt aac Asn Pro Asn Tyr Thr Ile Pro Glu Glu Gly Asp Ile Leu Lys Phe Asn 145 150 155 160	480
tcc aaa ttt gag tct ggg aat ctg cgc ana gta att caa att aga aaa Ser Lys Phe Glu Ser Gly Asn Leu Arg Xaa Val Ile Gln Ile Arg Lys 165 170 175	528
aat gaa tat gat ctt att ctg aac tca gac ata aac agc aat cat tat Asn Glu Tyr Asp Leu Ile Leu Asn Ser Asp Ile Asn Ser Asn His Tyr 180 185 190	576
cat cag tgg ttt tac ttt gaa gtc agt gga atg cga cca ggt gtt gct His Gln Trp Phe Tyr Phe Glu Val Ser Gly Met Arg Pro Gly Val Ala 195 200 205	624
tac agg ttt aac atc att aac tgt gaa aag tcc aac agt cag ttt aat Tyr Arg Phe Asn Ile Ile Asn Cys Glu Lys Ser Asn Ser Gln Phe Asn 210 215 220	672
tat ggt atg caa cca ctc atg tat tcg gtt cag gaa gca tta aat gcc Tyr Gly Met Gln Pro Leu Met Tyr Ser Val Gln Glu Ala Leu Asn Ala 225 230 235 240	720
aga cca tgg tgg att cgt atg ggg act gac att tgt tac tat aaa aat Arg Pro Trp Trp Ile Arg Met Gly Thr Asp Ile Cys Tyr Tyr Lys Asn 245 250 255	768
cat ttc tca aga agt tca gtt gct gca ggt ggg caa aag gga aaa tcc His Phe Ser Arg Ser Ser Val Ala Ala Gly Gly Gln Lys Gly Lys Ser 260 265 270	816
tac tat aca att aca ttt act gtc aat ttt cca cat aaa gat gat gtt Tyr Tyr Thr Ile Thr Phe Thr Val Asn Phe Pro His Lys Asp Asp Val 275 280 285	864

185

tgc tac ttt gct tat cac tat cca tat acg tat tca act tta cag atg Cys Tyr Phe Ala Tyr His Tyr Pro Tyr Thr Tyr Ser Thr Leu Gln Met 290 295 300	912
cat ctt caa aaa ttg gaa tca gca cac aat cct cag caa atc tat ttt His Leu Gln Lys Leu Glu Ser Ala His Asn Pro Gln Gln Ile Tyr Phe 305 310 315 320	960
cgg aaa gat gtg tta tgt gaa acc ctg tct gga aac agc tgc ccc ttg Arg Lys Asp Val Leu Cys Glu Thr Leu Ser Gly Asn Ser Cys Pro Leu 325 330 335	1008
gtg act ata aca gca atg cca gag tct aat tat tat gaa cat atc tgc Val Thr Ile Thr Ala Met Pro Glu Ser Asn Tyr Tyr Glu His Ile Cys 340 345 350	1056
cat ttc aga aat cgc cct tac gtt ttc ttg tct gct cgg gta cat cct His Phe Arg Asn Arg Pro Tyr Val Phe Leu Ser Ala Arg Val His Pro 355 360 365	1104
gga gaa act aat gca agt tgg gtt atg aaa gga acg ttg gaa tat ctc Gly Glu Thr Asn Ala Ser Trp Val Met Lys Gly Thr Leu Glu Tyr Leu 370 375 380	1152
atg agc aat aac ccc act gct cag agc tta cga gaa tct tat att ttt Met Ser Asn Asn Pro Thr Ala Gln Ser Leu Arg Glu Ser Tyr Ile Phe 385 390 395 400	1200
aaa att gtc cct atg tta aat cca gat ggt gtc atc aat gga aat cat Lys Ile Val Pro Met Leu Asn Pro Asp Gly Val Ile Asn Gly Asn His 405 410 415	1248
cgc tgt tct tta agt gga gag gat ttg aat agg cag tgg caa agt cca Arg Cys Ser Leu Ser Gly Glu Asp Leu Asn Arg Gln Trp Gln Ser Pro 420 425 430	1296
agt ccg gat tta cat cct aca att tac cat gct aag ggg ctg ttg caa Ser Pro Asp Leu His Pro Thr Ile Tyr His Ala Lys Gly Leu Leu Gln 435 440 445	1344
tac ttg gct gca gtg aag cgt tta ccc ttg gtt tat tgt gat tat cat Tyr Leu Ala Ala Val Lys Arg Leu Pro Leu Val Tyr Cys Asp Tyr His 450 455 460	1392

ggc Gly 465	cat His	tcc Ser	cga Arg	aag Lys	aag Lys 470	aat Asn	gta Val	ttt Phe	atg Met	tat Tyr 475	ggt Gly	tgc Cys	agc Ser	atc Ile	aaa Lys 480	1440
gag Glu	aca Thr	gtg Val	tgg Trp	cat His 485	acc Thr	aat Asn	gat Asp	aat Asn	gca Ala 490	act Thr	tca Ser	tgt Cys	gat Asp	gtt Val 495	gtg Val	1488
gag Glu	gat Asp	acg Thr	gga Gly 500	tac Tyr	agg Arg	aca Thr	ttg Leu	cct Pro 505	aag Lys	ata Ile	ctg Leu	agc Ser 510	cat His	atc Ile	gcc Ala	1536
cca Pro	gca Ala	ttt Phe 515	tgc Cys	atg Met	agc Ser	agc Ser	tgt Cys 520	agc Ser	ttc Phe	gta Val	gtg Val 525	gaa Glu	aaa Lys	tct Ser	aaa Lys	1584
gaa Glu	tcc Ser 530	aca Thr	gca Ala	cgt Arg	gtt Val	gta Val 535	gtt Val	tgg Trp	agg Arg	gaa Glu	ata Ile 540	gga Gly	gta Val	caa Gln	aga Arg	1632
agt Ser 545	tat Tyr	acc Thr	atg Met	gag Glu 550	agt Ser	act Thr	tta Leu	tgt Cys	ggc Gly 555	tgt Cys 555	gat Asp	cag Gln	gga Gly	aaa Lys	tac Tyr 560	1680
aag Lys	ggt Gly	tta Leu	cag Gln	att Ile 565	ggt Gly	acc Thr	cga Arg	gaa Glu 570	ctg Leu	gaa Glu	gag Glu	atg Met	gga Gly	gca Ala 575	aaa Lys	1728
ttt Phe	tgt Cys	gtt Val 580	ggt Gly	ctt Leu	tta Leu	cgt Arg	ttg Leu	aaa Lys 585	aga Arg	ctg Leu	acc Thr	tct Ser 590	cca Pro	ttg Leu	gag Glu	1776
tat Tyr	aat Asn	ctg Leu 595	cct Pro	tcc Ser	agc Ser	ctg Leu	ctt Leu 600	gac Asp	ttt Phe	gaa Glu	aat Asn	gat Asp 605	tta Leu	att Ile	gaa Glu	1824
tca Ser 610	agc Ser	tgc Cys	aaa Lys	gta Val	act Thr	agc Ser 615	cct Pro	acc Thr	act Thr	tat Tyr 620	gtc Val	ttg Leu	gat Asp	gaa Glu	gat Asp	1872
gaa Glu 625	cct Pro	cga Arg	ttc Phe	ctt Leu	gaa Glu 630	gaa Glu	gtt Val	gat Asp	tac Tyr	agt Ser 635	gca Ala	gaa Glu	agt Ser	aat Asn	gat Asp 640	1920

187

gag tta gat att gag ttg gct gaa aat gta gga gat tat gaa cct tct 1968
 Glu Leu Asp Ile Glu Leu Ala Glu Asn Val Gly Asp Tyr Glu Pro Ser
 645 650 655

gct caa gaa gaa gta ctt tct gac tct gaa tta tca aga aca tac cta 2016
 Ala Gln Glu Glu Val Leu Ser Asp Ser Glu Leu Ser Arg Thr Tyr Leu
 660 665 670

cct tga 2022
 Pro *

<210> 130
 <211> 673
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Thr Val Gln Leu Gly Lys Leu Cys Cys Thr Gly Val Glu Thr Glu Asp
 35 40 45
 Asp Glu Asp Thr Glu Ser Asn Ser Ser Val Glu Gln Ala Ser Val Glu
 50 55 60
 Val Pro Asp Gly Pro Thr Leu His Asp Pro Asp Leu Tyr Ile Glu Ile
 65 70 75 80
 Val Lys Asn Thr Lys Ser Val Pro Glu Tyr Ser Glu Val Ala Tyr Pro
 85 90 95
 Asp Tyr Phe Gly His Ile Pro Pro Pro Phe Lys Glu Pro Ile Leu Glu
 100 105 110
 Arg Pro Tyr Gly Val Gln Arg Thr Lys Ile Ala Gln Asp Ile Glu Arg
 115 120 125
 Leu Ile His Gln Ser Asp Ile Ile Asp Arg Val Val Tyr Asp Leu Asp
 130 135 140
 Asn Pro Asn Tyr Thr Ile Pro Glu Glu Gly Asp Ile Leu Lys Phe Asn
 145 150 155 160

Ser Lys Phe Glu Ser Gly Asn Leu Arg Xaa Val Ile Gln Ile Arg Lys
 165 170 175
 Asn Glu Tyr Asp Leu Ile Leu Asn Ser Asp Ile Asn Ser Asn His Tyr
 180 185 190
 His Gln Trp Phe Tyr Phe Glu Val Ser Gly Met Arg Pro Gly Val Ala
 195 200 205
 Tyr Arg Phe Asn Ile Ile Asn Cys Glu Lys Ser Asn Ser Gln Phe Asn
 210 215 220
 Tyr Gly Met Gln Pro Leu Met Tyr Ser Val Gln Glu Ala Leu Asn Ala
 225 230 235 240
 Arg Pro Trp Trp Ile Arg Met Gly Thr Asp Ile Cys Tyr Tyr Lys Asn
 245 250 255
 His Phe Ser Arg Ser Ser Val Ala Ala Gly Gly Gln Lys Gly Lys Ser
 260 265 270
 Tyr Tyr Thr Ile Thr Phe Thr Val Asn Phe Pro His Lys Asp Asp Val
 275 280 285
 Cys Tyr Phe Ala Tyr His Tyr Pro Tyr Thr Tyr Ser Thr Leu Gln Met
 290 295 300
 His Leu Gln Lys Leu Glu Ser Ala His Asn Pro Gln Gln Ile Tyr Phe
 305 310 315 320
 Arg Lys Asp Val Leu Cys Glu Thr Leu Ser Gly Asn Ser Cys Pro Leu
 325 330 335
 Val Thr Ile Thr Ala Met Pro Glu Ser Asn Tyr Tyr Glu His Ile Cys
 340 345 350
 His Phe Arg Asn Arg Pro Tyr Val Phe Leu Ser Ala Arg Val His Pro
 355 360 365
 Gly Glu Thr Asn Ala Ser Trp Val Met Lys Gly Thr Leu Glu Tyr Leu
 370 375 380
 Met Ser Asn Asn Pro Thr Ala Gln Ser Leu Arg Glu Ser Tyr Ile Phe
 385 390 395 400
 Lys Ile Val Pro Met Leu Asn Pro Asp Gly Val Ile Asn Gly Asn His
 405 410 415
 Arg Cys Ser Leu Ser Gly Glu Asp Leu Asn Arg Gln Trp Gln Ser Pro
 420 425 430
 Ser Pro Asp Leu His Pro Thr Ile Tyr His Ala Lys Gly Leu Leu Gln
 435 440 445
 Tyr Leu Ala Ala Val Lys Arg Leu Pro Leu Val Tyr Cys Asp Tyr His
 450 455 460
 Gly His Ser Arg Lys Lys Asn Val Phe Met Tyr Gly Cys Ser Ile Lys
 465 470 475 480
 Glu Thr Val Trp His Thr Asn Asp Asn Ala Thr Ser Cys Asp Val Val
 485 490 495
 Glu Asp Thr Gly Tyr Arg Thr Leu Pro Lys Ile Leu Ser His Ile Ala
 500 505 510

189

Pro	Ala	Phe	Cys	Met	Ser	Ser	Cys	Ser	Phe	Val	Val	Glu	Lys	Ser	Lys
515				520				525							
Glu	Ser	Thr	Ala	Arg	Val	Val	Val	Trp	Arg	Glu	Ile	Gly	Val	Gln	Arg
530				535				540							
Ser	Tyr	Thr	Met	Glu	Ser	Thr	Leu	Cys	Gly	Cys	Asp	Gln	Gly	Lys	Tyr
545				550				555				560			
Lys	Gly	Leu	Gln	Ile	Gly	Thr	Arg	Glu	Leu	Glu	Glu	Met	Gly	Ala	Lys
565				570				575							
Phe	Cys	Val	Gly	Leu	Leu	Arg	Leu	Lys	Arg	Leu	Thr	Ser	Pro	Leu	Glu
580				585				590							
Tyr	Asn	Leu	Pro	Ser	Ser	Leu	Leu	Asp	Phe	Glu	Asn	Asp	Leu	Ile	Glu
595				600				605							
Ser	Ser	Cys	Lys	Val	Thr	Ser	Pro	Thr	Thr	Tyr	Val	Leu	Asp	Glu	Asp
610				615				620							
Glu	Pro	Arg	Phe	Leu	Glu	Glu	Val	Asp	Tyr	Ser	Ala	Glu	Ser	Asn	Asp
625				630				635				640			
Glu	Leu	Asp	Ile	Glu	Leu	Ala	Glu	Asn	Val	Gly	Asp	Tyr	Glu	Pro	Ser
645				650				655							
Ala	Gln	Glu	Glu	Val	Leu	Ser	Asp	Ser	Glu	Leu	Ser	Arg	Thr	Tyr	Leu
660				665				670							
Pro															

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<212> DNA
<213> Homo sapiens
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Met	Ile	Gly	Pro	Ala	Val	Phe	Leu	Val	Ala	Ala	Gly	Phe	Ile	Gly	Cys	
1			5			10			15							
gat	tat	tct	ttg	gcc	gtt	gct	ttc	cta	act	ata	tca	aca	aca	ctg	gga	96
Asp	Tyr	Ser	Leu	Ala	Val	Ala	Phe	Leu	Thr	Ile	Ser	Thr	Thr	Leu	Gly	
			20			25						30				
ggc	ttt	tgc	tct	tct	gga	ttt	agc	atc	aac	cat	ctg	gat	att	gct	cct	144
Gly	Phe	Cys	Ser	Ser	Gly	Phe	Ser	Ile	Asn	His	Leu	Asp	Ile	Ala	Pro	
35						40						45				

190

tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt gcc act att 192
 Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile
 50 55 60

cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc cct gat aac 240
 Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn
 65 70 75 80

act gtt gga gaa tgg caa acc gtg ttc tat att gct gct gct att aat 288
 Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn
 85 90 95

gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt gaa gta caa 336
 Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln
 100 105 110

aac tgg gct ctc aat gat cac cat gga cac aga cac tga 375
 Asn Trp Ala Leu Asn Asp His His Gly His Arg His *
 115 120

<210> 132

<211> 124

<212> PRT

<213> Homo sapiens

<400> 132

Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe Ile Gly Cys
 1 5 10 15
 Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr Thr Leu Gly
 20 25 30
 Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp Ile Ala Pro
 35 40 45
 Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile
 50 55 60
 Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn
 65 70 75 80
 Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn
 85 90 95
 Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln
 100 105 110
 Asn Trp Ala Leu Asn Asp His His Gly His Arg His
 115 120

191

<210> 133
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(1485)

<221> misc_feature
 <222> (1)...(1485)
 <223> n = A,T,C or G

<400> 133

atg ccc gca gag tct gga aag aga ttc aaa ccc agc aag tat gtc ccg	48
Met Pro Ala Glu Ser Gly Lys Arg Phe Lys Pro Ser Lys Tyr Val Pro	
1 5 10 15	
gtc tct gca gcc gcc atc ttc cta gtg gga gct acg aca ctc ttc ttt	96
Val Ser Ala Ala Ala Ile Phe Leu Val Gly Ala Thr Thr Leu Phe Phe	
20 25 30	
gcc ttt acg tgt cca gga cta agc ctg tat gtg tca cct gca gtg ccc	144
Ala Phe Thr Cys Pro Gly Leu Ser Leu Tyr Val Ser Pro Ala Val Pro	
35 40 45	
atc tac aat gca att atg ttt ctc ttt gtg ttg gcc aac ttc agc atg	192
Ile Tyr Asn Ala Ile Met Phe Leu Phe Val Leu Ala Asn Phe Ser Met	
50 55 60	
gcc acc ttc atg gac cca ggg att ttc cct cga gct gag gag gat gag	240
Ala Thr Phe Met Asp Pro Gly Ile Phe Pro Arg Ala Glu Glu Asp Glu	
65 70 75 80	
gac aag gaa gat gat ttc cga gct ccc ctt tac aaa aca gtg gag ata	288
Asp Lys Glu Asp Asp Phe Arg Ala Pro Leu Tyr Lys Thr Val Glu Ile	
85 90 95	
aag ggc atc cag gtg cgc atg aaa tgg tgt gcc acc tgc cgc ttt tac	336
Lys Gly Ile Gln Val Arg Met Lys Trp Cys Ala Thr Cys Arg Phe Tyr	
100 105 110	
cgt ccc cct cga tgt tcc cac tgc agt gtc tgt gac aac tgt gtg gag	384

192

Arg	Pro	Pro	Arg	Cys	Ser	His	Cys	Ser	Val	Cys	Asp	Asn	Cys	Val	Glu	
	115						120					125				
gaa	ttt	gat	cat	cac	tgc	ccc	tgg	gtg	aat	aac	tgt	att	ggg	cgc	cgg	432
Glu	Phe	Asp	His	His	Cys	Pro	Trp	Val	Asn	Asn	Cys	Ile	Gly	Arg	Arg	
	130					135					140					
aac	tac	cgt	tat	ttt	ttc	ctt	ttc	ctc	ctt	tcc	ctg	aca	gcc	cac	att	480
Asn	Tyr	Arg	Tyr	Phe	Phe	Leu	Phe	Leu	Leu	Ser	Leu	Thr	Ala	His	Ile	
	145				150					155					160	
atg	ggg	gtg	ttt	ggc	ttt	ggc	ctc	ctt	tat	gtc	ctc	tac	cac	ata	gag	528
Met	Gly	Val	Phe	Gly	Phe	Gly	Leu	Leu	Tyr	Val	Leu	Tyr	His	Ile	Glu	
			165						170					175		
gaa	ctc	tca	ggg	gtc	cgc	acg	gct	gtc	aca	atg	gca	gta	atg	tgt	gtg	576
Glu	Leu	Ser	Gly	Val	Arg	Thr	Ala	Val	Thr	Met	Ala	Val	Met	Cys	Val	
		180					185						190			
gct	ggc	tta	ttc	ttc	atc	cct	gta	gct	ggc	ctc	acg	gga	ttt	cac	gtg	624
Ala	Gly	Leu	Phe	Phe	Ile	Pro	Val	Ala	Gly	Leu	Thr	Gly	Phe	His	Val	
		195				200						205				
gtt	ctg	gtg	gcc	agg	gga	cgc	aca	acc	aat	gaa	cag	gtt	acg	ggg	aaa	672
Val	Leu	Val	Ala	Arg	Gly	Arg	Thr	Thr	Asn	Glu	Gln	Val	Thr	Gly	Lys	
	210					215					220					
ttc	cgg	gga	ggg	gtg	aac	ccc	ttc	acc	aat	ggc	tgc	tgt	aac	aat	gtc	720
Phe	Arg	Gly	Gly	Val	Asn	Pro	Phe	Thr	Asn	Gly	Cys	Cys	Asn	Asn	Val	
	225				230					235					240	
agc	cgt	gtt	ctc	tgc	agt	tct	cca	gca	ccc	agg	tat	ttg	ggg	aga	cca	768
Ser	Arg	Val	Leu	Cys	Ser	Ser	Pro	Ala	Pro	Arg	Tyr	Leu	Gly	Arg	Pro	
			245						250					255		
aag	aaa	gag	aag	aca	att	gta	atc	aga	cct	ccc	ttc	ctt	cga	cca	gaa	816
Lys	Lys	Glu	Lys	Thr	Ile	Val	Ile	Arg	Pro	Pro	Phe	Leu	Arg	Pro	Glu	
		260					265					270				
gtt	tca	gat	ggg	cag	ata	act	gtg	aag	atc	atg	gat	aat	ggc	atc	cag	864
Val	Ser	Asp	Gly	Gln	Ile	Thr	Val	Lys	Ile	Met	Asp	Asn	Gly	Ile	Gln	
		275					280					285				
gga	gag	ctg	agg	aga	aca	aag	tct	aag	gga	agc	ctg	gag	ata	aca	gag	912

193

Gly	Glu	Leu	Arg	Arg	Thr	Lys	Ser	Lys	Gly	Ser	Leu	Glu	Ile	Thr	Glu		
290						295					300						
agc	cag	tct	gca	gat	gct	gaa	cct	cca	cct	cct	cct	aag	cca	gac	ctg	960	
Ser	Gln	Ser	Ala	Asp	Ala	Glu	Pro	Pro	Pro	Pro	Pro	Lys	Pro	Asp	Leu		
305					310					315					320		
agc	cgt	tac	aca	ggg	ttg	cga	aca	cac	ctc	ggc	ttg	gct	act	aat	gag	1008	
Ser	Arg	Tyr	Thr	Gly	Leu	Arg	Thr	His	Leu	Gly	Leu	Ala	Thr	Asn	Glu		
				325					330					335			
gat	agt	agc	tta	ttg	gcc	aag	gac	agc	ccc	ccg	aca	cct	acc	atg	tac	1056	
Asp	Ser	Ser	Leu	Leu	Ala	Lys	Asp	Ser	Pro	Pro	Thr	Pro	Thr	Met	Tyr		
			340					345						350			
aag	tat	cgg	ccg	ggg	tac	agt	agc	agc	agt	acg	tca	gct	gcc	atg	ccg	1104	
Lys	Tyr	Arg	Pro	Gly	Tyr	Ser	Ser	Ser	Ser	Thr	Ser	Ala	Ala	Met	Pro		
		355					360					365					
cat	tcc	tcc	agc	gcc	aag	ttg	agt	cgt	ggg	gac	agc	ttg	aag	gag	cca	1152	
His	Ser	Ser	Ser	Ala	Lys	Leu	Ser	Arg	Gly	Asp	Ser	Leu	Lys	Glu	Pro		
			370			375					380						
acc	tca	att	gca	gag	agc	agc	cgt	cac	ccc	agc	tac	cgc	tca	gag	ccc	1200	
Thr	Ser	Ile	Ala	Glu	Ser	Ser	Arg	His	Pro	Ser	Tyr	Arg	Ser	Glu	Pro		
385					390					395					400		
agc	ttg	gaa	cca	gag	agc	ttc	cgt	tct	cct	acc	ttt	ggc	aaa	agt	ttt	1248	
Ser	Leu	Glu	Pro	Glu	Ser	Phe	Arg	Ser	Pro	Thr	Phe	Gly	Lys	Ser	Phe		
				405					410					415			
cac	ttc	gat	cca	cta	tcc	agt	ggc	tca	cgc	tcc	tcc	agc	ctc	aag	tca	1296	
His	Phe	Asp	Pro	Leu	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Ser	Leu	Lys	Ser		
			420				425						430				
ncc	cag	ggc	aca	ggc	ttt	gag	ctg	ggc	cag	ttg	caa	tcc	att	cgt	tca	1344	
Xaa	Gln	Gly	Thr	Gly	Phe	Glu	Leu	Gly	Gln	Leu	Gln	Ser	Ile	Arg	Ser		
			435				440						445				
gag	ggc	acc	acc	tcc	acc	tcc	tat	aag	agc	ctg	gcc	aac	cag	aca	cgc	1392	
Glu	Gly	Thr	Thr	Ser	Thr	Ser	Tyr	Lys	Ser	Leu	Ala	Asn	Gln	Thr	Arg		
			450				455				460						
aat	gga	agc	cta	tct	tat	gac	agc	ttg	ctc	aca	cct	tca	gac	agc	cct	1440	

194

Asn Gly Ser Leu Ser Tyr Asp Ser Leu Leu Thr Pro Ser Asp Ser Pro
 465 470 475 480

gat ttt gag tca gtg cag gca ggg ctg agc cag acc cac ctt tag 1485
 Asp Phe Glu Ser Val Gln Ala Gly Leu Ser Gln Thr His Leu *
 485 490

<210> 134

<211> 494

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(494)

<223> Xaa = Any Amino Acid

<400> 134

Met Pro Ala Glu Ser Gly Lys Arg Phe Lys Pro Ser Lys Tyr Val Pro
 1 5 10 15
 Val Ser Ala Ala Ala Ile Phe Leu Val Gly Ala Thr Thr Leu Phe Phe
 20 25 30
 Ala Phe Thr Cys Pro Gly Leu Ser Leu Tyr Val Ser Pro Ala Val Pro
 35 40 45
 Ile Tyr Asn Ala Ile Met Phe Leu Phe Val Leu Ala Asn Phe Ser Met
 50 55 60
 Ala Thr Phe Met Asp Pro Gly Ile Phe Pro Arg Ala Glu Glu Asp Glu
 65 70 75 80
 Asp Lys Glu Asp Asp Phe Arg Ala Pro Leu Tyr Lys Thr Val Glu Ile
 85 90 95
 Lys Gly Ile Gln Val Arg Met Lys Trp Cys Ala Thr Cys Arg Phe Tyr
 100 105 110
 Arg Pro Pro Arg Cys Ser His Cys Ser Val Cys Asp Asn Cys Val Glu
 115 120 125
 Glu Phe Asp His His Cys Pro Trp Val Asn Asn Cys Ile Gly Arg Arg
 130 135 140
 Asn Tyr Arg Tyr Phe Phe Leu Phe Leu Leu Ser Leu Thr Ala His Ile
 145 150 155 160
 Met Gly Val Phe Gly Phe Gly Leu Leu Tyr Val Leu Tyr His Ile Glu
 165 170 175
 Glu Leu Ser Gly Val Arg Thr Ala Val Thr Met Ala Val Met Cys Val
 180 185 190
 Ala Gly Leu Phe Phe Ile Pro Val Ala Gly Leu Thr Gly Phe His Val

195

195	200	205
Val Leu Val Ala Arg Gly Arg Thr Thr Asn Glu Gln Val Thr Gly Lys		
210	215	220
Phe Arg Gly Gly Val Asn Pro Phe Thr Asn Gly Cys Cys Asn Asn Val		
225	230	235
Ser Arg Val Leu Cys Ser Ser Pro Ala Pro Arg Tyr Leu Gly Arg Pro		
245	250	255
Lys Lys Glu Lys Thr Ile Val Ile Arg Pro Pro Phe Leu Arg Pro Glu		
260	265	270
Val Ser Asp Gly Gln Ile Thr Val Lys Ile Met Asp Asn Gly Ile Gln		
275	280	285
Gly Glu Leu Arg Arg Thr Lys Ser Lys Gly Ser Leu Glu Ile Thr Glu		
290	295	300
Ser Gln Ser Ala Asp Ala Glu Pro Pro Pro Pro Pro Lys Pro Asp Leu		
305	310	315
Ser Arg Tyr Thr Gly Leu Arg Thr His Leu Gly Leu Ala Thr Asn Glu		
325	330	335
Asp Ser Ser Leu Leu Ala Lys Asp Ser Pro Pro Thr Pro Thr Met Tyr		
340	345	350
Lys Tyr Arg Pro Gly Tyr Ser Ser Ser Ser Thr Ser Ala Ala Met Pro		
355	360	365
His Ser Ser Ser Ala Lys Leu Ser Arg Gly Asp Ser Leu Lys Glu Pro		
370	375	380
Thr Ser Ile Ala Glu Ser Ser Arg His Pro Ser Tyr Arg Ser Glu Pro		
385	390	395
Ser Leu Glu Pro Glu Ser Phe Arg Ser Pro Thr Phe Gly Lys Ser Phe		
405	410	415
His Phe Asp Pro Leu Ser Ser Gly Ser Arg Ser Ser Ser Leu Lys Ser		
420	425	430
Xaa Gln Gly Thr Gly Phe Glu Leu Gly Gln Leu Gln Ser Ile Arg Ser		
435	440	445
Glu Gly Thr Thr Ser Thr Ser Tyr Lys Ser Leu Ala Asn Gln Thr Arg		
450	455	460
Asn Gly Ser Leu Ser Tyr Asp Ser Leu Leu Thr Pro Ser Asp Ser Pro		
465	470	475
Asp Phe Glu Ser Val Gln Ala Gly Leu Ser Gln Thr His Leu		
485	490	

<210> 135

<211> 246

<212> DNA

<213> Homo sapiens

<220>

196

<221> CDS

<222> (1)...(246)

<400> 135

atg gtt ggg ggg gac gca gat gcc agg tcc aag gcc ttg ctg gga gtc	48
Met Val Gly Gly Asp Ala Asp Ala Arg Ser Lys Ala Leu Leu Gly Val	
1 5 10 15	

tgc gtc ggg tca ggc acg gaa gcc tat gtc ctg gta ttg gac cct cac	96
Cys Val Gly Ser Gly Thr Glu Ala Tyr Val Leu Val Leu Asp Pro His	
20 25 30	

tac tgg ggc act cca aaa agc ccc agt gaa cta cag gct gct ggg tgg	144
Tyr Trp Gly Thr Pro Lys Ser Pro Ser Glu Leu Gln Ala Ala Gly Trp	
35 40 45	

gtg ggc tgg caa gag gtg agt gca gcc ttt gac ccc aac tcc ttc tac	192
Val Gly Trp Gln Glu Val Ser Ala Ala Phe Asp Pro Asn Ser Phe Tyr	
50 55 60	

aac ctg tgc ttg acc agc ctt agc tcc caa cag cag cag cgc acc ttg	240
Asn Leu Cys Leu Thr Ser Leu Ser Ser Gln Gln Gln Gln Arg Thr Leu	
65 70 75 80	

gac tga	246
Asp *	

<210> 136

<211> 81

<212> PRT

<213> Homo sapiens

<400> 136

Met Val Gly Gly Asp Ala Asp Ala Arg Ser Lys Ala Leu Leu Gly Val
1 5 10 15

Cys Val Gly Ser Gly Thr Glu Ala Tyr Val Leu Val Leu Asp Pro His
20 25 30

Tyr Trp Gly Thr Pro Lys Ser Pro Ser Glu Leu Gln Ala Ala Gly Trp
35 40 45

Val Gly Trp Gln Glu Val Ser Ala Ala Phe Asp Pro Asn Ser Phe Tyr
50 55 60

Asn Leu Cys Leu Thr Ser Leu Ser Ser Gln Gln Gln Gln Arg Thr Leu

197

65
Asp

70

75

80

<210> 137
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(552)

<400> 137

atg gaa cag cgg tta gct gag ttt cgg gcg gcg cgg aaa cgg gcg ggt 48
 Met Glu Gln Arg Leu Ala Glu Phe Arg Ala Ala Arg Lys Arg Ala Gly
 1 5 10 15

ctg gcg gcc caa ccc cct gct gcc agt cag ggc gca caa acc cca gga 96
 Leu Ala Ala Gln Pro Pro Ala Ala Ser Gln Gly Ala Gln Thr Pro Gly
 20 25 30

gag aag gcg gaa gca gca gcg act cta aag gca gcc cca ggc tgg cta 144
 Glu Lys Ala Glu Ala Ala Ala Thr Leu Lys Ala Ala Pro Gly Trp Leu
 35 40 45

aag cgg ttc ctg gta tgg aaa cct agg ccc gcg agt gcc cgg gcc cag 192
 Lys Arg Phe Leu Val Trp Lys Pro Arg Pro Ala Ser Ala Arg Ala Gln
 50 55 60

ccc ggc cta gtt cag gaa gcg gct cag ccc cag ggc agc aca tca gag 240
 Pro Gly Leu Val Gln Glu Ala Ala Gln Pro Gln Gly Ser Thr Ser Glu
 65 70 75 80

aca cca tgg aac aca gcc att cct ctg ccg tcg tgc tgg gac cag tct 288
 Thr Pro Trp Asn Thr Ala Ile Pro Leu Pro Ser Cys Trp Asp Gln Ser
 85 90 95

ttc ctg acc aat atc acc ttc ttg aag gtt ctt ctc tgg ttg gtc ctg 336
 Phe Leu Thr Asn Ile Thr Phe Leu Lys Val Leu Leu Trp Leu Val Leu
 100 105 110

ctg gga ctg ttt gtg gaa ctg gaa ttt ggc ctg gca tat ttt gtc ctg 384
 Leu Gly Leu Phe Val Glu Leu Glu Phe Gly Leu Ala Tyr Phe Val Leu

198

115	120	125	
tcc ttg ttc tat tgg atg tac gtc ggg aca cga ggc cct gaa gag aag			432
Ser Leu Phe Tyr Trp Met Tyr Val Gly Thr Arg Gly Pro Glu Glu Lys			
130	135	140	
aaa gag gga gag aag agc gcc tac tct gtg ttc aat cca ggc tgt gaa			480
Lys Glu Gly Glu Lys Ser Ala Tyr Ser Val Phe Asn Pro Gly Cys Glu			
145	150	155	160
gcc atc cag ggc acc ctg act gca gag cag ttg gag cgc gag tta cag			528
Ala Ile Gln Gly Thr Leu Thr Ala Glu Gln Leu Glu Arg Glu Leu Gln			
165	170	175	
ttg aga ccc ctg gca ggg aga tag			552
Leu Arg Pro Leu Ala Gly Arg *			
180			

<210> 138

<211> 183

<212> PRT

<213> Homo sapiens

<400> 138

Met Glu Gln Arg Leu Ala Glu Phe Arg Ala Ala Arg Lys Arg Ala Gly			
1	5	10	15
Leu Ala Ala Gln Pro Pro Ala Ala Ser Gln Gly Ala Gln Thr Pro Gly			
20	25	30	
Glu Lys Ala Glu Ala Ala Ala Thr Leu Lys Ala Ala Pro Gly Trp Leu			
35	40	45	
Lys Arg Phe Leu Val Trp Lys Pro Arg Pro Ala Ser Ala Arg Ala Gln			
50	55	60	
Pro Gly Leu Val Gln Glu Ala Ala Gln Pro Gln Gly Ser Thr Ser Glu			
65	70	75	80
Thr Pro Trp Asn Thr Ala Ile Pro Leu Pro Ser Cys Trp Asp Gln Ser			
85	90	95	
Phe Leu Thr Asn Ile Thr Phe Leu Lys Val Leu Leu Trp Leu Val Leu			
100	105	110	
Leu Gly Leu Phe Val Glu Leu Glu Phe Gly Leu Ala Tyr Phe Val Leu			
115	120	125	
Ser Leu Phe Tyr Trp Met Tyr Val Gly Thr Arg Gly Pro Glu Glu Lys			
130	135	140	
Lys Glu Gly Glu Lys Ser Ala Tyr Ser Val Phe Asn Pro Gly Cys Glu			

199

145 150 155 160
 Ala Ile Gln Gly Thr Leu Thr Ala Glu Gln Leu Glu Arg Glu Leu Gln
 165 170 175
 Leu Arg Pro Leu Ala Gly Arg
 180

<210> 139
 <211> 912
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(912)

<400> 139
 atg gcg gcg gcg gca ttg ggc agc tcc tca ggc tcg gcg tcc ccg gcc 48
 Met Ala Ala Ala Ala Leu Gly Ser Ser Ser Gly Ser Ala Ser Pro Ala
 1 5 10 15

 gtg gct gag ctc tgc cag aac acc ccg gag acc ttt ttg gag gcc tcc 96
 Val Ala Glu Leu Cys Gln Asn Thr Pro Glu Thr Phe Leu Glu Ala Ser
 20 25 30

 aag ctg ctg ctc acc tat gct gac aac atc ctc aga aac cct aat gat 144
 Lys Leu Leu Leu Thr Tyr Ala Asp Asn Ile Leu Arg Asn Pro Asn Asp
 35 40 45

 gaa aaa tat aga tcc atc cgg att gga aac aca gcc ttt tct act aga 192
 Glu Lys Tyr Arg Ser Ile Arg Ile Gly Asn Thr Ala Phe Ser Thr Arg
 50 55 60

 ctc ttg cct gtc aga gga gct gtt gaa tgt tta ttt gaa atg ggc ttt 240
 Leu Leu Pro Val Arg Gly Ala Val Glu Cys Leu Phe Glu Met Gly Phe
 65 70 75 80

 gaa gag gga gaa aca cat ctc atc ttt cct aaa aaa gct tca gtg gag 288
 Glu Glu Gly Glu Thr His Leu Ile Phe Pro Lys Lys Ala Ser Val Glu
 85 90 95

 cag ctg caa aaa att cgt gac ctg att gcc ata gag aga agt agc aga 336
 Gln Leu Gln Lys Ile Arg Asp Leu Ile Ala Ile Glu Arg Ser Ser Arg
 100 105 110

200

ctg gat ggc tca aat aag agc cac aaa gta aag tca tct cag .caa cct Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro 115 120 125	384
gca gcc agt acc cag ctt cct aca aca cca tct tca aat ccc agt ggg Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly 130 135 140	432
tta aac cag cac aca agg aac cgt caa ggg cag tca tca gat cca cca Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro 145 150 155 160	480
tct gct tca acg gtt gct gct gac tca gcc att cta gaa gtt ctt cag Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln 165 170 175	528
tcc aac att cag cat gtg ctg gtc tat gaa aat cct gct ctt cag gag Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu 180 185 190	576
aaa gcg ttg gct tgt att ccg gtc caa gaa cta aaa agg aaa tca caa Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln 195 200 205	624
gaa aag tta tcg aga gct aga aaa ttg gat aaa ggt atc aat ata agt Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser 210 215 220	672
gat gag gat ttt ctt ttg ctg gag ctt ttg cac tgg ttt aag gaa gaa Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu 225 230 235 240	720
ttt ttt cac tgg gtg aat aac gtt ttg tgc agc aaa tgt ggt gga cag Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln 245 250 255	768
act agg tct aga gat aga tca tta ctg ccc agt gat gat gag ctg aag Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys 260 265 270	816
tgg ggt gca aag gaa gtg gaa gat cat tac tgt gat gcc tgc cag ttc Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe 275 280 285	864

201

agc aat cga ttc cca aga tgg gtg ccc tgg atg gta aaa tca gaa taa 912
 Ser Asn Arg Phe Pro Arg Trp Val Pro Trp Met Val Lys Ser Glu *
 290 295 300

<210> 140

<211> 303

<212> PRT

<213> Homo sapiens

<400> 140

Met Ala Ala Ala Ala Leu Gly Ser Ser Ser Gly Ser Ala Ser Pro Ala
 1 5 10 15
 Val Ala Glu Leu Cys Gln Asn Thr Pro Glu Thr Phe Leu Glu Ala Ser
 20 25 30
 Lys Leu Leu Leu Thr Tyr Ala Asp Asn Ile Leu Arg Asn Pro Asn Asp
 35 40 45
 Glu Lys Tyr Arg Ser Ile Arg Ile Gly Asn Thr Ala Phe Ser Thr Arg
 50 55 60
 Leu Leu Pro Val Arg Gly Ala Val Glu Cys Leu Phe Glu Met Gly Phe
 65 70 75 80
 Glu Glu Gly Glu Thr His Leu Ile Phe Pro Lys Lys Ala Ser Val Glu
 85 90 95
 Gln Leu Gln Lys Ile Arg Asp Leu Ile Ala Ile Glu Arg Ser Ser Arg
 100 105 110
 Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro
 115 120 125
 Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly
 130 135 140
 Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro
 145 150 155 160
 Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln
 165 170 175
 Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu
 180 185 190
 Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln
 195 200 205
 Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser
 210 215 220
 Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu
 225 230 235 240
 Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln
 245 250 255
 Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys

202

		260						265					270				
Trp	Gly	Ala	Lys	Glu	Val	Glu	Asp	His	Tyr	Cys	Asp	Ala	Cys	Gln	Phe		
		275						280					285				
Ser	Asn	Arg	Phe	Pro	Arg	Trp	Val	Pro	Trp	Met	Val	Lys	Ser	Glu			
		290					295					300					

<210> 141
 <211> 750
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(750)

<400> 141	
atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg ggc ctg ctg ctc	48
Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu	
1 5 10 15	
ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc cgg ggt cgg cgg	96
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg	
20 25 30	
cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag tcc gca gaa gac	144
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp	
35 40 45	
tta act gat ggt tca tat gat gat gtt cta aat gct gaa caa ctt cag	192
Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln	
50 55 60	
aaa ctc ctt tac ctg ctg gag tca acg gag gat cct gta att att gaa	240
Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu	
65 70 75 80	
aga gct ttg att act ttg ggt aac aat gca gcc ttt tca gtt aac caa	288
Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln	
85 90 95	
gct att att cgt gaa ttg ggt ggt att cca att gtt gca aac aaa atc	336
Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile	
100 105 110	

203

aac cat tcc aac cag agt att aaa gag aaa gct tta aat gca cta aat 384
 Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
 115 120 125

aac ctg agt gtg aat gtt gaa aat caa atc aag ata aag gtg caa gtt 432
 Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val
 130 135 140

ttg aaa ctg ctt ttg aat ttg tct gaa aat cca gcc atg aca gaa gga 480
 Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly
 145 150 155 160

ctt ctc cgt gcc caa gtg gat tca tca ttc ctt tcc ctt tat gac agc 528
 Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser
 165 170 175

cac gta gca aag gag att ctt ctt cga gta ctt acg cta ttt cag aat 576
 His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn
 180 185 190

ata aag aac tgc ctc aaa ata gaa ggc cat tta gct gtg cag cct act 624
 Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr
 195 200 205

ttc act gaa ggt tca ttg ttt ttc ctg tta cat gga gaa gaa tgt gcc 672
 Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala
 210 215 220

cag aaa ata aga gct tta gtt gat cac cat gat gca gag gtg aag gaa 720
 Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu
 225 230 235 240

aag gtt gta aca ata ata ccc aaa atc tga 750
 Lys Val Val Thr Ile Ile Pro Lys Ile *
 245

<210> 142

<211> 249

<212> PRT

<213> Homo sapiens

<400> 142

Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu

204

```

      1             5             10             15
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
      20             25             30
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
      35             40             45
Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
      50             55             60
Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
      65             70             75             80
Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln
      85             90             95
Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile
      100            105            110
Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
      115            120            125
Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val
      130            135            140
Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly
      145            150            155            160
Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser
      165            170            175
His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn
      180            185            190
Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr
      195            200            205
Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala
      210            215            220
Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu
      225            230            235            240
Lys Val Val Thr Ile Ile Pro Lys Ile
      245

```

<210> 143

<211> 846

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(846)

<221> misc_feature

<222> (1)...(846)

<223> n = A.T.C or G

205

<400> 143

atg ctg ccc aag tcc cgg cga gcc cta act atc cag gng atc gct gcg	48
Met Leu Pro Lys Ser Arg Arg Ala Leu Thr Ile Gln Xaa Ile Ala Ala	
1 5 10 15	
ctg gcc agg tcc tcc ctg cat ggt att tcc cag gtg gtg aag gac cac	96
Leu Ala Arg Ser Ser Leu His Gly Ile Ser Gln Val Val Lys Asp His	
20 25 30	
gtg acc aag cct acc gcc atg gcc cag ggc cga gtg gct cac ctc att	144
Val Thr Lys Pro Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile	
35 40 45	
gag tgg aag ggc tgg agc aag ccg agt gac tca cct gct gcc ctg gaa	192
Glu Trp Lys Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu	
50 55 60	
tca gcc ttt tcc tcc tat tca gac ctc agc gag ggc gaa caa gag gct	240
Ser Ala Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala	
65 70 75 80	
cgc ttt gca gca gga gtg gct gag cag ttt gcc atc gcg gaa gcc aag	288
Arg Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys	
85 90 95	
ctc cga gca tgg tct tcg gtg gat ggc gag gac tcc act gat gac tcc	336
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp Ser	
100 105 110	
tat gat gag gac ttt gct ggg gga atg gac aca gac atg gct ggg cag	384
Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala Gly Gln	
115 120 125	
ctg ccc ctg ggg ccg cac ctc cag gac ctg ttc acc ggc cac cgg ttc	432
Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly His Arg Phe	
130 135 140	
tcc cgg cct gtg cgc cag ggc tcc gtg gag cct gag agc gac tgc tca	480
Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu Ser Asp Cys Ser	
145 150 155 160	
cag acc gtg tcc cca gac acc ctg tgc tct agt ctg tgc agc ctg gag	528
Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser Leu Cys Ser Leu Glu	

206

165	170	175	
gat ggg ttg ttg ggc tcc ccg gcc cgg ctg gcc tcc cag ctg ctg ggc			576
Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu Ala Ser Gln Leu Leu Gly			
180	185	190	
gat gag ctg ctt ctc gcc aaa ctg ccc ccc agc cgg gaa agt gcc ttc			624
Asp Glu Leu Leu Leu Ala Lys Leu Pro Pro Ser Arg Glu Ser Ala Phe			
195	200	205	
cgc agc ctg ggc cca ctg gag gcc cag gac tca ctc tac aac tcg ccc			672
Arg Ser Leu Gly Pro Leu Glu Ala Gln Asp Ser Leu Tyr Asn Ser Pro			
210	215	220	
ctc aca gag tcc tgc ctt tcc ccc gcg gag gag gag cca gcc ccc tgc			720
Leu Thr Glu Ser Cys Leu Ser Pro Ala Glu Glu Glu Pro Ala Pro Cys			
225	230	235	240
aag gac tgc cag cca ctc tgc cca cca cta acg ggc agc tgg gaa cgg			768
Lys Asp Cys Gln Pro Leu Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg			
245	250	255	
cag cgg caa gcc tct gac ctg gcc tct tct ggg gtg gtg tcc tta gat			816
Gln Arg Gln Ala Ser Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp			
260	265	270	
gag gat gag gca gag cca gag gaa cag tga			846
Glu Asp Glu Ala Glu Pro Glu Glu Gln *			
275	280		

<210> 144

<211> 281

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(281)

<223> Xaa = Any Amino Acid

<400> 144

Met	Leu	Pro	Lys	Ser	Arg	Arg	Ala	Leu	Thr	Ile	Gln	Xaa	Ile	Ala	Ala
1				5				10					15		

207

Leu Ala Arg Ser Ser Leu His Gly Ile Ser Gln Val Val Lys Asp His
 20 25 30
 Val Thr Lys Pro Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile
 35 40 45
 Glu Trp Lys Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu
 50 55 60
 Ser Ala Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala
 65 70 75 80
 Arg Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
 85 90 95
 Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp Ser
 100 105 110
 Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala Gly Gln
 115 120 125
 Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly His Arg Phe
 130 135 140
 Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu Ser Asp Cys Ser
 145 150 155 160
 Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser Leu Cys Ser Leu Glu
 165 170 175
 Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu Ala Ser Gln Leu Leu Gly
 180 185 190
 Asp Glu Leu Leu Leu Ala Lys Leu Pro Pro Ser Arg Glu Ser Ala Phe
 195 200 205
 Arg Ser Leu Gly Pro Leu Glu Ala Gln Asp Ser Leu Tyr Asn Ser Pro
 210 215 220
 Leu Thr Glu Ser Cys Leu Ser Pro Ala Glu Glu Glu Pro Ala Pro Cys
 225 230 235 240
 Lys Asp Cys Gln Pro Leu Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg
 245 250 255
 Gln Arg Gln Ala Ser Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp
 260 265 270
 Glu Asp Glu Ala Glu Pro Glu Glu Gln
 275 280

<210> 145

<211> 1353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1353)

208

<400> 145

atg	ctg	gtg	act	gcc	tac	ctt	gct	ttt	gta	ggc	ctc	ctg	gcc	tcc	tgc	48
Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	Cys	
1				5					10					15		

ctg	ggg	ctg	gaa	ctg	tca	aga	tgc	cgg	gct	aaa	ccc	cct	gga	agg	gcc	96
Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	Arg	Ala	
			20					25					30			

tgc	agc	aat	ccc	tcc	ttc	ctt	cgg	ttt	caa	ctg	gac	ttc	tat	cag	gtc	144
Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	Tyr	Gln	Val	
		35					40					45				

tac	ttc	ctg	gcc	ctg	gca	gct	gat	tgg	ctt	cag	gcc	ccc	tac	ctc	tat	192
Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	Pro	Tyr	Leu	Tyr	
	50					55					60					

aaa	ctc	tac	cag	cat	tac	tac	ttc	ctg	gaa	ggc	caa	att	gcc	atc	ctc	240
Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	Gln	Ile	Ala	Ile	Leu	
65					70					75					80	

tat	gtc	tgt	ggc	ctt	gcc	tct	aca	gtc	ctc	ttt	ggc	cta	gtg	gcc	tcc	288
Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	Phe	Gly	Leu	Val	Ala	Ser	
			85						90					95		

tcc	ctt	gtg	gat	tgg	ctg	ggc	cgc	aag	aat	tct	tgt	gtc	ctc	ttc	tcc	336
Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	Asn	Ser	Cys	Val	Leu	Phe	Ser	
			100					105						110		

ctg	act	tac	tca	cta	tgc	tgc	tta	acc	aaa	ctc	tct	caa	gac	tac	ttt	384
Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	
		115					120					125				

gtg	ctg	cta	gtg	ggg	cga	gca	ctt	ggc	ggg	ctg	tcc	aca	gcc	ctg	ctc	432
Val	Leu	Leu	Val	Gly	Arg	Ala	Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	
	130					135					140					

ttc	tca	gcc	ttc	gag	gcc	tgg	tat	atc	cat	gag	cac	gtg	gaa	cgg	cat	480
Phe	Ser	Ala	Phe	Glu	Ala	Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	
145					150					155				160		

gac	ttc	cct	gct	gag	tgg	atc	cca	gct	acc	ttt	gct	cga	gct	gcc	ttc	528
Asp	Phe	Pro	Ala	Glu	Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	
			165						170					175		

209

tgg aac cat gtg ctg gct gta gtg gca ggt gtg gca gct gag gct gta	576
Trp Asn His Val Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val	
180 185 190	
gcc agc tgg ata ggg ctg ggg cct gta gcg ccc ttt gtg gct gcc atc	624
Ala Ser Trp Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile	
195 200 205	
cct ctc ctg gct ctg gca ggg gcc ttg gcc ctt cga aac tgg ggg gag	672
Pro Leu Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu	
210 215 220	
aac tat gac cgg cag cgt gcc ttc tca agg acc tgt gct gga ggc ctg	720
Asn Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu	
225 230 235 240	
cgc tgc ctc ctg tcg gac cgc cgc gtg ctg ctg ttg ggc acc ata caa	768
Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile Gln	
245 250 255	
gct cta ttt gag agt gtc atc ttc atc ttt gtc ttc ctc tgg aca cct	816
Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp Thr Pro	
260 265 270	
gtg ctg gac cca cac ggg gcc cct ctg ggc att atc ttc tcc agc ttc	864
Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe Ser Ser Phe	
275 280 285	
atg gca gcc agc ctg ctt ggc tct tcc ctg tac cgt atc gcc acc tcc	912
Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg Ile Ala Thr Ser	
290 295 300	
aag agg tac cac ctt cag ccc atg cac ctg ctg tcc ctt gct gtg ctc	960
Lys Arg Tyr His Leu Gln Pro Met His Leu Leu Ser Leu Ala Val Leu	
305 310 315 320	
atc gtc gtc ttc tct ctc ttc atg ttg act ttc tct acc agc cca ggc	1008
Ile Val Val Phe Ser Leu Phe Met Leu Thr Phe Ser Thr Ser Pro Gly	
325 330 335	
cag gag agt ccg gtg gag tcc ttc ata gcc ttt cta ctt att gag ttg	1056
Gln Glu Ser Pro Val Glu Ser Phe Ile Ala Phe Leu Leu Ile Glu Leu	
340 345 350	

210

gct tgt gga tta tac ttt ccc agc atg agc ttc cta cgg aga aag gtg 1104
Ala Cys Gly Leu Tyr Phe Pro Ser Met Ser Phe Leu Arg Arg Lys Val
355 360 365

atc cct gag aca gag cag gct ggt gta ctc aac tgg ttc cgg gta cct 1152
Ile Pro Glu Thr Glu Gln Ala Gly Val Leu Asn Trp Phe Arg Val Pro
370 375 380

ctg cac tca ctg gct tgc cta ggg ctc ctt gtc ctc cat gac agt gat 1200
Leu His Ser Leu Ala Cys Leu Gly Leu Leu Val Leu His Asp Ser Asp
385 390 395 400

cga aaa aca ggc act cgg aat atg ttc agc att tgc tct gct gtc atg 1248
Arg Lys Thr Gly Thr Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met
405 410 415

gtg atg gct ctg ctg gca gtg gtg gga ctc ttc acc gtg gta agg cat 1296
Val Met Ala Leu Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His
420 425 430

gat gct gag ctg cgg gta cct tca cct act gag gag ccc tat gcc cct 1344
Asp Ala Glu Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro
435 440 445

gag ctg taa 1353
Glu Leu *
450

<210> 146

<211> 450

<212> PRT

<213> Homo sapiens

<400> 146

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser Cys
1 5 10 15
Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly Arg Ala
20 25 30
Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe Tyr Gln Val
35 40 45
Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala Pro Tyr Leu Tyr
50 55 60

211

Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly Gln Ile Ala Ile Leu
 65 70 75 80
 Tyr Val Cys Gly Leu Ala Ser Thr Val Leu Phe Gly Leu Val Ala Ser
 85 90 95
 Ser Leu Val Asp Trp Leu Gly Arg Lys Asn Ser Cys Val Leu Phe Ser
 100 105 110
 Leu Thr Tyr Ser Leu Cys Cys Leu Thr Lys Leu Ser Gln Asp Tyr Phe
 115 120 125
 Val Leu Leu Val Gly Arg Ala Leu Gly Gly Leu Ser Thr Ala Leu Leu
 130 135 140
 Phe Ser Ala Phe Glu Ala Trp Tyr Ile His Glu His Val Glu Arg His
 145 150 155 160
 Asp Phe Pro Ala Glu Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe
 165 170 175
 Trp Asn His Val Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val
 180 185 190
 Ala Ser Trp Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile
 195 200 205
 Pro Leu Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu
 210 215 220
 Asn Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
 225 230 235 240
 Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile Gln
 245 250 255
 Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp Thr Pro
 260 265 270
 Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe Ser Ser Phe
 275 280 285
 Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg Ile Ala Thr Ser
 290 295 300
 Lys Arg Tyr His Leu Gln Pro Met His Leu Leu Ser Leu Ala Val Leu
 305 310 315 320
 Ile Val Val Phe Ser Leu Phe Met Leu Thr Phe Ser Thr Ser Pro Gly
 325 330 335
 Gln Glu Ser Pro Val Glu Ser Phe Ile Ala Phe Leu Leu Ile Glu Leu
 340 345 350
 Ala Cys Gly Leu Tyr Phe Pro Ser Met Ser Phe Leu Arg Arg Lys Val
 355 360 365
 Ile Pro Glu Thr Glu Gln Ala Gly Val Leu Asn Trp Phe Arg Val Pro
 370 375 380
 Leu His Ser Leu Ala Cys Leu Gly Leu Leu Val Leu His Asp Ser Asp
 385 390 395 400
 Arg Lys Thr Gly Thr Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met
 405 410 415

212

Val Met Ala Leu Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His
 420 425 430
 Asp Ala Glu Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro
 435 440 445
 Glu Leu
 450

<210> 147
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(465)

<221> misc_feature
 <222> (1)...(465)
 <223> n = A,T,C or G

<400> 147

atg gcg ggg ccg gtg aag gac cgc gag gcc ttc cag agg ctc aac ttc	48
Met Ala Gly Pro Val Lys Asp Arg Glu Ala Phe Gln Arg Leu Asn Phe	
1 5 10 15	
ctg tac cag gcc gcc cat tgt gtc ctt gcc cag gac ccc gag aac cag	96
Leu Tyr Gln Ala Ala His Cys Val Leu Ala Gln Asp Pro Glu Asn Gln	
20 25 30	
gcg ctg gcg agg ttt tac tgc tac act gag agg acc att gcg aag ngg	144
Ala Leu Ala Arg Phe Tyr Cys Tyr Thr Glu Arg Thr Ile Ala Lys Xaa	
35 40 45	
ctc gtc ttg cgg cgg gat ccc tcg gtg aag agg act ctc tgt cga ggc	192
Leu Val Leu Arg Arg Asp Pro Ser Val Lys Arg Thr Leu Cys Arg Gly	
50 55 60	
tgc tct tcc ctc ctc gtc ccg ggc ctc acc tgc acc cag cgc cag aga	240
Cys Ser Ser Leu Leu Val Pro Gly Leu Thr Cys Thr Gln Arg Gln Arg	
65 70 75 80	
cgc tgc agg gga cag cgc tgg acc gta cag acc tgc cta aca tgc cag	288
Arg Cys Arg Gly Gln Arg Trp Thr Val Gln Thr Cys Leu Thr Cys Gln	
85 90 95	

213

cgc agc caa cgc ttc ctc aat gat ccc ggg cat tta ctc tgg gga gac 336
 Arg Ser Gln Arg Phe Leu Asn Asp Pro Gly His Leu Leu Trp Gly Asp
 100 105 110

agg cct gag gcc cag ctc ggg agc caa gca gat tcc aaa cca cta caa 384
 Arg Pro Glu Ala Gln Leu Gly Ser Gln Ala Asp Ser Lys Pro Leu Gln
 115 120 125

ccc ttg cca aac aca gcc cac tcc att tca gac cgc ctt cct gag gag 432
 Pro Leu Pro Asn Thr Ala His Ser Ile Ser Asp Arg Leu Pro Glu Glu
 130 135 140

aaa atg cag act cag ggt tcc agt aac cag tga 465
 Lys Met Gln Thr Gln Gly Ser Ser Asn Gln *
 145 150

<210> 148

<211> 154

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Gly Pro Val Lys Asp Arg Glu Ala Phe Gln Arg Leu Asn Phe
 1 5 10 15
 Leu Tyr Gln Ala Ala His Cys Val Leu Ala Gln Asp Pro Glu Asn Gln
 20 25 30
 Ala Leu Ala Arg Phe Tyr Cys Tyr Thr Glu Arg Thr Ile Ala Lys Xaa
 35 40 45
 Leu Val Leu Arg Arg Asp Pro Ser Val Lys Arg Thr Leu Cys Arg Gly
 50 55 60
 Cys Ser Ser Leu Leu Val Pro Gly Leu Thr Cys Thr Gln Arg Gln Arg
 65 70 75 80
 Arg Cys Arg Gly Gln Arg Trp Thr Val Gln Thr Cys Leu Thr Cys Gln
 85 90 95
 Arg Ser Gln Arg Phe Leu Asn Asp Pro Gly His Leu Leu Trp Gly Asp
 100 105 110
 Arg Pro Glu Ala Gln Leu Gly Ser Gln Ala Asp Ser Lys Pro Leu Gln
 115 120 125
 Pro Leu Pro Asn Thr Ala His Ser Ile Ser Asp Arg Leu Pro Glu Glu
 130 135 140
 Lys Met Gln Thr Gln Gly Ser Ser Asn Gln
 145 150

214

<210> 149
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(390)

<400> 149
 atg atc ccc ctc ctc aga gag agc tta cac ccc atg ctg ctc tcc atc 48
 Met Ile Pro Leu Leu Arg Glu Ser Leu His Pro Met Leu Leu Ser Ile
 1 5 10 15

atc atc act gtt gca gac aac ctc aac tcc aag aac tca ggg att tac 96
 Ile Ile Thr Val Ala Asp Asn Leu Asn Ser Lys Asn Ser Gly Ile Tyr
 20 25 30

gct gct gcc gtg gca gtg ctg gtg gcc tca gtt tac ccc cgg aag cct 144
 Ala Ala Ala Val Ala Val Leu Val Ala Ser Val Tyr Pro Arg Lys Pro
 35 40 45

caa gct gta gag cgg cat gtc ctt ccc atc ctc tgg cac ttc ctg aac 192
 Gln Ala Val Glu Arg His Val Leu Pro Ile Leu Trp His Phe Leu Asn
 50 55 60

acc gcc acc agg aat ggc acc ctg cct gga ccc agc ggg aac atc cgc 240
 Thr Ala Thr Arg Asn Gly Thr Leu Pro Gly Pro Ser Gly Asn Ile Arg
 65 70 75 80

ggg gtg gtg tgc cgg ctg tcc agg agc ctc cag gag cac cat ggg ctc 288
 Gly Val Val Cys Arg Leu Ser Arg Ser Leu Gln Glu His His Gly Leu
 85 90 95

ccg cct gct gga ctt tgc cgc cag cca gcc aaa gca cgt cct caa gac 336
 Pro Pro Ala Gly Leu Cys Arg Gln Pro Ala Lys Ala Arg Pro Gln Asp
 100 105 110

gct cca gga act ctt aga ctc aga gtc ctt ggg agg cag ccg caa ggc 384
 Ala Pro Gly Thr Leu Arg Leu Arg Val Leu Gly Arg Gln Pro Gln Gly
 115 120 125

cac tga 390

215

His *

<210> 150
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 150
 Met Ile Pro Leu Leu Arg Glu Ser Leu His Pro Met Leu Leu Ser Ile
 1 5 10 15
 Ile Ile Thr Val Ala Asp Asn Leu Asn Ser Lys Asn Ser Gly Ile Tyr
 20 25 30
 Ala Ala Ala Val Ala Val Leu Val Ala Ser Val Tyr Pro Arg Lys Pro
 35 40 45
 Gln Ala Val Glu Arg His Val Leu Pro Ile Leu Trp His Phe Leu Asn
 50 55 60
 Thr Ala Thr Arg Asn Gly Thr Leu Pro Gly Pro Ser Gly Asn Ile Arg
 65 70 75 80
 Gly Val Val Cys Arg Leu Ser Arg Ser Leu Gln Glu His His Gly Leu
 85 90 95
 Pro Pro Ala Gly Leu Cys Arg Gln Pro Ala Lys Ala Arg Pro Gln Asp
 100 105 110
 Ala Pro Gly Thr Leu Arg Leu Arg Val Leu Gly Arg Gln Pro Gln Gly
 115 120 125
 His

<210> 151
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(567)

<400> 151
 atg gtc cct gcc cct cag cat gtc act gag cta gag ctg ggc atg tac 48
 Met Val Pro Ala Pro Gln His Val Thr Glu Leu Glu Leu Gly Met Tyr
 1 5 10 15
 • gcc ctg ctg gga gtc ttc tgc gtg gcc atc ttc atc ttc ttg gtc aat 96

216

Ala	Leu	Leu	Gly	Val	Phe	Cys	Val	Ala	Ile	Phe	Ile	Phe	Leu	Val	Asn	
			20					25					30			
ggt	gtg	gtc	ttc	gtc	ctg	cgc	tat	cag	cgc	aaa	gaa	cct	ccc	gac	agt	144
Gly	Val	Val	Phe	Val	Leu	Arg	Tyr	Gln	Arg	Lys	Glu	Pro	Pro	Asp	Ser	
		35				40					45					
gcc	act	gac	ccc	acc	tcc	ccc	cag	ccc	cac	aac	tgg	gtc	tgg	ctg	ggc	192
Ala	Thr	Asp	Pro	Thr	Ser	Pro	Gln	Pro	His	Asn	Trp	Val	Trp	Leu	Gly	
	50					55				60						
act	gac	cag	gag	gaa	ctg	agc	cgc	cag	ctg	gac	cgg	cag	tcc	cct	ggc	240
Thr	Asp	Gln	Glu	Glu	Leu	Ser	Arg	Gln	Leu	Asp	Arg	Gln	Ser	Pro	Gly	
65					70					75					80	
ccg	ccc	aag	ggg	gag	ggg	agc	tgc	ccc	tgt	gag	agt	ggg	gga	gga	ggg	288
Pro	Pro	Lys	Gly	Glu	Gly	Ser	Cys	Pro	Cys	Glu	Ser	Gly	Gly	Gly	Gly	
			85					90					95			
gag	gcc	cct	acc	ctg	gcc	cct	ggc	cct	cct	ggg	ggc	acc	acc	agc	tcc	336
Glu	Ala	Pro	Thr	Leu	Ala	Pro	Gly	Pro	Pro	Gly	Gly	Thr	Thr	Ser	Ser	
		100					105					110				
tca	agc	acc	ctg	gcc	cga	aag	gag	gct	ggg	ggg	cgg	cgg	aag	cga	gta	384
Ser	Ser	Thr	Leu	Ala	Arg	Lys	Glu	Ala	Gly	Gly	Arg	Arg	Lys	Arg	Val	
		115				120					125					
gag	ttt	gtg	aca	ttt	gcg	cca	gcc	cct	cca	gcc	cag	tca	cct	gag	gag	432
Glu	Phe	Val	Thr	Phe	Ala	Pro	Ala	Pro	Pro	Ala	Gln	Ser	Pro	Glu	Glu	
	130					135				140						
cct	gta	ggg	gcc	cct	gct	gtg	cag	tcc	atc	ctt	gtg	gca	ggc	gag	gag	480
Pro	Val	Gly	Ala	Pro	Ala	Val	Gln	Ser	Ile	Leu	Val	Ala	Gly	Glu	Glu	
145					150					155					160	
gac	atc	cgc	tgg	gtg	tgt	gag	gac	atg	ggg	ctg	aag	gac	cct	gag	gag	528
Asp	Ile	Arg	Trp	Val	Cys	Glu	Asp	Met	Gly	Leu	Lys	Asp	Pro	Glu	Glu	
			165					170					175			
ctt	cgc	aac	tac	atg	gag	agg	atc	cgg	ggc	agc	tcc	tga				567
Leu	Arg	Asn	Tyr	Met	Glu	Arg	Ile	Arg	Gly	Ser	Ser	*				
		180						185								

217

<210> 152
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 152
 Met Val Pro Ala Pro Gln His Val Thr Glu Leu Glu Leu Gly Met Tyr
 1 5 10 15
 Ala Leu Leu Gly Val Phe Cys Val Ala Ile Phe Ile Phe Leu Val Asn
 20 25 30
 Gly Val Val Phe Val Leu Arg Tyr Gln Arg Lys Glu Pro Pro Asp Ser
 35 40 45
 Ala Thr Asp Pro Thr Ser Pro Gln Pro His Asn Trp Val Trp Leu Gly
 50 55 60
 Thr Asp Gln Glu Glu Leu Ser Arg Gln Leu Asp Arg Gln Ser Pro Gly
 65 70 75 80
 Pro Pro Lys Gly Glu Gly Ser Cys Pro Cys Glu Ser Gly Gly Gly Gly
 85 90 95
 Glu Ala Pro Thr Leu Ala Pro Gly Pro Pro Gly Gly Thr Thr Ser Ser
 100 105 110
 Ser Ser Thr Leu Ala Arg Lys Glu Ala Gly Gly Arg Arg Lys Arg Val
 115 120 125
 Glu Phe Val Thr Phe Ala Pro Ala Pro Pro Ala Gln Ser Pro Glu Glu
 130 135 140
 Pro Val Gly Ala Pro Ala Val Gln Ser Ile Leu Val Ala Gly Glu Glu
 145 150 155 160
 Asp Ile Arg Trp Val Cys Glu Asp Met Gly Leu Lys Asp Pro Glu Glu
 165 170 175
 Leu Arg Asn Tyr Met Glu Arg Ile Arg Gly Ser Ser
 180 185

<210> 153
 <211> 735
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(735)

<400> 153
 atg gct acg gga acg cgc tat gcc ggg aag gtg gtg gtc gtg acc ggg
 Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr Gly
 1 5 10 15

48

218

ggc ggc cgc ggc atc gga gct ggc atc gtg cgc gcc ttc gtg aac agc Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val Asn Ser 20 25 30	96
ggg gcc cga gtg gtt atc tgc gac aag gat gag tct ggg ggc cgg gcc Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly Gly Arg Ala 35 40 45	144
ctg gag cag gag ctc cct gga gct gtc ttt atc ctc tgt gat gtg act Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu Cys Asp Val Thr 50 55 60	192
cag gaa gat gat gtg aag acc ctg gtt tct gag acc atc cgc cga ttt Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu Thr Ile Arg Arg Phe 65 70 75 80	240
ggc cgc ctg gat tgt gtt gtc aac aac gct ggc cac cac cca ccc cca Gly Arg Leu Asp Cys Val Val Asn Asn Ala Gly His His Pro Pro Pro 85 90 95	288
cag agg cct gag gag acc tct gcc cag gga ttc cgc cag ctg ctg gag Gln Arg Pro Glu Glu Thr Ser Ala Gln Gly Phe Arg Gln Leu Leu Glu 100 105 110	336
ctg aac cta ctg ggg acg tac acc ttg acc aag ctc gcc ctc ccc tac Leu Asn Leu Leu Gly Thr Tyr Thr Leu Thr Lys Leu Ala Leu Pro Tyr 115 120 125	384
ctg cgg aag agt caa ggg aat gtc atc aac atc tcc agc ctg gtg ggg Leu Arg Lys Ser Gln Gly Asn Val Ile Asn Ile Ser Ser Leu Val Gly 130 135 140	432
gca atc ggc cag gcc cag gca gtt ccc tat gtg gcc acc aag ggg gca Ala Ile Gly Gln Ala Gln Ala Val Pro Tyr Val Ala Thr Lys Gly Ala 145 150 155 160	480
gta aca gcc atg acc aaa gct ttg gcc ctg gat gaa agt cca tat ggt Val Thr Ala Met Thr Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly 165 170 175	528
gtc cga gtc aac tgt atc tcc cca gga aac atc tgg acc ccg ctg tgg Val Arg Val Asn Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp 180 185 190	576

219

gag gag ctg gca gcc tta atg cca gac cct agg gcc aca atc cga gag 624
 Glu Glu Leu Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu
 195 200 205

ggc atg ctg ccc agc cac tgg gcc gca tgg gcc agc ccg ctg agg tcg 672
 Gly Met Leu Pro Ser His Trp Ala Ala Trp Ala Ser Pro Leu Arg Ser
 210 215 220

ggg ctg cgg cag tgt tcc tgg cct ccg aag cca act tct gca cgg gca 720
 Gly Leu Arg Gln Cys Ser Trp Pro Pro Lys Pro Thr Ser Ala Arg Ala
 225 230 235 240

ttg aac tgc tcg tga 735
 Leu Asn Cys Ser *

<210> 154
 <211> 244
 <212> PRT
 <213> Homo sapiens

<400> 154
 Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr Gly
 1 5 10 15
 Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val Asn Ser
 20 25 30
 Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly Gly Arg Ala
 35 40 45
 Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu Cys Asp Val Thr
 50 55 60
 Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu Thr Ile Arg Arg Phe
 65 70 75 80
 Gly Arg Leu Asp Cys Val Val Asn Asn Ala Gly His His Pro Pro Pro
 85 90 95
 Gln Arg Pro Glu Glu Thr Ser Ala Gln Gly Phe Arg Gln Leu Leu Glu
 100 105 110
 Leu Asn Leu Leu Gly Thr Tyr Thr Leu Thr Lys Leu Ala Leu Pro Tyr
 115 120 125
 Leu Arg Lys Ser Gln Gly Asn Val Ile Asn Ile Ser Ser Leu Val Gly
 130 135 140
 Ala Ile Gly Gln Ala Gln Ala Val Pro Tyr Val Ala Thr Lys Gly Ala
 145 150 155 160

220

Val Thr Ala Met Thr Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly
 165 170 175
 Val Arg Val Asn Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp
 180 185 190
 Glu Glu Leu Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu
 195 200 205
 Gly Met Leu Pro Ser His Trp Ala Ala Trp Ala Ser Pro Leu Arg Ser
 210 215 220
 Gly Leu Arg Gln Cys Ser Trp Pro Pro Lys Pro Thr Ser Ala Arg Ala
 225 230 235 240
 Leu Asn Cys Ser

<210> 155

<211> 975

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(975)

<221> misc_feature

<222> (1)...(975)

<223> n = A,T,C or G

<400> 155

atg atg ctg gca cag ggc ctt ctg ctg cat tnc ntn ccn nna gac tgg 48
 Met Met Leu Ala Gln Gly Leu Leu Leu His Xaa Xaa Xaa Xaa Asp Trp
 1 5 10 15

aca tgg gcc gag ggc atg ggc ctg ggc ccc cct gag ctg tca ggg tca 96
 Thr Trp Ala Glu Gly Met Gly Leu Gly Pro Pro Glu Leu Ser Gly Ser
 20 25 30

gcc tct ccc agc cgg tac cat ggg cct gcc cgc tgg atg ccc cca cgc 144
 Ala Ser Pro Ser Arg Tyr His Gly Pro Ala Arg Trp Met Pro Pro Arg
 35 40 45

tgg gcc cag ggt gcc cct gag ctg gag cag gaa cgc cgg cac cgg cag 192
 Trp Ala Gln Gly Ala Pro Glu Leu Glu Gln Glu Arg Arg His Arg Gln
 50 55 60

att gtg tcc tgg ttc gcc gac cac ccc cgg gcc ccc ttt ggc cta cac 240

221

Ile	Val	Ser	Trp	Phe	Ala	Asp	His	Pro	Arg	Ala	Pro	Phe	Gly	Leu	His	
65					70					75					80	
cgg	ctg	gtg	gag	ctt	ggg	cag	agc	tca	ggc	aag	aag	gca	ggt	gac	tgg	288
Arg	Leu	Val	Glu	Leu	Gly	Gln	Ser	Ser	Gly	Lys	Lys	Ala	Gly	Asp	Trp	
				85					90					95		
tat	ggg	cca	tcg	cta	gtg	gca	cac	atc	ctc	agg	aaa	gcc	gtg	gag	agc	336
Tyr	Gly	Pro	Ser	Leu	Val	Ala	His	Ile	Leu	Arg	Lys	Ala	Val	Glu	Ser	
			100					105					110			
tgc	tcc	gac	gtc	acc	cgc	ctg	gtg	gtg	tac	gtt	tct	cag	gac	tgc	aca	384
Cys	Ser	Asp	Val	Thr	Arg	Leu	Val	Val	Tyr	Val	Ser	Gln	Asp	Cys	Thr	
		115					120					125				
gtg	tac	aag	gcg	gat	gtg	gca	cgc	ctg	gtg	gcc	agg	cca	gac	ccc	aca	432
Val	Tyr	Lys	Ala	Asp	Val	Ala	Arg	Leu	Val	Ala	Arg	Pro	Asp	Pro	Thr	
	130					135				140						
gcc	gag	tgg	aag	tct	gtg	gtc	atc	ctg	gtg	ccc	gtg	cga	ctg	ggt	ggc	480
Ala	Glu	Trp	Lys	Ser	Val	Val	Ile	Leu	Val	Pro	Val	Arg	Leu	Gly	Gly	
145					150					155				160		
gag	act	ctc	aac	ccc	gtg	tat	gtg	ccc	tgc	gtg	aag	gaa	ctc	ctg	cgt	528
Glu	Thr	Leu	Asn	Pro	Val	Tyr	Val	Pro	Cys	Val	Lys	Glu	Leu	Leu	Arg	
			165					170						175		
tgc	gag	ctg	tgc	ctg	ggc	atc	atg	ggg	ggg	aaa	ccg	cga	cac	tca	ctg	576
Cys	Glu	Leu	Cys	Leu	Gly	Ile	Met	Gly	Gly	Lys	Pro	Arg	His	Ser	Leu	
			180					185					190			
tac	ttc	att	ggc	tac	caa	gat	gac	ttc	ctg	ctg	tac	ctg	gac	cct	cac	624
Tyr	Phe	Ile	Gly	Tyr	Gln	Asp	Asp	Phe	Leu	Leu	Tyr	Leu	Asp	Pro	His	
		195					200					205				
tac	tgc	cag	ccc	act	gtg	gat	gtc	agc	cag	gcc	gac	ttc	ccc	ctg	gag	672
Tyr	Cys	Gln	Pro	Thr	Val	Asp	Val	Ser	Gln	Ala	Asp	Phe	Pro	Leu	Glu	
	210					215				220						
tcc	ttc	cac	tgc	acc	tcg	ccc	cgc	aag	atg	gcc	ttt	gcc	aag	atg	gac	720
Ser	Phe	His	Cys	Thr	Ser	Pro	Arg	Lys	Met	Ala	Phe	Ala	Lys	Met	Asp	
225					230					235				240		
cca	agc	tgt	acc	gtg	ggc	ttc	tat	gct	gga	gac	agg	aag	gag	ttt	gag	768

223

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65              70              75              80
Arg Leu Val Glu Leu Gly Gln Ser Ser Gly Lys Lys Ala Gly Asp Trp
              85              90              95
Tyr Gly Pro Ser Leu Val Ala His Ile Leu Arg Lys Ala Val Glu Ser
              100             105             110
Cys Ser Asp Val Thr Arg Leu Val Val Tyr Val Ser Gln Asp Cys Thr
              115             120             125
Val Tyr Lys Ala Asp Val Ala Arg Leu Val Ala Arg Pro Asp Pro Thr
              130             135             140
Ala Glu Trp Lys Ser Val Val Ile Leu Val Pro Val Arg Leu Gly Gly
145             150             155             160
Glu Thr Leu Asn Pro Val Tyr Val Pro Cys Val Lys Glu Leu Leu Arg
              165             170             175
Cys Glu Leu Cys Leu Gly Ile Met Gly Gly Lys Pro Arg His Ser Leu
              180             185             190
Tyr Phe Ile Gly Tyr Gln Asp Asp Phe Leu Leu Tyr Leu Asp Pro His
              195             200             205
Tyr Cys Gln Pro Thr Val Asp Val Ser Gln Ala Asp Phe Pro Leu Glu
              210             215             220
Ser Phe His Cys Thr Ser Pro Arg Lys Met Ala Phe Ala Lys Met Asp
225             230             235             240
Pro Ser Cys Thr Val Gly Phe Tyr Ala Gly Asp Arg Lys Glu Phe Glu
              245             250             255
Thr Leu Cys Ser Glu Leu Thr Arg Val Leu Ser Ser Ser Ser Ala Thr
              260             265             270
Glu Arg Tyr Pro Met Phe Thr Leu Ala Glu Gly His Ala Gln Asp His
              275             280             285
Ser Leu Asp Asp Leu Cys Ser Gln Leu Ala Gln Pro Thr Leu Arg Leu
              290             295             300
Pro Arg Thr Gly Arg Leu Leu Arg Ala Lys Arg Pro Ser Ser Glu Asp
305             310             315             320
Phe Val Phe Leu

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<210> 157
 <211> 669
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(669)

<400> 157

224

atg atc ctt gta gga ctc tgg tta att cag tgg ctg ctc tta aaa tac	48
Met Ile Leu Val Gly Leu Trp Leu Ile Gln Trp Leu Leu Leu Lys Tyr	
1 5 10 15	
aag tct att att agc aga aga ttt ttc tgc ata gtt ggc acg ctg tac	96
Lys Ser Ile Ile Ser Arg Arg Phe Phe Cys Ile Val Gly Thr Leu Tyr	
20 25 30	
ctg tat cgg tgt att aca atg tat gta act aca ctc cca gta cct ggt	144
Leu Tyr Arg Cys Ile Thr Met Tyr Val Thr Thr Leu Pro Val Pro Gly	
35 40 45	
atg cat ttc aac tgt tct ccg aag ctt ttc gga gac tgg gaa gcc caa	192
Met His Phe Asn Cys Ser Pro Lys Leu Phe Gly Asp Trp Glu Ala Gln	
50 55 60	
ctg cga aga ata atg aag ctc att gct gga ggt ggc ttg tct atc act	240
Leu Arg Arg Ile Met Lys Leu Ile Ala Gly Gly Gly Leu Ser Ile Thr	
65 70 75 80	
ggc tct cac aac atg tgt ggg gac tat ctg tac agc ggc cac acg gtc	288
Gly Ser His Asn Met Cys Gly Asp Tyr Leu Tyr Ser Gly His Thr Val	
85 90 95	
atg cta aca ctt acc tac tta ttt atc aaa gag tat tcc cct cgg cga	336
Met Leu Thr Leu Thr Tyr Leu Phe Ile Lys Glu Tyr Ser Pro Arg Arg	
100 105 110	
ctc tgg tgg tat cac tgg att tgc tgg ctt ctc agc gta gtt gga atc	384
Leu Trp Trp Tyr His Trp Ile Cys Trp Leu Leu Ser Val Val Gly Ile	
115 120 125	
ttc tgt att ctc tta gcg cat gac cac tac act gtg gac gtg gtg gtg	432
Phe Cys Ile Leu Leu Ala His Asp His Tyr Thr Val Asp Val Val Val	
130 135 140	
gca tat tac atc acc acg aga ctc ttc tgg tgg tat cac act atg gcc	480
Ala Tyr Tyr Ile Thr Thr Arg Leu Phe Trp Trp Tyr His Thr Met Ala	
145 150 155 160	
aat cag caa gtg cta aag gaa gct tcc cag atg aac ctc ctg gcc agg	528
Asn Gln Gln Val Leu Lys Glu Ala Ser Gln Met Asn Leu Leu Ala Arg	
165 170 175	

225

gtg tgg tgg tac agg cca ttt cag tac ttt gaa aag aat gtc caa gga 576
 Val Trp Trp Tyr Arg Pro Phe Gln Tyr Phe Glu Lys Asn Val Gln Gly
 180 185 190

att gta cct cga tct tac cat tgg cct ttc ccc tgg cca gta gtc cac 624
 Ile Val Pro Arg Ser Tyr His Trp Pro Phe Pro Trp Pro Val Val His
 195 200 205

ctc agt agg caa gtt aaa tac agc cgg ctg gtg aat gac aca taa 669
 Leu Ser Arg Gln Val Lys Tyr Ser Arg Leu Val Asn Asp Thr *
 210 215 220

<210> 158

<211> 222

<212> PRT

<213> Homo sapiens

<400> 158

Met Ile Leu Val Gly Leu Trp Leu Ile Gln Trp Leu Leu Leu Lys Tyr
 1 5 10 15
 Lys Ser Ile Ile Ser Arg Arg Phe Phe Cys Ile Val Gly Thr Leu Tyr
 20 25 30
 Leu Tyr Arg Cys Ile Thr Met Tyr Val Thr Thr Leu Pro Val Pro Gly
 35 40 45
 Met His Phe Asn Cys Ser Pro Lys Leu Phe Gly Asp Trp Glu Ala Gln
 50 55 60
 Leu Arg Arg Ile Met Lys Leu Ile Ala Gly Gly Gly Leu Ser Ile Thr
 65 70 75 80
 Gly Ser His Asn Met Cys Gly Asp Tyr Leu Tyr Ser Gly His Thr Val
 85 90 95
 Met Leu Thr Leu Thr Tyr Leu Phe Ile Lys Glu Tyr Ser Pro Arg Arg
 100 105 110
 Leu Trp Trp Tyr His Trp Ile Cys Trp Leu Leu Ser Val Val Gly Ile
 115 120 125
 Phe Cys Ile Leu Leu Ala His Asp His Tyr Thr Val Asp Val Val Val
 130 135 140
 Ala Tyr Tyr Ile Thr Thr Arg Leu Phe Trp Trp Tyr His Thr Met Ala
 145 150 155 160
 Asn Gln Gln Val Leu Lys Glu Ala Ser Gln Met Asn Leu Leu Ala Arg
 165 170 175
 Val Trp Trp Tyr Arg Pro Phe Gln Tyr Phe Glu Lys Asn Val Gln Gly
 180 185 190
 Ile Val Pro Arg Ser Tyr His Trp Pro Phe Pro Trp Pro Val Val His

226

195 200 205
 Leu Ser Arg Gln Val Lys Tyr Ser Arg Leu Val Asn Asp Thr
 210 215 220

<210> 159

<211> 540

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(540)

<221> misc_feature

<222> (1)...(540)

<223> n = A,T,C or G

<400> 159

atg gcc gct ccc cgc ngc agg gcc gcg ccc tgg acg acg gcc ctg ctg 48
 Met Ala Ala Pro Arg Xaa Arg Ala Ala Pro Trp Thr Thr Ala Leu Leu
 1 5 10 15

ctg ctc cta gcc tcg cag gtc ctg tct ccg gga agc tgc gcg gac gag 96
 Leu Leu Leu Ala Ser Gln Val Leu Ser Pro Gly Ser Cys Ala Asp Glu
 20 25 30

gag gag gtc ccc gag gag tgg gtg ctc ctg cac gtc gtc cag ggc cag 144
 Glu Glu Val Pro Glu Glu Trp Val Leu Leu His Val Val Gln Gly Gln
 35 40 45

ata ggc gcc ggg aac tac agc tac ctg cgg ctg aac cac gag ggc aag 192
 Ile Gly Ala Gly Asn Tyr Ser Tyr Leu Arg Leu Asn His Glu Gly Lys
 50 55 60

ata gtc ctc agg atg cgc acc tnc aag gga gat gcg gat ctg tac gtc 240
 Ile Val Leu Arg Met Arg Thr Xaa Lys Gly Asp Ala Asp Leu Tyr Val
 65 70 75 80

tcc gcc agc agc ctg cac ccc agc ttc gac gac tac gag ctg caa tcg 288
 Ser Ala Ser Ser Leu His Pro Ser Phe Asp Asp Tyr Glu Leu Gln Ser
 85 90 95

gcc acc tgn cgg ccc gga cgc cgt gtc cat ccc cgc gca ctt ccg gcg 336
 Ala Thr Xaa Arg Pro Gly Arg Arg Val His Pro Arg Ala Leu Pro Ala

227

100	105	110	
ccc agt ggg cat cgg cgt cta tgg aca ccc ctc cca cct gga gag cga			384
Pro Ser Gly His Arg Arg Leu Trp Thr Pro Leu Pro Pro Gly Glu Arg			
115	120	125	
gtt cga gat gaa ggt gta cta cga cgg cac ggt ncg agc agc acc cgt			432
Val Arg Asp Glu Gly Val Leu Arg Arg His Gly Xaa Ser Ser Thr Arg			
130	135	140	
tcg gcg agg ccg cct acc ccg ccg acg gcg cag atg ccg gcc aga agc			480
Ser Ala Arg Pro Pro Thr Pro Pro Thr Ala Gln Met Pro Ala Arg Ser			
145	150	155	160
acg ctg gtg ccc cgg aag acg cct cgc aag agg agg aat ctg ttc tct			528
Thr Leu Val Pro Arg Lys Thr Pro Arg Lys Arg Arg Asn Leu Phe Ser			
165	170	175	
gga cga tat taa			540
Gly Arg Tyr *			

<210> 160

<211> 179

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(179)

<223> Xaa = Any Amino Acid

<400> 160

Met	Ala	Ala	Pro	Arg	Xaa	Arg	Ala	Ala	Pro	Trp	Thr	Thr	Ala	Leu	Leu
1				5					10					15	
Leu	Leu	Leu	Ala	Ser	Gln	Val	Leu	Ser	Pro	Gly	Ser	Cys	Ala	Asp	Glu
			20						25				30		
Glu	Glu	Val	Pro	Glu	Glu	Trp	Val	Leu	Leu	His	Val	Val	Gln	Gly	Gln
		35					40					45			
Ile	Gly	Ala	Gly	Asn	Tyr	Ser	Tyr	Leu	Arg	Leu	Asn	His	Glu	Gly	Lys
	50					55				60					
Ile	Val	Leu	Arg	Met	Arg	Thr	Xaa	Lys	Gly	Asp	Ala	Asp	Leu	Tyr	Val
65					70					75				80	

228

Ser Ala Ser Ser Leu His Pro Ser Phe Asp Asp Tyr Glu Leu Gln Ser
 85 90 95
 Ala Thr Xaa Arg Pro Gly Arg Arg Val His Pro Arg Ala Leu Pro Ala
 100 105 110
 Pro Ser Gly His Arg Arg Leu Trp Thr Pro Leu Pro Pro Gly Glu Arg
 115 120 125
 Val Arg Asp Glu Gly Val Leu Arg Arg His Gly Xaa Ser Ser Thr Arg
 130 135 140
 Ser Ala Arg Pro Pro Thr Pro Pro Thr Ala Gln Met Pro Ala Arg Ser
 145 150 155 160
 Thr Leu Val Pro Arg Lys Thr Pro Arg Lys Arg Arg Asn Leu Phe Ser
 165 170 175
 Gly Arg Tyr

<210> 161
 <211> 1290
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1290)

<400> 161
 atg act gct gct ctg gcc gtc gtc acg acg tcg ggt ttg gaa gat ggg 48
 Met Thr Ala Ala Leu Ala Val Val Thr Thr Ser Gly Leu Glu Asp Gly
 1 5 10 15

 gtg cct agg tcc cgt ggc gaa ggg acc ggg gaa gtg gtc ttg gag cgg 96
 Val Pro Arg Ser Arg Gly Glu Gly Thr Gly Glu Val Val Leu Glu Arg
 20 25 30

 ggg ccc ggc gcg gcc tac cac atg ttc gtg gtg atg gag gac ttg gtg 144
 Gly Pro Gly Ala Ala Tyr His Met Phe Val Val Met Glu Asp Leu Val
 35 40 45

 gag aag ctg aag ctg ctc cgc tac gag gag gag ttc ctc cgg aag agc 192
 Glu Lys Leu Lys Leu Leu Arg Tyr Glu Glu Glu Phe Leu Arg Lys Ser
 50 55 60

 aac ctg aag gcc ccg tcc aga cac tat ttt gca ctg cct acc aac cct 240
 Asn Leu Lys Ala Pro Ser Arg His Tyr Phe Ala Leu Pro Thr Asn Pro
 65 70 75 80

229

ggc gaa cag ttc tac atg ttt tgt act ctt gct gct tgg ttg att aat	288
Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn	
85 90 95	
aaa gcg gga cgt ccc ttt gag cag cct caa gaa tat gat gac cct aat	336
Lys Ala Gly Arg Pro Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn	
100 105 110	
gca aca ata tct aac ata cta tcc gag ctt cgg tca ttt gga aga act	384
Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr	
115 120 125	
gca gat ttt cct cct tca aaa tta aag tca ggt tat gga gaa cat gta	432
Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu His Val	
130 135 140	
tgc tat gtt ctt gat tgc ttc gct gaa gaa gca ttg aaa tat att ggt	480
Cys Tyr Val Leu Asp Cys Phe Ala Glu Glu Ala Leu Lys Tyr Ile Gly	
145 150 155 160	
ttc acc tgg aaa agg cca ata tac cca gta gaa gaa tta gaa gaa gaa	528
Phe Thr Trp Lys Arg Pro Ile Tyr Pro Val Glu Glu Leu Glu Glu Glu	
165 170 175	
agc gtt gca gaa gat gat gca gaa tta aca tta aat aaa gtg gat gaa	576
Ser Val Ala Glu Asp Asp Ala Glu Leu Thr Leu Asn Lys Val Asp Glu	
180 185 190	
gaa ttt gtg gaa gaa gag aca gat aat gaa gaa aac ttt att gat ctc	624
Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu	
195 200 205	
aac gtt tta aag gcc cag aca tat cac ttg gat atg aac gag act gcc	672
Asn Val Leu Lys Ala Gln Thr Tyr His Leu Asp Met Asn Glu Thr Ala	
210 215 220	
aaa caa gaa gat att ttg gaa tcc aca aca gat gct gca gaa tgg agc	720
Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser	
225 230 235 240	
cta gaa gtg gaa cgt gta cta ccg caa ctg aaa gtc acg att agg act	768
Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr	
245 250 255	

230

gac aat aag gat tgg aga atc cat gtt gac caa atg cac cag cac aga Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Arg 260 265 270	816
agt gga att gaa tct gct cta aag gag acc aag gga ttt ttg gac aaa Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys 275 280 285	864
ctc cat aat gaa att act agg act ttg gaa aag atc agc agc cga gaa Leu His Asn Glu Ile Thr Arg Thr Leu Glu Lys Ile Ser Ser Arg Glu 290 295 300	912
aag tac atc aac aat cag ctt gag aat ttg gtt caa gaa tat cgt gca Lys Tyr Ile Asn Asn Gln Leu Glu Asn Leu Val Gln Glu Tyr Arg Ala 305 310 315 320	960
gct caa gcc cag ctg agt gag gca aag gag cga tac cag cag gga aat Ala Gln Ala Gln Leu Ser Glu Ala Lys Glu Arg Tyr Gln Gln Gly Asn 325 330 335	1008
gga gga gtg acg gaa aga acc aga ctc ctc tct gag gtt atg gaa gaa Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Met Glu Glu 340 345 350	1056
tta gaa aag gta aaa caa gaa atg gaa gaa aag ggc agc agc atg act Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr 355 360 365	1104
gat ggt gct cct ttg gtg aag att aaa cag agc tta aca aaa ctg aag Asp Gly Ala Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys 370 375 380	1152
caa gaa act gta gag atg gac att aga att ggc att gtg gaa cac aca Gln Glu Thr Val Glu Met Asp Ile Arg Ile Gly Ile Val Glu His Thr 385 390 395 400	1200
cta ctc caa tca aag ctg aag gag aag tcc aac atg act agg aac atg Leu Leu Gln Ser Lys Leu Lys Glu Lys Ser Asn Met Thr Arg Asn Met 405 410 415	1248
cat gcc aca gtt att cca gaa cca gca aca ggc ttt tat taa His Ala Thr Val Ile Pro Glu Pro Ala Thr Gly Phe Tyr *	1290
420 425	

231

<210> 162
 <211> 429
 <212> PRT
 <213> Homo sapiens

<400> 162

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Met Thr Ala Ala Leu Ala Val Val Thr Thr Ser Gly Leu Glu Asp Gly
 1          5          10          15
Val Pro Arg Ser Arg Gly Glu Gly Thr Gly Glu Val Val Leu Glu Arg
          20          25          30
Gly Pro Gly Ala Ala Tyr His Met Phe Val Val Met Glu Asp Leu Val
          35          40          45
Glu Lys Leu Lys Leu Leu Arg Tyr Glu Glu Glu Phe Leu Arg Lys Ser
          50          55          60
Asn Leu Lys Ala Pro Ser Arg His Tyr Phe Ala Leu Pro Thr Asn Pro
65          70          75          80
Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn
          85          90          95
Lys Ala Gly Arg Pro Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn
          100          105          110
Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr
          115          120          125
Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu His Val
          130          135          140
Cys Tyr Val Leu Asp Cys Phe Ala Glu Glu Ala Leu Lys Tyr Ile Gly
145          150          155          160
Phe Thr Trp Lys Arg Pro Ile Tyr Pro Val Glu Glu Leu Glu Glu Glu
          165          170          175
Ser Val Ala Glu Asp Asp Ala Glu Leu Thr Leu Asn Lys Val Asp Glu
          180          185          190
Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu
          195          200          205
Asn Val Leu Lys Ala Gln Thr Tyr His Leu Asp Met Asn Glu Thr Ala
          210          215          220
Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser
225          230          235          240
Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr
          245          250          255
Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Arg
          260          265          270
Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys
          275          280          285

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232

Leu His Asn Glu Ile Thr Arg Thr Leu Glu Lys Ile Ser Ser Arg Glu
 290 295 300
 Lys Tyr Ile Asn Asn Gln Leu Glu Asn Leu Val Gln Glu Tyr Arg Ala
 305 310 315 320
 Ala Gln Ala Gln Leu Ser Glu Ala Lys Glu Arg Tyr Gln Gln Gly Asn
 325 330 335
 Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Met Glu Glu
 340 345 350
 Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr
 355 360 365
 Asp Gly Ala Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys
 370 375 380
 Gln Glu Thr Val Glu Met Asp Ile Arg Ile Gly Ile Val Glu His Thr
 385 390 395 400
 Leu Leu Gln Ser Lys Leu Lys Glu Lys Ser Asn Met Thr Arg Asn Met
 405 410 415
 His Ala Thr Val Ile Pro Glu Pro Ala Thr Gly Phe Tyr
 420 425

<210> 163

<211> 456

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(456)

<400> 163

atg gaa gga cag cgg caa gaa agc cac gca acc cta aca ctc gcc cag	48
Met Glu Gly Gln Arg Gln Glu Ser His Ala Thr Leu Thr Leu Ala Gln	
1 5 10 15	
 gct cat ttc aac aat gga gag tac gcg gag gcc gag gca ctg tac tcc	96
Ala His Phe Asn Asn Gly Glu Tyr Ala Glu Ala Glu Ala Leu Tyr Ser	
20 25 30	
 gct tac att cgc cgg tgc gct tgc gcg gcc tcc agc gac gag agt ccc	144
Ala Tyr Ile Arg Arg Cys Ala Cys Ala Ala Ser Ser Asp Glu Ser Pro	
35 40 45	
 ggg agc aaa tgc agc cct gag gat ttg gct act gca tat aac aac agg	192
Gly Ser Lys Cys Ser Pro Glu Asp Leu Ala Thr Ala Tyr Asn Asn Arg	
50 55 60	

233

ggg caa atc aag tac ttc agg gtt gat ttt tat gaa gcc atg gat gac 240
 Gly Gln Ile Lys Tyr Phe Arg Val Asp Phe Tyr Glu Ala Met Asp Asp
 65 70 75 80

tac aca tct gcc ata gaa gtc caa ccc aat ttt gaa gtt cca tat tac 288
 Tyr Thr Ser Ala Ile Glu Val Gln Pro Asn Phe Glu Val Pro Tyr Tyr
 85 90 95

aac aga ggg ttg ata ctg tat agg ctg gga tat ttt gat gat gct ttg 336
 Asn Arg Gly Leu Ile Leu Tyr Arg Leu Gly Tyr Phe Asp Asp Ala Leu
 100 105 110

gaa gat ttc aag aag gtc tta gac tta aat cct gga ttt caa gat gct 384
 Glu Asp Phe Lys Lys Val Leu Asp Leu Asn Pro Gly Phe Gln Asp Ala
 115 120 125

act ttg agc tta aaa cag act att cta gac aaa gaa gaa aaa caa aga 432
 Thr Leu Ser Leu Lys Gln Thr Ile Leu Asp Lys Glu Glu Lys Gln Arg
 130 135 140

aga aat gtt gca aaa aat tat tga 456
 Arg Asn Val Ala Lys Asn Tyr *
 145 150

<210> 164

<211> 151

<212> PRT

<213> Homo sapiens

<400> 164

Met Glu Gly Gln Arg Gln Glu Ser His Ala Thr Leu Thr Leu Ala Gln
 1 5 10 15
 Ala His Phe Asn Asn Gly Glu Tyr Ala Glu Ala Glu Ala Leu Tyr Ser
 20 25 30
 Ala Tyr Ile Arg Arg Cys Ala Cys Ala Ala Ser Ser Asp Glu Ser Pro
 35 40 45
 Gly Ser Lys Cys Ser Pro Glu Asp Leu Ala Thr Ala Tyr Asn Asn Arg
 50 55 60
 Gly Gln Ile Lys Tyr Phe Arg Val Asp Phe Tyr Glu Ala Met Asp Asp
 65 70 75 80
 Tyr Thr Ser Ala Ile Glu Val Gln Pro Asn Phe Glu Val Pro Tyr Tyr
 85 90 95

234

Asn Arg Gly Leu Ile Leu Tyr Arg Leu Gly Tyr Phe Asp Asp Ala Leu
 100 105 110
 Glu Asp Phe Lys Lys Val Leu Asp Leu Asn Pro Gly Phe Gln Asp Ala
 115 120 125
 Thr Leu Ser Leu Lys Gln Thr Ile Leu Asp Lys Glu Glu Lys Gln Arg
 130 135 140
 Arg Asn Val Ala Lys Asn Tyr
 145 150

<210> 165
 <211> 1032
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1032)

<400> 165

atg atg ctg ctg ctc tat gaa gaa ggc ctc cgg gtt gtc ata cac acc	48
Met Met Leu Leu Leu Tyr Glu Glu Gly Leu Arg Val Val Ile His Thr	
1 5 10 15	
tcc aac ctc atc cat gct gac tgg cac cag aaa act caa gga ata tgg	96
Ser Asn Leu Ile His Ala Asp Trp His Gln Lys Thr Gln Gly Ile Trp	
20 25 30	
ttg agc ccc tta tac cca cga att gct gat gga acc cac aaa tct gga	144
Leu Ser Pro Leu Tyr Pro Arg Ile Ala Asp Gly Thr His Lys Ser Gly	
35 40 45	
gag tcg cca aca cat ttt aaa gct gat ctc atc agt tac ttg atg gct	192
Glu Ser Pro Thr His Phe Lys Ala Asp Leu Ile Ser Tyr Leu Met Ala	
50 55 60	
tat aat gcc cct tct ctc aag gag tgg ata gat gtc att cac aag cac	240
Tyr Asn Ala Pro Ser Leu Lys Glu Trp Ile Asp Val Ile His Lys His	
65 70 75 80	
gat ctc tct gaa aca aat gtt tat ctt att ggt tca acc cca gga cgc	288
Asp Leu Ser Glu Thr Asn Val Tyr Leu Ile Gly Ser Thr Pro Gly Arg	
85 90 95	
ttt caa gga agt caa aaa gat aat tgg gga cat ttt aga ctt aag aag	336

235

Phe	Gln	Gly	Ser	Gln	Lys	Asp	Asn	Trp	Gly	His	Phe	Arg	Leu	Lys	Lys		
			100					105					110				
ctt	ctg	aaa	gac	cat	gcc	tca	tcc	atg	cct	aac	gca	gag	tcc	tgg	cct		384
Leu	Leu	Lys	Asp	His	Ala	Ser	Ser	Met	Pro	Asn	Ala	Glu	Ser	Trp	Pro		
		115					120					125					
gtc	gta	ggc	cag	ttt	tca	agc	gtt	ggc	tcc	ttg	gga	gcc	gat	gaa	tca		432
Val	Val	Gly	Gln	Phe	Ser	Ser	Val	Gly	Ser	Leu	Gly	Ala	Asp	Glu	Ser		
		130				135					140						
aag	tgg	tta	tgt	tct	gag	ttt	aaa	gag	agc	atg	ctg	aca	ctg	ggg	aag		480
Lys	Trp	Leu	Cys	Ser	Glu	Phe	Lys	Glu	Ser	Met	Leu	Thr	Leu	Gly	Lys		
		145			150					155					160		
gaa	agc	aag	act	cca	gga	aaa	agc	tct	gtt	cct	ctt	tac	ttg	atc	tat		528
Glu	Ser	Lys	Thr	Pro	Gly	Lys	Ser	Ser	Val	Pro	Leu	Tyr	Leu	Ile	Tyr		
			165						170					175			
cct	tct	gtg	gaa	aat	gtg	cgg	acc	agt	tta	gaa	gga	tat	cct	gct	ggg		576
Pro	Ser	Val	Glu	Asn	Val	Arg	Thr	Ser	Leu	Glu	Gly	Tyr	Pro	Ala	Gly		
		180					185						190				
ggc	tct	ctt	ccc	tat	agc	atc	cag	aca	gct	gaa	aaa	cag	aat	tgg	ctg		624
Gly	Ser	Leu	Pro	Tyr	Ser	Ile	Gln	Thr	Ala	Glu	Lys	Gln	Asn	Trp	Leu		
		195					200					205					
cat	tcc	tat	ttt	cac	aaa	tgg	tca	gct	gag	act	tct	ggc	cgc	agc	aat		672
His	Ser	Tyr	Phe	His	Lys	Trp	Ser	Ala	Glu	Thr	Ser	Gly	Arg	Ser	Asn		
		210				215					220						
gcc	atg	cca	cat	att	aag	aca	tat	atg	agg	cct	tct	cca	gac	ttc	agt		720
Ala	Met	Pro	His	Ile	Lys	Thr	Tyr	Met	Arg	Pro	Ser	Pro	Asp	Phe	Ser		
	225				230				235					240			
aaa	att	gct	tgg	ttc	ctt	gtc	aca	agc	gca	aat	ctg	tcc	aag	gct	gcc		768
Lys	Ile	Ala	Trp	Phe	Leu	Val	Thr	Ser	Ala	Asn	Leu	Ser	Lys	Ala	Ala		
			245						250					255			
tgg	gga	gca	ttg	gag	aag	aat	ggc	acc	cag	ctg	atg	atc	cgc	tcc	tac		816
Trp	Gly	Ala	Leu	Glu	Lys	Asn	Gly	Thr	Gln	Leu	Met	Ile	Arg	Ser	Tyr		
		260					265						270				
gag	ctc	ggg	gtc	ctt	ttc	ctc	cct	tca	gca	ttt	ggc	cta	gac	agt	ttc		864

236

Glu Leu Gly Val Leu Phe Leu Pro Ser Ala Phe Gly Leu Asp Ser Phe
 275 280 285
 aaa gtg aaa cag aag ttc ttc gct ggc agc cag gag cca atg gcc acc 912
 Lys Val Lys Gln Lys Phe Phe Ala Gly Ser Gln Glu Pro Met Ala Thr
 290 295 300
 ttt cct gtg cca tat gat ttg cct cca gaa ctg tat gga agt aaa gat 960
 Phe Pro Val Pro Tyr Asp Leu Pro Pro Glu Leu Tyr Gly Ser Lys Asp
 305 310 315 320
 cgg cca tgg ata tgg aac att cct tat gtc aaa gca ccg gat acg cat 1008
 Arg Pro Trp Ile Trp Asn Ile Pro Tyr Val Lys Ala Pro Asp Thr His
 325 330 335
 ggg aac atg tgg gtg ccc tcc tga 1032
 Gly Asn Met Trp Val Pro Ser *
 340

<210> 166

<211> 343

<212> PRT

<213> Homo sapiens

<400> 166

Met Met Leu Leu Leu Tyr Glu Glu Gly Leu Arg Val Val Ile His Thr
 1 5 10 15
 Ser Asn Leu Ile His Ala Asp Trp His Gln Lys Thr Gln Gly Ile Trp
 20 25 30
 Leu Ser Pro Leu Tyr Pro Arg Ile Ala Asp Gly Thr His Lys Ser Gly
 35 40 45
 Glu Ser Pro Thr His Phe Lys Ala Asp Leu Ile Ser Tyr Leu Met Ala
 50 55 60
 Tyr Asn Ala Pro Ser Leu Lys Glu Trp Ile Asp Val Ile His Lys His
 65 70 75 80
 Asp Leu Ser Glu Thr Asn Val Tyr Leu Ile Gly Ser Thr Pro Gly Arg
 85 90 95
 Phe Gln Gly Ser Gln Lys Asp Asn Trp Gly His Phe Arg Leu Lys Lys
 100 105 110
 Leu Leu Lys Asp His Ala Ser Ser Met Pro Asn Ala Glu Ser Trp Pro
 115 120 125
 Val Val Gly Gln Phe Ser Ser Val Gly Ser Leu Gly Ala Asp Glu Ser
 130 135 140

237

Lys Trp Leu Cys Ser Glu Phe Lys Glu Ser Met Leu Thr Leu Gly Lys
 145 150 155 160
 Glu Ser Lys Thr Pro Gly Lys Ser Ser Val Pro Leu Tyr Leu Ile Tyr
 165 170 175
 Pro Ser Val Glu Asn Val Arg Thr Ser Leu Glu Gly Tyr Pro Ala Gly
 180 185 190
 Gly Ser Leu Pro Tyr Ser Ile Gln Thr Ala Glu Lys Gln Asn Trp Leu
 195 200 205
 His Ser Tyr Phe His Lys Trp Ser Ala Glu Thr Ser Gly Arg Ser Asn
 210 215 220
 Ala Met Pro His Ile Lys Thr Tyr Met Arg Pro Ser Pro Asp Phe Ser
 225 230 235 240
 Lys Ile Ala Trp Phe Leu Val Thr Ser Ala Asn Leu Ser Lys Ala Ala
 245 250 255
 Trp Gly Ala Leu Glu Lys Asn Gly Thr Gln Leu Met Ile Arg Ser Tyr
 260 265 270
 Glu Leu Gly Val Leu Phe Leu Pro Ser Ala Phe Gly Leu Asp Ser Phe
 275 280 285
 Lys Val Lys Gln Lys Phe Phe Ala Gly Ser Gln Glu Pro Met Ala Thr
 290 295 300
 Phe Pro Val Pro Tyr Asp Leu Pro Pro Glu Leu Tyr Gly Ser Lys Asp
 305 310 315 320
 Arg Pro Trp Ile Trp Asn Ile Pro Tyr Val Lys Ala Pro Asp Thr His
 325 330 335
 Gly Asn Met Trp Val Pro Ser
 340

<210> 167
 <211> 594
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(594)

<400> 167

atg cca ccc gcg ggg ctc cgc cgg gcc gcg ccg ctc acc gca atc gct 48
 Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile Ala
 1 5 10 15

ctg ttg gtg ctg ggg gct ccc cta gtg ctg gcc ggc gag gac tgc ctg 96
 Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp Cys Leu
 20 25 30

238

tgg tac ctg gac cgg aat ggc tcc tgg cat ccg ggg ttt aac tgc gag	144
Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe Asn Cys Glu	
35 40 45	
ttc ttc acc ttc tgc tgc ggg acc tgc tac cat ccg tac tgc tgc agg	192
Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg Tyr Cys Cys Arg	
50 55 60	
gac ctg acc ttg ctt atc acc gag agg cag cag aag cac tgc ctg gcc	240
Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln Lys His Cys Leu Ala	
65 70 75 80	
ttc agc ccc aag acc ata gca ggc atc gcc tca gct gtg atc ctc ttt	288
Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala Ser Ala Val Ile Leu Phe	
85 90 95	
gtt gct gtg gtt gcc acc acc atc tgc tgc ttc ctc tgt tcc tgt tgc	336
Val Ala Val Val Ala Thr Thr Ile Cys Cys Phe Leu Cys Ser Cys Cys	
100 105 110	
tac ctg tac cgc cgg cgc cag cag ctc cag agc cca ttt gaa ggc cag	384
Tyr Leu Tyr Arg Arg Arg Gln Gln Leu Gln Ser Pro Phe Glu Gly Gln	
115 120 125	
gag att cca atg aca ggc atc cca gtg cag cca gta tac cca tac ccc	432
Glu Ile Pro Met Thr Gly Ile Pro Val Gln Pro Val Tyr Pro Tyr Pro	
130 135 140	
cag gac ccc aaa gct ggc cct gca ccc cca cag cct ggc ttc atg tac	480
Gln Asp Pro Lys Ala Gly Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr	
145 150 155 160	
cca cct agt ggt cct gct ccc caa tat cca ctc tac cca gct ggg ccc	528
Pro Pro Ser Gly Pro Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro	
165 170 175	
cca gtc tac aac cct gca gct cct cct ccc tat atg cca cca cag ccc	576
Pro Val Tyr Asn Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro	
180 185 190	
tct tac ccg gga gcc tga	594
Ser Tyr Pro Gly Ala *	
195	

239

<210> 168
 <211> 197
 <212> PRT
 <213> Homo sapiens

<400> 168
 Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile Ala
 1 5 10 15
 Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp Cys Leu
 20 25 30
 Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe Asn Cys Glu
 35 40 45
 Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg Tyr Cys Cys Arg
 50 55 60
 Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln Lys His Cys Leu Ala
 65 70 75 80
 Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala Ser Ala Val Ile Leu Phe
 85 90 95
 Val Ala Val Val Ala Thr Thr Ile Cys Cys Phe Leu Cys Ser Cys Cys
 100 105 110
 Tyr Leu Tyr Arg Arg Arg Gln Gln Leu Gln Ser Pro Phe Glu Gly Gln
 115 120 125
 Glu Ile Pro Met Thr Gly Ile Pro Val Gln Pro Val Tyr Pro Tyr Pro
 130 135 140
 Gln Asp Pro Lys Ala Gly Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr
 145 150 155 160
 Pro Pro Ser Gly Pro Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro
 165 170 175
 Pro Val Tyr Asn Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro
 180 185 190
 Ser Tyr Pro Gly Ala
 195

<210> 169
 <211> 669
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(669)

240

<400> 169
 atg cgt gtg ggc ctc gcg ctg atc ttg gtg ggc cac gtg aac ctg ctg 48
 Met Arg Val Gly Leu Ala Leu Ile Leu Val Gly His Val Asn Leu Leu
 1 5 10 15

ctg ggg gcc gtg ctg cat ggc acc gtc ctg cgg cac gtg gcc aat ccc 96
 Leu Gly Ala Val Leu His Gly Thr Val Leu Arg His Val Ala Asn Pro
 20 25 30

cgc ggc gct gtc acg ccg gag tac acc gta gcc aat gtc atc tct gtc 144
 Arg Gly Ala Val Thr Pro Glu Tyr Thr Val Ala Asn Val Ile Ser Val
 35 40 45

ggc tcg ggg ctg ctg agc gtt tcc gtg gga ctt gtg gcc ctc ctg gcg 192
 Gly Ser Gly Leu Leu Ser Val Ser Val Gly Leu Val Ala Leu Leu Ala
 50 55 60

tcc agg aac ctt ctt cgc cct cca ctg cac tgg gtc ctg ctg gca cta 240
 Ser Arg Asn Leu Leu Arg Pro Pro Leu His Trp Val Leu Leu Ala Leu
 65 70 75 80

gct ctg gtg aac ctg ctc ttg tcc gtt gcc tgc tcc ctg ggc ctc ctt 288
 Ala Leu Val Asn Leu Leu Leu Ser Val Ala Cys Ser Leu Gly Leu Leu
 85 90 95

ctt gct gtg tca ctc act gtg gcc aac ggt ggc cgc cgc ctt att gct 336
 Leu Ala Val Ser Leu Thr Val Ala Asn Gly Gly Arg Arg Leu Ile Ala
 100 105 110

gac tgc cac cca gga ctg ctg gat cct ctg gta cca ctg gat gag ggg 384
 Asp Cys His Pro Gly Leu Leu Asp Pro Leu Val Pro Leu Asp Glu Gly
 115 120 125

ccg gga cat act gac tgc ccc ttt gac ccc aca aga atc tat gat aca 432
 Pro Gly His Thr Asp Cys Pro Phe Asp Pro Thr Arg Ile Tyr Asp Thr
 130 135 140

gcc ttg gct ctc tgg atc cct tct ttg ctc atg tct gca ggg gag gct 480
 Ala Leu Ala Leu Trp Ile Pro Ser Leu Leu Met Ser Ala Gly Glu Ala
 145 150 155 160

gct cta tct ggt tac tgc tgt gtg gct gca ctc act cta cgt gga gtt 528
 Ala Leu Ser Gly Tyr Cys Cys Val Ala Ala Leu Thr Leu Arg Gly Val
 165 170 175

241

ggg ccc tgc agg aag gac gga ctt cag ggg cag cta gag gaa atg aca 576
 Gly Pro Cys Arg Lys Asp Gly Leu Gln Gly Gln Leu Glu Glu Met Thr
 180 185 190

gag ctt gaa tct cct aaa tgt aaa agg cag gaa aat gag cag cta ctg 624
 Glu Leu Glu Ser Pro Lys Cys Lys Arg Gln Glu Asn Glu Gln Leu Leu
 195 200 205

gat caa aat caa gaa atc cgg gca tca cag aga agt tgg gtt tag 669
 Asp Gln Asn Gln Glu Ile Arg Ala Ser Gln Arg Ser Trp Val *
 210 215 220

<210> 170

<211> 222

<212> PRT

<213> Homo sapiens

<400> 170

Met Arg Val Gly Leu Ala Leu Ile Leu Val Gly His Val Asn Leu Leu
 1 5 10 15
 Leu Gly Ala Val Leu His Gly Thr Val Leu Arg His Val Ala Asn Pro
 20 25 30
 Arg Gly Ala Val Thr Pro Glu Tyr Thr Val Ala Asn Val Ile Ser Val
 35 40 45
 Gly Ser Gly Leu Leu Ser Val Ser Val Gly Leu Val Ala Leu Leu Ala
 50 55 60
 Ser Arg Asn Leu Leu Arg Pro Pro Leu His Trp Val Leu Leu Ala Leu
 65 70 75 80
 Ala Leu Val Asn Leu Leu Leu Ser Val Ala Cys Ser Leu Gly Leu Leu
 85 90 95
 Leu Ala Val Ser Leu Thr Val Ala Asn Gly Gly Arg Arg Leu Ile Ala
 100 105 110
 Asp Cys His Pro Gly Leu Leu Asp Pro Leu Val Pro Leu Asp Glu Gly
 115 120 125
 Pro Gly His Thr Asp Cys Pro Phe Asp Pro Thr Arg Ile Tyr Asp Thr
 130 135 140
 Ala Leu Ala Leu Trp Ile Pro Ser Leu Leu Met Ser Ala Gly Glu Ala
 145 150 155 160
 Ala Leu Ser Gly Tyr Cys Cys Val Ala Ala Leu Thr Leu Arg Gly Val
 165 170 175
 Gly Pro Cys Arg Lys Asp Gly Leu Gln Gly Gln Leu Glu Glu Met Thr
 180 185 190

242

Glu Leu Glu Ser Pro Lys Cys Lys Arg Gln Glu Asn Glu Gln Leu Leu
 195 200 205
 Asp Gln Asn Gln Glu Ile Arg Ala Ser Gln Arg Ser Trp Val
 210 215 220

<210> 171
 <211> 345
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(345)

<400> 171

atg ctg ctg tgg ctt ctt gtc ttc tct gct ctg ggt atc cag gcc tgg 48
 Met Leu Leu Trp Leu Leu Val Phe Ser Ala Leu Gly Ile Gln Ala Trp
 1 5 10 15

ggt gat tcc tcc tgg aac aaa aca caa gct aaa cag gta tca gag ggg 96
 Gly Asp Ser Ser Trp Asn Lys Thr Gln Ala Lys Gln Val Ser Glu Gly
 20 25 30

ctc cag tac cta ttt gag aac atc tcc cag ctc act gaa aaa gat gtc 144
 Leu Gln Tyr Leu Phe Glu Asn Ile Ser Gln Leu Thr Glu Lys Asp Val
 35 40 45

tcc acc acg gtc tct cgc aag gca tgg ggg gca gaa gct gtt ggc tgc 192
 Ser Thr Thr Val Ser Arg Lys Ala Trp Gly Ala Glu Ala Val Gly Cys
 50 55 60

agt att cag ctg acc acg cca gtg aat gtc ctt gtt ata cac cat gtc 240
 Ser Ile Gln Leu Thr Thr Pro Val Asn Val Leu Val Ile His His Val
 65 70 75 80

cct gga ctg gag tgt cac gac cag aca gtc tgc agc cag aga ctg cgg 288
 Pro Gly Leu Glu Cys His Asp Gln Thr Val Cys Ser Gln Arg Leu Arg
 85 90 95

gaa ctg cag gcc cat cat gtc cac aac aac agt ggg tgt gat gtg gcc 336
 Glu Leu Gln Ala His His Val His Asn Asn Ser Gly Cys Asp Val Ala
 100 105 110

tac aag taa 345

243

Tyr Lys *

<210> 172
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 172
 Met Leu Leu Trp Leu Leu Val Phe Ser Ala Leu Gly Ile Gln Ala Trp
 1 5 10 15
 Gly Asp Ser Ser Trp Asn Lys Thr Gln Ala Lys Gln Val Ser Glu Gly
 20 25 30
 Leu Gln Tyr Leu Phe Glu Asn Ile Ser Gln Leu Thr Glu Lys Asp Val
 35 40 45
 Ser Thr Thr Val Ser Arg Lys Ala Trp Gly Ala Glu Ala Val Gly Cys
 50 55 60
 Ser Ile Gln Leu Thr Thr Pro Val Asn Val Leu Val Ile His His Val
 65 70 75 80
 Pro Gly Leu Glu Cys His Asp Gln Thr Val Cys Ser Gln Arg Leu Arg
 85 90 95
 Glu Leu Gln Ala His His Val His Asn Asn Ser Gly Cys Asp Val Ala
 100 105 110
 Tyr Lys

<210> 173
 <211> 924
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(924)

<400> 173
 atg gag cag ctg cag gag gcc ctg aag gta cgc aag gat gat gcc cac 48
 Met Glu Gln Leu Gln Glu Ala Leu Lys Val Arg Lys Asp Asp Ala His
 1 5 10 15
 gcc ctc cac ctg ctg gca ctg ctc ttc tct gcc cag aag cac cac cag 96
 Ala Leu His Leu Leu Ala Leu Leu Phe Ser Ala Gln Lys His His Gln
 20 25 30

244

cat gcc ctg gat gtt gtc aac atg gcc atc acc gag cac cct gag aac His Ala Leu Asp Val Val Asn Met Ala Ile Thr Glu His Pro Glu Asn 35 40 45	144
ttc aac ctg atg ttc acc aag gtg aag ctg gag cag gtg ctg aaa ggc Phe Asn Leu Met Phe Thr Lys Val Lys Leu Glu Gln Val Leu Lys Gly 50 55 60	192
cca gag gaa gcc ctc gtg acc tgc aga caa gtg ctg agg ctg tgg cag Pro Glu Glu Ala Leu Val Thr Cys Arg Gln Val Leu Arg Leu Trp Gln 65 70 75 80	240
acc ctg tac agc ttc tcc cag ctg gga ggc cta gaa aag gat ggc agc Thr Leu Tyr Ser Phe Ser Gln Leu Gly Gly Leu Glu Lys Asp Gly Ser 85 90 95	288
ttc ggt gag ggc ctc acc atg aag aag cag agt ggc atg cac ctg act Phe Gly Glu Gly Leu Thr Met Lys Lys Gln Ser Gly Met His Leu Thr 100 105 110	336
ttg cct gat gcc cat gat gca gac tct ggc tcc cgg cgg gct tcg tcc Leu Pro Asp Ala His Asp Ala Asp Ser Gly Ser Arg Arg Ala Ser Ser 115 120 125	384
atc gcc gcc tcc cgg ctg gag gag gcc atg tca gag ctg act atg ccc Ile Ala Ala Ser Arg Leu Glu Glu Ala Met Ser Glu Leu Thr Met Pro 130 135 140	432
tct tcg gtc ctg aag cag ggc ccc atg cag ctg tgg acc acg ctg gaa Ser Ser Val Leu Lys Gln Gly Pro Met Gln Leu Trp Thr Thr Leu Glu 145 150 155 160	480
cag atc tgg ctg cag gct gct gag ctg ttc atg gag cag cag cac ctc Gln Ile Trp Leu Gln Ala Ala Glu Leu Phe Met Glu Gln Gln His Leu 165 170 175	528
aag gaa gca ggt ttc tgc atc cag gag gcg gcg ggc ctc ttc ccc act Lys Glu Ala Gly Phe Cys Ile Gln Glu Ala Ala Gly Leu Phe Pro Thr 180 185 190	576
tct cac tca gta ctc tat atg cgg ggc cgg ctg gct gag gtg aag ggc Ser His Ser Val Leu Tyr Met Arg Gly Arg Leu Ala Glu Val Lys Gly 195 200 205	624

245

aac ctg gag gag gcc aag cag ctg tac aag gag gcg ctc acg gtg aac 672
 Asn Leu Glu Glu Ala Lys Gln Leu Tyr Lys Glu Ala Leu Thr Val Asn
 210 215 220

cca gat ggc gtg cgc atc atg cat agc ctg ggt ctg atg ctg agt cgg 720
 Pro Asp Gly Val Arg Ile Met His Ser Leu Gly Leu Met Leu Ser Arg
 225 230 235 240

ctg ggc cac aag agc ttg gcc cag aag gtg ctt cgt gat gcc gtg gag 768
 Leu Gly His Lys Ser Leu Ala Gln Lys Val Leu Arg Asp Ala Val Glu
 245 250 255

agg cag agt acg tgc cac gag gcg tgg cag ggc ctg ggc gag gtg ctg 816
 Arg Gln Ser Thr Cys His Glu Ala Trp Gln Gly Leu Gly Glu Val Leu
 260 265 270

cag gcc cag ggc cag aac gag gct gcc gtt gac tgc ttc ctc acc gcc 864
 Gln Ala Gln Gly Gln Asn Glu Ala Ala Val Asp Cys Phe Leu Thr Ala
 275 280 285

ctt gag ctg gag gcc agc agc cct gta ctg ccc ttc tcc atc atc ccc 912
 Leu Glu Leu Glu Ala Ser Ser Pro Val Leu Pro Phe Ser Ile Ile Pro
 290 295 300

aga gag ctc tga 924
 Arg Glu Leu *
 305

<210> 174

<211> 307

<212> PRT

<213> Homo sapiens

<400> 174

Met Glu Gln Leu Gln Glu Ala Leu Lys Val Arg Lys Asp Asp Ala His
 1 5 10 15
 Ala Leu His Leu Leu Ala Leu Leu Phe Ser Ala Gln Lys His His Gln
 20 25 30
 His Ala Leu Asp Val Val Asn Met Ala Ile Thr Glu His Pro Glu Asn
 35 40 45
 Phe Asn Leu Met Phe Thr Lys Val Lys Leu Glu Gln Val Leu Lys Gly
 50 55 60

246

Pro Glu Glu Ala Leu Val Thr Cys Arg Gln Val Leu Arg Leu Trp Gln
 65 70 75 80
 Thr Leu Tyr Ser Phe Ser Gln Leu Gly Gly Leu Glu Lys Asp Gly Ser
 85 90 95
 Phe Gly Glu Gly Leu Thr Met Lys Lys Gln Ser Gly Met His Leu Thr
 100 105 110
 Leu Pro Asp Ala His Asp Ala Asp Ser Gly Ser Arg Arg Ala Ser Ser
 115 120 125
 Ile Ala Ala Ser Arg Leu Glu Glu Ala Met Ser Glu Leu Thr Met Pro
 130 135 140
 Ser Ser Val Leu Lys Gln Gly Pro Met Gln Leu Trp Thr Thr Leu Glu
 145 150 155 160
 Gln Ile Trp Leu Gln Ala Ala Glu Leu Phe Met Glu Gln Gln His Leu
 165 170 175
 Lys Glu Ala Gly Phe Cys Ile Gln Glu Ala Ala Gly Leu Phe Pro Thr
 180 185 190
 Ser His Ser Val Leu Tyr Met Arg Gly Arg Leu Ala Glu Val Lys Gly
 195 200 205
 Asn Leu Glu Glu Ala Lys Gln Leu Tyr Lys Glu Ala Leu Thr Val Asn
 210 215 220
 Pro Asp Gly Val Arg Ile Met His Ser Leu Gly Leu Met Leu Ser Arg
 225 230 235 240
 Leu Gly His Lys Ser Leu Ala Gln Lys Val Leu Arg Asp Ala Val Glu
 245 250 255
 Arg Gln Ser Thr Cys His Glu Ala Trp Gln Gly Leu Gly Glu Val Leu
 260 265 270
 Gln Ala Gln Gly Gln Asn Glu Ala Ala Val Asp Cys Phe Leu Thr Ala
 275 280 285
 Leu Glu Leu Glu Ala Ser Ser Pro Val Leu Pro Phe Ser Ile Ile Pro
 290 295 300
 Arg Glu Leu
 305

<210> 175

<211> 627

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(627)

<221> misc_feature

<222> (1)...(627)

247

<223> n = A,T,C or G

<400> 175

atg gga ctc ggc gcg cga ggt gct tgg gcc gcg ctg ctc ctg ggg acg	48
Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly Thr	
1 5 10 15	

ctg cag gtg cta gcg ctg ctg ggg gcc gcc cat gaa agc gca ncc atg	96
Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala Xaa Met	
20 25 30	

gcg gca tct gca aac ata gag aat tct ggg ctt cca cac aac tcc agt	144
Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His Asn Ser Ser	
35 40 45	

gct aac tca aca gag act ctc caa cat gtg cct tct gac cat aca aat	192
Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser Asp His Thr Asn	
50 55 60	

gaa act tcc aac agt act gtg aaa cca cca act tca gtt gcc tca gac	240
Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr Ser Val Ala Ser Asp	
65 70 75 80	

tcc agt aat aca acg gtc acc acc atg aaa cct aca gcg gca tct aat	288
Ser Ser Asn Thr Thr Val Thr Thr Met Lys Pro Thr Ala Ala Ser Asn	
85 90 95	

aca aca aca cca ggg atg gtc tca aca aat atg act tct acc acc tta	336
Thr Thr Thr Pro Gly Met Val Ser Thr Asn Met Thr Ser Thr Thr Leu	
100 105 110	

aag tct aca ccc aaa aca aca agt gtt tca cag aac aca tct cag ata	384
Lys Ser Thr Pro Lys Thr Thr Ser Val Ser Gln Asn Thr Ser Gln Ile	
115 120 125	

tca aca tcc aca atg acc gta acc cac aat agt tca gtg aca tct gct	432
Ser Thr Ser Thr Met Thr Val Thr His Asn Ser Ser Val Thr Ser Ala	
130 135 140	

gct tca tca gta aca atc aca aca act atg cat tct gaa gca aag aaa	480
Ala Ser Ser Val Thr Ile Thr Thr Thr Met His Ser Glu Ala Lys Lys	
145 150 155 160	

gga tca aaa ttt gat act ggg agc ttt gtt ggt ggt att gta tta acg	528
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248

Gly Ser Lys Phe Asp Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr
 165 170 175

ctg gga gtt tta tct att ctt tac att gga tgc aaa atg tat tac tca 576
 Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser
 180 185 190

aga aga ggc att cgg tat cga acc ata gat gaa cat gat gcc atc att 624
 Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile
 195 200 205

taa 627
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<210> 176

<211> 208

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(208)

<223> Xaa = Any Amino Acid

<400> 176

Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly Thr
 1 5 10 15

Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala Xaa Met
 20 25 30

Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His Asn Ser Ser
 35 40 45

Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser Asp His Thr Asn
 50 55 60

Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr Ser Val Ala Ser Asp
 65 70 75 80

Ser Ser Asn Thr Thr Val Thr Thr Met Lys Pro Thr Ala Ala Ser Asn
 85 90 95

Thr Thr Thr Pro Gly Met Val Ser Thr Asn Met Thr Ser Thr Thr Leu
 100 105 110

Lys Ser Thr Pro Lys Thr Thr Ser Val Ser Gln Asn Thr Ser Gln Ile
 115 120 125

Ser Thr Ser Thr Met Thr Val Thr His Asn Ser Ser Val Thr Ser Ala

249

130		135		140
Ala Ser Ser Val Thr Ile Thr Thr Thr Met His Ser Glu Ala Lys Lys				
145		150		155
Gly Ser Lys Phe Asp Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr				
	165		170	175
Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser				
	180		185	190
Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile				
195		200		205

<210> 177

<211> 1401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1401)

<221> misc_feature

<222> (1)...(1401)

<223> n = A,T,C or G

<400> 177

atg gtc tgg gcc tct ctg ggg gct gcc tgg gtg gca nat ggt gtt cag	48
Met Val Trp Ala Ser Leu Gly Ala Ala Trp Val Ala Xaa Gly Val Gln	
1 5 10 15	
tgc gac agg aca gtt gta aac ggc atc atc gca acc gtc gtg gtc agt	96
Cys Asp Arg Thr Val Val Asn Gly Ile Ile Ala Thr Val Val Val Ser	
20 25 30	
tgg atc atc atc gct gcc aca gtg gtt tcc att atc att gtc ttt gac	144
Trp Ile Ile Ile Ala Ala Thr Val Val Ser Ile Ile Ile Val Phe Asp	
35 40 45	
cct ctt ggg ggg aaa atg gct cca tat tcc tct gcc ggc ccc agc cac	192
Pro Leu Gly Gly Lys Met Ala Pro Tyr Ser Ser Ala Gly Pro Ser His	
50 55 60	
ctg gat agt cat gat tca agc cag tta ctt aat ggc ctc aag aca gca	240
Leu Asp Ser His Asp Ser Ser Gln Leu Leu Asn Gly Leu Lys Thr Ala	
65 70 75 80	

250

gct aca agc gtg tgg gaa acc aga atc aag ctc ttg tgc tgt tgc att	288
Ala Thr Ser Val Trp Glu Thr Arg Ile Lys Leu Leu Cys Cys Cys Ile	
85 90 95	
ggg aaa gac gac cat act cgg gtt gct ttt tcg agt acg gca gag ctt	336
Gly Lys Asp Asp His Thr Arg Val Ala Phe Ser Ser Thr Ala Glu Leu	
100 105 110	
ttc tca acc tac ttt tca gac aca gat ctg gtg ccc agc gac att gcg	384
Phe Ser Thr Tyr Phe Ser Asp Thr Asp Leu Val Pro Ser Asp Ile Ala	
115 120 125	
gcg ggc ctc gcc ctg ctt cat cag caa cag gac aat atc agg aac aac	432
Ala Gly Leu Ala Leu Leu His Gln Gln Gln Asp Asn Ile Arg Asn Asn	
130 135 140	
caa gag cct gcc cag gtg gtc tgc cat gcc cca ggg agc tcc cag gaa	480
Gln Glu Pro Ala Gln Val Val Cys His Ala Pro Gly Ser Ser Gln Glu	
145 150 155 160	
gct gat ctg gat gca gaa tta gaa aac tgc cat cat tac atg cag ttt	528
Ala Asp Leu Asp Ala Glu Leu Glu Asn Cys His His Tyr Met Gln Phe	
165 170 175	
gca gca gcg gcc tat ggg tgg ccc ctc tac atc tac aga aac ccc ctc	576
Ala Ala Ala Ala Tyr Gly Trp Pro Leu Tyr Ile Tyr Arg Asn Pro Leu	
180 185 190	
acg ggg ctg tgc agg att ggt ggt gac tgc tgc aga agc aga acc aca	624
Thr Gly Leu Cys Arg Ile Gly Gly Asp Cys Cys Arg Ser Arg Thr Thr	
195 200 205	
gac tat gac ttg gtc gga ggc gat cag ctc aac tgt cac ttc ggc tcc	672
Asp Tyr Asp Leu Val Gly Gly Asp Gln Leu Asn Cys His Phe Gly Ser	
210 215 220	
atc ctg cac acc aca ggg ctg cag tac agg gac ttc atc cac gtc agc	720
Ile Leu His Thr Thr Gly Leu Gln Tyr Arg Asp Phe Ile His Val Ser	
225 230 235 240	
ttc cat gac aag gtt tac gag ctg ccg ttt tta gtg gct ctg gat cac	768
Phe His Asp Lys Val Tyr Glu Leu Pro Phe Leu Val Ala Leu Asp His	
245 250 255	

251

agg aaa gag tct gtt gtg gtc gct gtg agg ggg acc atg tct ctg cag	816
Arg Lys Glu Ser Val Val Val Ala Val Arg Gly Thr Met Ser Leu Gln	
260 265 270	
gat gtc ctt acg gac ctg tca gcg gag agt gag gtg ctg gac gtg gag	864
Asp Val Leu Thr Asp Leu Ser Ala Glu Ser Glu Val Leu Asp Val Glu	
275 280 285	
tgt gag gtg cag gac cgc ctg gca cac aag ggt att tct caa gct gcc	912
Cys Glu Val Gln Asp Arg Leu Ala His Lys Gly Ile Ser Gln Ala Ala	
290 295 300	
aga tac gtt tac caa cga ctc atc aac gac ggg att ttg agc caa gcc	960
Arg Tyr Val Tyr Gln Arg Leu Ile Asn Asp Gly Ile Leu Ser Gln Ala	
305 310 315 320	
ttc agc att gct cct gag tac cgg ctg gtc ata gtg ggc cac agc ctc	1008
Phe Ser Ile Ala Pro Glu Tyr Arg Leu Val Ile Val Gly His Ser Leu	
325 330 335	
ggg ggn ggg gcg gcc gcc ctg ctg gcc acc atg ctc aga gcc gcc tac	1056
Gly Xaa Gly Ala Ala Ala Leu Leu Ala Thr Met Leu Arg Ala Ala Tyr	
340 345 350	
ccg cag gtc agg tgc tac gcc ttc tcc cca ccc cgg ggg ctg tgg agc	1104
Pro Gln Val Arg Cys Tyr Ala Phe Ser Pro Pro Arg Gly Leu Trp Ser	
355 360 365	
aaa gct ctg cag gaa tat tct cag agc ttc atc gtg tca ctc gtc ctg	1152
Lys Ala Leu Gln Glu Tyr Ser Gln Ser Phe Ile Val Ser Leu Val Leu	
370 375 380	
ggg aag gat gtg att ccc agg ctc agt gtg acc aac ttg gaa gat ctg	1200
Gly Lys Asp Val Ile Pro Arg Leu Ser Val Thr Asn Leu Glu Asp Leu	
385 390 395 400	
aag aga aga atc ttg cga gtg gtc gcg cac tgc aat aaa ccc aag tac	1248
Lys Arg Arg Ile Leu Arg Val Val Ala His Cys Asn Lys Pro Lys Tyr	
405 410 415	
aag atc ttg ctg cac ggt ttg tgg tac gaa ctg ttt gga gga aac ccc	1296
Lys Ile Leu Leu His Gly Leu Trp Tyr Glu Leu Phe Gly Gly Asn Pro	
420 425 430	

252

aac aac ttg ccc agc aca agg ggt ctc cag tgt gga cgt ggc ctg acc 1344
 Asn Asn Leu Pro Ser Thr Arg Gly Leu Gln Cys Gly Arg Gly Leu Thr
 435 440 445

agg gcc act gga aac tgt ccc agg aac gat gga ctc acg ctt ttg tcc 1392
 Arg Ala Thr Gly Asn Cys Pro Arg Asn Asp Gly Leu Thr Leu Leu Ser
 450 455 460

tta aac tga 1401
 Leu Asn *
 465

<210> 178

<211> 466

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(466)

<223> Xaa = Any Amino Acid

<400> 178

Met Val Trp Ala Ser Leu Gly Ala Ala Trp Val Ala Xaa Gly Val Gln
 1 5 10 15
 Cys Asp Arg Thr Val Val Asn Gly Ile Ile Ala Thr Val Val Val Ser
 20 25 30
 Trp Ile Ile Ile Ala Ala Thr Val Val Ser Ile Ile Ile Val Phe Asp
 35 40 45
 Pro Leu Gly Gly Lys Met Ala Pro Tyr Ser Ser Ala Gly Pro Ser His
 50 55 60
 Leu Asp Ser His Asp Ser Ser Gln Leu Leu Asn Gly Leu Lys Thr Ala
 65 70 75 80
 Ala Thr Ser Val Trp Glu Thr Arg Ile Lys Leu Leu Cys Cys Cys Ile
 85 90 95
 Gly Lys Asp Asp His Thr Arg Val Ala Phe Ser Ser Thr Ala Glu Leu
 100 105 110
 Phe Ser Thr Tyr Phe Ser Asp Thr Asp Leu Val Pro Ser Asp Ile Ala
 115 120 125
 Ala Gly Leu Ala Leu Leu His Gln Gln Gln Asp Asn Ile Arg Asn Asn
 130 135 140
 Gln Glu Pro Ala Gln Val Val Cys His Ala Pro Gly Ser Ser Gln Glu
 145 150 155 160

253

[illegible]

<210> 179

<211> 909

<212> DNA

254

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(909)

<221> misc_feature

<222> (1)...(909)

<223> n = A,T,C or G

<400> 179

atg	tcc	cca	agg	act	agg	cca	cgc	agg	tcc	act	ggc	tat	tct	gag	gtg	48
Met	Ser	Pro	Arg	Thr	Arg	Pro	Arg	Arg	Ser	Thr	Gly	Tyr	Ser	Glu	Val	
1				5					10					15		

ata	gtt	gtc	gtt	gga	gga	tgt	gag	cga	gtt	gga	gga	ttt	aat	ctt	cca	96
Ile	Val	Val	Val	Gly	Gly	Cys	Glu	Arg	Val	Gly	Gly	Phe	Asn	Leu	Pro	
			20					25					30			

tac	act	gag	tgc	tac	gat	cct	gta	aca	gga	gaa	tgg	aag	tct	ttg	gct	144
Tyr	Thr	Glu	Cys	Tyr	Asp	Pro	Val	Thr	Gly	Glu	Trp	Lys	Ser	Leu	Ala	
		35				40						45				

aag	ctt	cca	gaa	ttt	acc	aaa	tca	gag	tat	gca	gtc	tgt	gct	cta	agg	192
Lys	Leu	Pro	Glu	Phe	Thr	Lys	Ser	Glu	Tyr	Ala	Val	Cys	Ala	Leu	Arg	
	50					55					60					

aat	gac	att	ctt	gtt	tca	ggt	gga	aga	atc	aac	agc	cgt	gat	gtc	tgg	240
Asn	Asp	Ile	Leu	Val	Ser	Gly	Gly	Arg	Ile	Asn	Ser	Arg	Asp	Val	Trp	
65					70				75					80		

att	tat	aac	tca	cag	tta	aat	att	tgg	ntc	aga	gtt	gcc	tct	ctc	aat	288
Ile	Tyr	Asn	Ser	Gln	Leu	Asn	Ile	Trp	Xaa	Arg	Val	Ala	Ser	Leu	Asn	
			85					90						95		

aaa	ggc	aga	tgg	cgt	cac	aaa	atg	gct	gtc	ctc	ctt	ggt	aaa	gta	tat	336
Lys	Gly	Arg	Trp	Arg	His	Lys	Met	Ala	Val	Leu	Leu	Gly	Lys	Val	Tyr	
		100						105					110			

gtt	gtc	ggt	ggc	tat	gat	ggg	caa	aac	aga	ctt	agc	agc	gta	gaa	tgt	384
Val	Val	Gly	Gly	Tyr	Asp	Gly	Gln	Asn	Arg	Leu	Ser	Ser	Val	Glu	Cys	
		115				120						125				

tat	gat	tcc	ttt	tca	aat	cga	tgg	act	gaa	gtt	gct	ccc	ctt	aag	gaa	432
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

255

Tyr	Asp	Ser	Phe	Ser	Asn	Arg	Trp	Thr	Glu	Val	Ala	Pro	Leu	Lys	Glu		
130						135					140						
gcc	gtg	agt	tct	cct	gca	gtg	act	agc	tgt	gta	ggc	aaa	ctg	ttt	gtg	480	
Ala	Val	Ser	Ser	Pro	Ala	Val	Thr	Ser	Cys	Val	Gly	Lys	Leu	Phe	Val		
145					150					155					160		
att	ggt	gga	gga	cct	gat	gat	aat	act	tgt	tct	gat	aag	gtt	caa	tct	528	
Ile	Gly	Gly	Gly	Pro	Asp	Asp	Asn	Thr	Cys	Ser	Asp	Lys	Val	Gln	Ser		
				165					170					175			
tat	gat	cca	gaa	acc	aat	tct	tgg	cta	ctt	cgt	gca	gct	atc	cca	att	576	
Tyr	Asp	Pro	Glu	Thr	Asn	Ser	Trp	Leu	Leu	Arg	Ala	Ala	Ile	Pro	Ile		
			180					185					190				
gcc	aaa	agg	tgt	ata	aca	gct	gta	tcc	cta	aac	aac	ctg	atc	tat	gtt	624	
Ala	Lys	Arg	Cys	Ile	Thr	Ala	Val	Ser	Leu	Asn	Asn	Leu	Ile	Tyr	Val		
	195						200					205					
gcc	ggt	gga	ctg	acc	aag	gca	ata	tac	tgt	tac	gat	cca	gtt	gaa	gat	672	
Ala	Gly	Gly	Leu	Thr	Lys	Ala	Ile	Tyr	Cys	Tyr	Asp	Pro	Val	Glu	Asp		
	210					215					220						
tac	tgg	atg	cac	gta	cag	aat	aca	ttc	agc	cgt	cag	gaa	aac	tgt	ggt	720	
Tyr	Trp	Met	His	Val	Gln	Asn	Thr	Phe	Ser	Arg	Gln	Glu	Asn	Cys	Gly		
225					230					235					240		
atg	tct	gtg	tgt	aat	ggt	aaa	ata	tat	atc	ctg	ggc	gga	aga	cgg	gaa	768	
Met	Ser	Val	Cys	Asn	Gly	Lys	Ile	Tyr	Ile	Leu	Gly	Gly	Arg	Arg	Glu		
				245					250					255			
aat	gga	gaa	gcc	aca	gac	act	att	ctc	tgt	tat	gat	cct	gca	aca	agt	816	
Asn	Gly	Glu	Ala	Thr	Asp	Thr	Ile	Leu	Cys	Tyr	Asp	Pro	Ala	Thr	Ser		
			260					265					270				
atc	atc	aca	ggg	gta	gct	gca	atg	ccc	agg	cca	gtg	tcc	tat	cat	ggc	864	
Ile	Ile	Thr	Gly	Val	Ala	Ala	Met	Pro	Arg	Pro	Val	Ser	Tyr	His	Gly		
		275					280					285					
tgt	gtg	act	att	cat	aga	tac	aat	gag	aaa	tgc	ttt	aaa	ctc	tga		909	
Cys	Val	Thr	Ile	His	Arg	Tyr	Asn	Glu	Lys	Cys	Phe	Lys	Leu	*			
	290					295					300						

256

<210> 180
 <211> 302
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(302)
 <223> Xaa = Any Amino Acid

<400> 180
 Met Ser Pro Arg Thr Arg Pro Arg Arg Ser Thr Gly Tyr Ser Glu Val
 1 5 10 15
 Ile Val Val Val Gly Gly Cys Glu Arg Val Gly Gly Phe Asn Leu Pro
 20 25 30
 Tyr Thr Glu Cys Tyr Asp Pro Val Thr Gly Glu Trp Lys Ser Leu Ala
 35 40 45
 Lys Leu Pro Glu Phe Thr Lys Ser Glu Tyr Ala Val Cys Ala Leu Arg
 50 55 60
 Asn Asp Ile Leu Val Ser Gly Gly Arg Ile Asn Ser Arg Asp Val Trp
 65 70 75 80
 Ile Tyr Asn Ser Gln Leu Asn Ile Trp Xaa Arg Val Ala Ser Leu Asn
 85 90 95
 Lys Gly Arg Trp Arg His Lys Met Ala Val Leu Leu Gly Lys Val Tyr
 100 105 110
 Val Val Gly Gly Tyr Asp Gly Gln Asn Arg Leu Ser Ser Val Glu Cys
 115 120 125
 Tyr Asp Ser Phe Ser Asn Arg Trp Thr Glu Val Ala Pro Leu Lys Glu
 130 135 140
 Ala Val Ser Ser Pro Ala Val Thr Ser Cys Val Gly Lys Leu Phe Val
 145 150 155 160
 Ile Gly Gly Gly Pro Asp Asp Asn Thr Cys Ser Asp Lys Val Gln Ser
 165 170 175
 Tyr Asp Pro Glu Thr Asn Ser Trp Leu Leu Arg Ala Ala Ile Pro Ile
 180 185 190
 Ala Lys Arg Cys Ile Thr Ala Val Ser Leu Asn Asn Leu Ile Tyr Val
 195 200 205
 Ala Gly Gly Leu Thr Lys Ala Ile Tyr Cys Tyr Asp Pro Val Glu Asp
 210 215 220
 Tyr Trp Met His Val Gln Asn Thr Phe Ser Arg Gln Glu Asn Cys Gly
 225 230 235 240
 Met Ser Val Cys Asn Gly Lys Ile Tyr Ile Leu Gly Gly Arg Arg Glu
 245 250 255
 Asn Gly Glu Ala Thr Asp Thr Ile Leu Cys Tyr Asp Pro Ala Thr Ser

257

260 265 270
 Ile Ile Thr Gly Val Ala Ala Met Pro Arg Pro Val Ser Tyr His Gly
 275 280 285
 Cys Val Thr Ile His Arg Tyr Asn Glu Lys Cys Phe Lys Leu
 290 295 300

<210> 181
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(405)
 <221> misc_feature
 <222> (1)...(405)
 <223> n = A,T,C or G

<400> 181
 atg ccg ctc cta cga gga ctg ctg tgg ctc cag gtg ctg tgt gcg ggc 48
 Met Pro Leu Leu Arg Gly Leu Leu Trp Leu Gln Val Leu Cys Ala Gly
 1 5 10 15
 cct ctc cat aca gag gct gtg gta ctt ctg gtt cct tct gat gat ggg 96
 Pro Leu His Thr Glu Ala Val Val Leu Leu Val Pro Ser Asp Asp Gly
 20 25 30
 cgt gct ttt ctg ctg cgg anc ggc ttc ttc atc cgg agg cgc atg tac 144
 Arg Ala Phe Leu Leu Arg Xaa Gly Phe Phe Ile Arg Arg Arg Met Tyr
 35 40 45
 ccc ccg ccg ctg atc gag gag cca gcc ttc aat gtg tcc tac acc agg 192
 Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn Val Ser Tyr Thr Arg
 50 55 60
 cag ccc cca aat ccc ggc cca gga gcc cag cag ccg ggg ccg ccc tat 240
 Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln Pro Gly Pro Pro Tyr
 65 70 75 80
 tac acc gac cca gga gga ccg ggg atg aac cct gtc ggg aat tcc atg 288
 Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro Val Gly Asn Ser Met
 85 90 95

258

gca atg gct ttc cag gtc cca ccc aac tca ccc cag ggg agt gtg gcc 336
 Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro Gln Gly Ser Val Ala
 100 105 110

tgc ccg ccc cct cca gcc tac tgc aac acg cct ccg ccc ccg tac gaa 384
 Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro Pro Pro Pro Tyr Glu
 115 120 125

cag gta gtg aag gcc aag tag 405
 Gln Val Val Lys Ala Lys *
 130

<210> 182

<211> 134

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(134)

<223> Xaa = Any Amino Acid

<400> 182

Met Pro Leu Leu Arg Gly Leu Leu Trp Leu Gln Val Leu Cys Ala Gly
 1 5 10 15
 Pro Leu His Thr Glu Ala Val Val Leu Leu Val Pro Ser Asp Asp Gly
 20 25 30
 Arg Ala Phe Leu Leu Arg Xaa Gly Phe Phe Ile Arg Arg Arg Met Tyr
 35 40 45
 Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn Val Ser Tyr Thr Arg
 50 55 60
 Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln Pro Gly Pro Pro Tyr
 65 70 75 80
 Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro Val Gly Asn Ser Met
 85 90 95
 Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro Gln Gly Ser Val Ala
 100 105 110
 Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro Pro Pro Pro Tyr Glu
 115 120 125
 Gln Val Val Lys Ala Lys
 130

<210> 183

260

gag gca cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg	432
Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr	
130 135 140	
tct gcc cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat	480
Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp	
145 150 155 160	
gct aac tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc	528
Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile	
165 170 175	
cca ttt aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag	576
Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys	
180 185 190	
ctg ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac	624
Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His	
195 200 205	
agc gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc	672
Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val	
210 215 220	
cca tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt	720
Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly	
225 230 235 240	
agc atc acg ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt	768
Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg	
245 250 255	
gag gat gtg gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg	816
Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val	
260 265 270	
gtc ctc aca ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct	864
Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser	
275 280 285	
ggt ttg aac ttg ctc gga aag cgt aag aca aga tga	900
Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg *	
290 295	

261

<210> 184
 <211> 299
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(299)
 <223> Xaa = Any Amino Acid

<400> 184

Met	Glu	Arg	Ala	Phe	Gln	Thr	Ala	Leu	Trp	Leu	Leu	Gln	Pro	Glu	Val
1			5					10					15		
Val	Phe	Ile	Leu	Gly	Asp	Ile	Phe	Asp	Glu	Gly	Lys	Trp	Ser	Thr	Pro
			20					25					30		
Xaa	Ala	Trp	Ala	Asp	Asp	Val	Glu	Arg	Phe	Gln	Lys	Met	Phe	Arg	His
		35					40					45			
Pro	Ser	His	Val	Gln	Leu	Lys	Val	Val	Ala	Gly	Asn	His	Asp	Ile	Gly
	50					55					60				
Phe	His	Tyr	Glu	Met	Asn	Thr	Tyr	Lys	Val	Glu	Arg	Phe	Glu	Lys	Val
65					70					75				80	
Phe	Ser	Ser	Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val	Met
				85					90					95	
Val	Asn	Ser	Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser	Glu
			100					105					110		
Thr	Glu	Ala	Glu	Leu	Ile	Glu	Val	Ser	His	Arg	Leu	Asn	Cys	Ser	Arg
	115						120					125			
Glu	Ala	Arg	Gly	Ser	Ser	Arg	Cys	Gly	Pro	Gly	Pro	Leu	Leu	Pro	Thr
	130					135					140				
Ser	Ala	Pro	Val	Leu	Leu	Gln	His	Tyr	Pro	Leu	Tyr	Arg	Arg	Ser	Asp
145					150					155				160	
Ala	Asn	Cys	Ser	Gly	Glu	Asp	Ala	Ala	Pro	Ala	Glu	Glu	Arg	Asp	Ile
			165						170					175	
Pro	Phe	Lys	Glu	Asn	Tyr	Asp	Val	Leu	Ser	Arg	Glu	Ala	Ser	Gln	Lys
			180					185					190		
Leu	Leu	Trp	Trp	Leu	Gln	Pro	Arg	Leu	Val	Leu	Ser	Gly	His	Thr	His
	195						200					205			
Ser	Ala	Cys	Glu	Val	His	His	Gly	Gly	Arg	Val	Pro	Glu	Leu	Ser	Val
	210					215					220				
Pro	Ser	Phe	Ser	Trp	Arg	Asn	Arg	Asn	Asn	Pro	Ser	Phe	Ile	Met	Gly
225					230					235				240	
Ser	Ile	Thr	Pro	Thr	Asp	Tyr	Thr	Leu	Ser	Lys	Cys	Tyr	Leu	Pro	Arg

263

100	105	110	
cga ctt tgt tac ctg aaa gag cag gaa gat att gca tgg tct gct ctt			384
Arg Leu Cys Tyr Leu Lys Glu Gln Glu Asp Ile Ala Trp Ser Ala Leu			
115	120	125	
gtg aag ttg ttt gat ccc gtg aaa tct ccc aga tgt tat gct gtt att			432
Val Lys Leu Phe Asp Pro Val Lys Ser Pro Arg Cys Tyr Ala Val Ile			
130	135	140	
gcc ctg aag aag cag cag tga			453
Ala Leu Lys Lys Gln Gln *			
145	150		

<210> 186
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 186

Met Ser Ala Cys Leu Ala Leu Glu Arg Val Ala Ala Gly Gln Gly Leu			
1	5	10	15
Pro Thr Glu Ser Leu Phe Tyr Arg Ala Val Leu Gln Asp Ile Ile Lys			
20	25	30	
Asp Cys Tyr Gly Ile Thr Lys Cys Asp Arg His Val Gly Lys Ile Tyr			
35	40	45	
Ser Lys Cys Ser Ser Phe Leu Asp Tyr Val Arg Arg Ser Leu Lys Lys			
50	55	60	
Leu Gly Leu Asp Glu Ser Lys Leu Pro Glu Lys Ile Ile Met Asn Tyr			
65	70	75	80
Tyr Glu Lys Tyr Lys Pro Arg Met Asn Glu Leu Glu Ala Phe Asn Met			
85	90	95	
Leu Lys Val Val Leu Ala Pro Cys Ile Glu Thr Leu Ile Leu Leu Asp			
100	105	110	
Arg Leu Cys Tyr Leu Lys Glu Gln Glu Asp Ile Ala Trp Ser Ala Leu			
115	120	125	
Val Lys Leu Phe Asp Pro Val Lys Ser Pro Arg Cys Tyr Ala Val Ile			
130	135	140	
Ala Leu Lys Lys Gln Gln			
145	150		

<210> 187
 <211> 1491

264

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1491)

<400> 187

atg	gcg	ctg	tgg	cgc	ggc	tcc	gcg	tac	gcg	ggc	ttc	ctg	gcg	ctg	gcc	48
Met	Ala	Leu	Trp	Arg	Gly	Ser	Ala	Tyr	Ala	Gly	Phe	Leu	Ala	Leu	Ala	
1				5					10					15		

gtg	ggc	tgc	gtc	ttc	ctg	ctg	gag	cca	gag	ctg	cca	ggc	tcg	gcg	ctg	96
Val	Gly	Cys	Val	Phe	Leu	Leu	Glu	Pro	Glu	Leu	Pro	Gly	Ser	Ala	Leu	
			20					25					30			

cgc	tct	ctc	tgg	agc	tcg	ctg	tgt	ctg	ggg	ccc	gcg	cct	gcg	ccc	ccg	144
Arg	Ser	Leu	Trp	Ser	Ser	Leu	Cys	Leu	Gly	Pro	Ala	Pro	Ala	Pro	Pro	
			35				40					45				

gga	ccc	gtc	tcc	ccc	gag	ggc	cgg	ttg	gcg	gca	gcc	tgg	gac	gcg	ctt	192
Gly	Pro	Val	Ser	Pro	Glu	Gly	Arg	Leu	Ala	Ala	Ala	Trp	Asp	Ala	Leu	
	50					55					60					

atc	gtg	cgg	cca	gtc	cgg	cgc	tgg	cgc	cgc	gtg	gca	gtg	gga	gtc	aat	240
Ile	Val	Arg	Pro	Val	Arg	Arg	Trp	Arg	Arg	Val	Ala	Val	Gly	Val	Asn	
	65				70					75					80	

gca	tgt	gtt	gat	gtg	gtg	ctc	tca	ggg	gtg	aag	ctc	ttg	cag	gca	ctt	288
Ala	Cys	Val	Asp	Val	Val	Leu	Ser	Gly	Val	Lys	Leu	Leu	Gln	Ala	Leu	
				85					90					95		

ggc	ctt	agt	cct	ggg	aat	ggg	aaa	gat	cac	agc	att	ctg	cat	tca	agg	336
Gly	Leu	Ser	Pro	Gly	Asn	Gly	Lys	Asp	His	Ser	Ile	Leu	His	Ser	Arg	
			100					105					110			

aat	gat	ctg	gaa	gaa	gcc	ttc	att	cac	ttc	atg	ggg	aag	gga	gca	gct	384
Asn	Asp	Leu	Glu	Glu	Ala	Phe	Ile	His	Phe	Met	Gly	Lys	Gly	Ala	Ala	
		115					120					125				

gct	gag	cgc	ttc	ttc	agt	gat	aag	gaa	act	ttt	cac	gac	att	gcc	cag	432
Ala	Glu	Arg	Phe	Phe	Ser	Asp	Lys	Glu	Thr	Phe	His	Asp	Ile	Ala	Gln	
	130					135						140				

266

ctt ggg ctg aat gaa cag gag ctg tta ttt ctc acc cag tca gcc tct	1008
Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala Ser	
325 330 335	
gga cct cac tct tct ctc tct tcc tgg aac ggt gtt cct gat gtg ggc	1056
Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val Gly	
340 345 350	
atg gtc agt gac atc ctc ttc tgg atc ttg aaa gaa cat ggg agg agt	1104
Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg Ser	
355 360 365	
aaa agc aga gcc tcg gat ctc acc agg atc cat ttc cac acg ctg gtc	1152
Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu Val	
370 375 380	
tac cac atc ctg gca act gtg gat gga cac tgg gcc aac cag ctg gca	1200
Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu Ala	
385 390 395 400	
gcc gtg gct gca gga gct cgt gtg gct ggg aca cag gcc tgc gcc aca	1248
Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala Thr	
405 410 415	
gaa acc ata gac acc agc cga gtg tct ctg agg gca ccc caa gag ttc	1296
Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu Phe	
420 425 430	
atg act tcc cat tcg gag gca ggc tcc agg att gta tta aac cca aac	1344
Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro Asn	
435 440 445	
aag cca gta gta gaa tgg cac aga gag gga ata tcc ttc cac ttc aca	1392
Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe Thr	
450 455 460	
cca gta ttg gtg tgt aaa gac ccc att cga act gta ggc ctt gga gat	1440
Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly Asp	
465 470 475 480	
gcc att tca gcc gaa gga ctc ttc tat tcg gaa gta cac cct cac tat	1488
Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His Tyr	
485 490 495	

267

tag

1491

*

<210> 188
 <211> 496
 <212> PRT
 <213> Homo sapiens

<400> 188

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Met Ala Leu Trp Arg Gly Ser Ala Tyr Ala Gly Phe Leu Ala Leu Ala
 1           5           10           15
Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
      20           25           30
Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
      35           40           45
Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
      50           55           60
Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
65           70           75           80
Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
      85           90           95
Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
      100          105          110
Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Gly Lys Gly Ala Ala
      115          120          125
Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
      130          135          140
Val Ala Ser Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala
      145          150          155          160
Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu
      165          170          175
Leu Cys Gly Pro Val Gly Pro Lys Leu His Glu Leu Leu Asp Asp Asn
      180          185          190
Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu
      195          200          205
Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro
      210          215          220
His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met
      225          230          235          240
Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp
      245          250          255
Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu

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268

260	265	270
Leu Gln Arg	Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile	
275	280	285
Pro Thr Gly Ile Pro Val His	Leu Glu Leu Ala Ser Met Thr Asn Arg	
290	295	300
Glu Leu Met Ser Ser Ile Val His Gln Val Phe Pro Ala Val Thr Ser		
305	310	315
Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala Ser		
325	330	335
Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val Gly		
340	345	350
Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg Ser		
355	360	365
Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu Val		
370	375	380
Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu Ala		
385	390	395
Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala Thr		
405	410	415
Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu Phe		
420	425	430
Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro Asn		
435	440	445
Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe Thr		
450	455	460
Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly Asp		
465	470	475
Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His Tyr		
485	490	495

<210> 189

<211> 339

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(339)

<400> 189

atg ggg tct cgg ttg tcc cag cct ttt gag tcc tat atc act gcg cct	
Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro	
1 5 10 15	

48

269

ccc ggt acc gcc gcc gcg ccc gcc aaa cct gcg ccc cca gct aca ccc 96
 Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro
 20 25 30

gga gcg ccg acc tcc cca gca gaa cac cgc ctg ttg aag acc tgc tgg 144
 Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
 35 40 45

agc tgt cgc gtg ctt tct ggg ttg ggg ctg atg ggg gcg ggc ggg tac 192
 Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
 50 55 60

gtg tac tgg gtg gca cgg aag ccc atg aag atg gga tac ccc ccg agt 240
 Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser
 65 70 75 80

cca tgg acc att acg cag atg gtc atc ggc ctc agc att gcc acc tgg 288
 Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp
 85 90 95

ggt atc gtt gtc atg gca gac ccc aaa ggg aag gcc tac cgc gtt gtt 336
 Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val
 100 105 110

tga 339
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<210> 190

<211> 112

<212> PRT

<213> Homo sapiens

<400> 190

Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro
 1 5 10 15

Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro
 20 25 30

Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
 35 40 45

Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
 50 55 60

Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser

270

65		70		75		80
Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp						
		85		90		95
Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val						
	100		105		110	

<210> 191

<211> 630

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(630)

<400> 191

atg gcg gcg gcc atg gca gca tct tcc ctg acg gtc acc tta ggg cgg	48
Met Ala Ala Ala Met Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg	
1 5 10 15	

ctg gcg tcc gcg tgc agc cac agc atc ctg aga cct tcg ggg ccc gga	96
Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly	
20 25 30	

gca gcc tcc ctt tgg tct gct tct cga agg ttc aat tca cag agc act	144
Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr	
35 40 45	

tca tat cta cca gga tat gtt cct aaa aca tcc ctg agt tca cca cct	192
Ser Tyr Leu Pro Gly Tyr Val Pro Lys Thr Ser Leu Ser Ser Pro Pro	
50 55 60	

tgg cca gaa gtt gtt ctg cca gac cca gtt gag gag acc aga cac cat	240
Trp Pro Glu Val Val Leu Pro Asp Pro Val Glu Glu Thr Arg His His	
65 70 75 80	

gca gag gtc gtg aag aag gtg aat gag atg atc gtc acg ggg cag tat	288
Ala Glu Val Val Lys Lys Val Asn Glu Met Ile Val Thr Gly Gln Tyr	
85 90 95	

ggc agg ctc ttt gcc gtg gtg cac ttt gcc agc cgc cag tgg aag gtg	336
Gly Arg Leu Phe Ala Val Val His Phe Ala Ser Arg Gln Trp Lys Val	
100 105 110	

271

acc tct gaa gac ctg atc tta att gga aat gaa cta gac ctt gcg tgt	384
Thr Ser Glu Asp Leu Ile Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys	
115 120 125	
gga gag aga att cga ctg gag aag gtc ctg ctg gtt ggg gca gac aac	432
Gly Glu Arg Ile Arg Leu Glu Lys Val Leu Leu Val Gly Ala Asp Asn	
130 135 140	
ttc acg ctg ctt ggc aag cca ctc ctc gga aag gat ctt gtt cga gta	480
Phe Thr Leu Leu Gly Lys Pro Leu Leu Gly Lys Asp Leu Val Arg Val	
145 150 155 160	
gaa gcc aca gtc att gaa aag aca gaa tca tgg cca aga atc att atg	528
Glu Ala Thr Val Ile Glu Lys Thr Glu Ser Trp Pro Arg Ile Ile Met	
165 170 175	
aga ttc agg aaa agg aaa aac ttc aag aag aaa aga atc gtc acg acc	576
Arg Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ile Val Thr Thr	
180 185 190	
ccg cag act gtc ctc cgg ata aac agc att gag att gct ccg tgt ttg	624
Pro Gln Thr Val Leu Arg Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu	
195 200 205	
ttg tga	630
Leu *	

<210> 192

<211> 209

<212> PRT

<213> Homo sapiens

<400> 192

Met Ala Ala Ala Met Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg	
1 5 10 15	
Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly	
20 25 30	
Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr	
35 40 45	
Ser Tyr Leu Pro Gly Tyr Val Pro Lys Thr Ser Leu Ser Ser Pro Pro	
50 55 60	
Trp Pro Glu Val Val Leu Pro Asp Pro Val Glu Glu Thr Arg His His	

272

[illegible]

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<210> 193
<211> 351
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(351)
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<400> 193																
atg	ggg	tct	cgg	ttg	tcc	cag	cct	ttt	gag	tcc	tat	atc	act	gcg	cct	48
Met	Gly	Ser	Arg	Leu	Ser	Gln	Pro	Phe	Glu	Ser	Tyr	Ile	Thr	Ala	Pro	
1		5			10					15						
ccc	ggt	acc	gcc	gcc	gcg	ccc	gcc	aaa	cct	gcg	ccc	cca	gct	aca	ccc	96
Pro	Gly	Thr	Ala	Ala	Ala	Pro	Ala	Lys	Pro	Ala	Pro	Pro	Ala	Thr	Pro	
			20		25					30						
gga	gcg	ccg	acc	tcc	cca	gca	gaa	cac	cgc	ctg	ttg	aag	acc	tgc	tgg	144
Gly	Ala	Pro	Thr	Ser	Pro	Ala	Glu	His	Arg	Leu	Leu	Lys	Thr	Cys	Trp	
35			40					45								
agc	tgt	cgc	gtg	ctt	tct	ggg	ttg	ggg	ctg	atg	ggg	gcg	ggc	ggg	tac	192
Ser	Cys	Arg	Val	Leu	Ser	Gly	Leu	Gly	Leu	Met	Gly	Ala	Gly	Gly	Tyr	

273

50	55	60	
gtg tac tgg gtg gca cgg aag ccc atg aag atg gga tac ccc ccg agt	240		
Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser			
65 70 75 80			
cca tgg acc att acg cag atg gtc atc ggc ctc agt gag aat caa ggc	288		
Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Glu Asn Gln Gly			
85 90 95			
att gcc acc tgg ggt atc gtt gtc atg gca gac ccc aaa ggg aag gcc	336		
Ile Ala Thr Trp Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala			
100 105 110			
tac cgc gtt gtt tga	351		
Tyr Arg Val Val *			
115			

<210> 194
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 194

Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro	
1 5 10 15	
Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro	
20 25 30	
Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp	
35 40 45	
Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr	
50 55 60	
Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser	
65 70 75 80	
Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Glu Asn Gln Gly	
85 90 95	
Ile Ala Thr Trp Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala	
100 105 110	
Tyr Arg Val Val	
115	

<210> 195
 <211> 1047

274

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1047)

<400> 195

atg cgg ctc ctc ggc tgg tgg caa gta ttg ctg tgg gtg ctg gga ctt	48
Met Arg Leu Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu	
1 5 10 15	
ccc gtc cgc ggc gtg gag gtt gca gag gaa agt ggt cgc tta tgg tca	96
Pro Val Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser	
20 25 30	
gag gag cag cct gct cac cct ctc cag gtg ggg gct gtg tac ctg ggt	144
Glu Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly	
35 40 45	
gag gag gag ctc ctg cat gac ccg atg ggc cag gac agg gca gca gaa	192
Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala Glu	
50 55 60	
gag gcc aat gcg gtg ctg ggg ctg gac acc caa ggc gat cac atg gtg	240
Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His Met Val	
65 70 75 80	
atg ctg tct gtg att cct ggg gaa gct gag gac aaa gtg agt tca gag	288
Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val Ser Ser Glu	
85 90 95	
cct agc ggc gtc acc tgt ggt gct gga gga gcg gag gac tca agg tgc	336
Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu Asp Ser Arg Cys	
100 105 110	
aac gtc cga gag agc ctt ttc tct ctg gat ggc gct gga gca cac ttc	384
Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly Ala Gly Ala His Phe	
115 120 125	
cct gac aga gaa gag gag tat tac aca gag cca gaa gtg gcg gaa tct	432
Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu Pro Glu Val Ala Glu Ser	
130 135 140	

276

tta att agt ttt att atg tat gct acc att cga act gag agt att cgg 1008
 Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu Ser Ile Arg
 325 330 335

tgg cta att cca gga caa gag cag gaa cat gtg gag tag 1047
 Trp Leu Ile Pro Gly Gln Glu Gln His Val Glu *
 340 345

<210> 196

<211> 348

<212> PRT

<213> Homo sapiens

<400> 196

Met Arg Leu Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu
 1 5 10 15
 Pro Val Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser
 20 25 30
 Glu Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
 35 40 45
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala Glu
 50 55 60
 Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His Met Val
 65 70 75 80
 Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val Ser Ser Glu
 85 90 95
 Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu Asp Ser Arg Cys
 100 105 110
 Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly Ala Gly Ala His Phe
 115 120 125
 Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu Pro Glu Val Ala Glu Ser
 130 135 140
 Asp Ala Ala Pro Thr Glu Asp Ser Asn Asn Thr Glu Ser Leu Lys Ser
 145 150 155 160
 Pro Lys Val Asn Cys Glu Glu Arg Asn Ile Thr Gly Leu Glu Asn Phe
 165 170 175
 Thr Leu Lys Ile Leu Asn Met Ser Gln Asp Leu Met Asp Phe Leu Asn
 180 185 190
 Pro Asn Gly Ser Asp Cys Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys
 195 200 205
 Arg Phe Ser Ala Ser Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala
 210 215 220
 Phe Pro Ala Leu His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser

277

225 230 235 240
 Leu Ser Thr Arg Phe Gly Thr Val Ala Val Pro Asn Ile Leu Leu Phe
 245 250 255
 Gln Gly Ala Lys Pro Met Ala Arg Phe Asn His Thr Asp Arg Thr Leu
 260 265 270
 Glu Thr Leu Lys Ile Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys
 275 280 285
 Lys Asn Val Val Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro Ser
 290 295 300
 Thr Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu Phe Phe
 305 310 315 320
 Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu Ser Ile Arg
 325 330 335
 Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu
 340 345

<210> 197
 <211> 444
 <212> DNA
 <213> Homo sapiens
 1 3
 <220> 1 3
 <221> CDS
 <222> (1)...(444)

<400> 197
 atg gcc ttc cca aag aag aaa ctt cag ggt ctt gtg gct gca acc atc 48
 Met Ala Phe Pro Lys Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile
 1 5 10 15

 acg cca atg act gag aat gga gaa atc aac ttt tca gta att ggt cag 96
 Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln
 20 25 30

 tat gtg gat tat ctt gtg aaa gaa cag gga gtg aag aac att ttt gtg 144
 Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
 35 40 45

 aat ggc aca aca gga gaa ggc ctg tcc ctg agc gtc tca gag cgt cgc 192
 Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
 50 55 60

 cag gtt gca gag gag tgg gtg aca aaa ggg aag gac aag ctg gat cag 240
 Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln

278

65	70	75	80	
gtg ata att cac gta gga gca ctg agc ttg aag gag tca cag gaa ctg				288
Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu				
	85	90	95	
gcc caa cat gca gca gaa ata gga gct gat ggc atc gct gtc att gca				336
Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala				
	100	105	110	
ccg ttc ttc ctc aag cca tgg acc aaa gat atc ctg att aat ttc cta				384
Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu				
	115	120	125	
aag gaa gtg gct gct gcg ccc ctg ccc tgc cat ttt att act atc aca				432
Lys Glu Val Ala Ala Ala Pro Leu Pro Cys His Phe Ile Thr Ile Thr				
	130	135	140	
ttc ctg cct tga				444
Phe Leu Pro *				
145				

<210> 198
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 198
 Met Ala Phe Pro Lys Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile
 1 5 10 15
 Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln
 20 25 30
 Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
 35 40 45
 Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
 50 55 60
 Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln
 65 70 75 80
 Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu
 85 90 95
 Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
 100 105 110
 Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu

279

115 120 125
 Lys Glu Val Ala Ala Ala Pro Leu Pro Cys His Phe Ile Thr Ile Thr
 130 135 140
 Phe Leu Pro
 145

<210> 199
 <211> 705
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(705)

<221> misc_feature
 <222> (1)...(705)
 <223> n = A,T,C or G

<400> 199
 atg atg tct caa ggt agt cag ttt ttg tat tca act ttt ggc tat acc 48
 Met Met Ser Gln Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr
 1 5 10 15

 cta ctg gca gcc ata gta gag aga gct tca gga tgt aaa tat ttg gac 96
 Leu Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
 20 25 30

 tat atg cag aaa ata ttc cat gac ttg gat atg ctg acg act gtg cag 144
 Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val Gln
 35 40 45

 gaa gaa aac gag cca gtg att tac aat aga gca aga ttt tat gtt tac 192
 Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg Phe Tyr Val Tyr
 50 55 60

 aat aaa aag aaa cgt ctt gtc aac aca cct tac gtg gat aac tcc tat 240
 Asn Lys Lys Lys Arg Leu Val Asn Thr Pro Tyr Val Asp Asn Ser Tyr
 65 70 75 80

 aaa tgg gct ggt ggt gga ttt ctg tct aca gtg ggt gac ctt ctg aaa 288
 Lys Trp Ala Gly Gly Gly Phe Leu Ser Thr Val Gly Asp Leu Leu Lys
 85 90 95

280

ttt ggg aat gca atg ctt tat ggt tac caa gtt ggg ctg ttt aag aac	336
Phe Gly Asn Ala Met Leu Tyr Gly Tyr Gln Val Gly Leu Phe Lys Asn	
100 105 110	
tca aat gaa aat ctt tta cct gga tac ctc aaa cca gaa aca atg gtt	384
Ser Asn Glu Asn Leu Leu Pro Gly Tyr Leu Lys Pro Glu Thr Met Val	
115 120 125	
atg atg tgg acc cca gtc cct aac aca gag atg tct tgg gat aaa gag	432
Met Met Trp Thr Pro Val Pro Asn Thr Glu Met Ser Trp Asp Lys Glu	
130 135 140	
ggg aaa tat gca atg gcg tgg ggt gtt gtg gaa ang aaa caa acg tat	480
Gly Lys Tyr Ala Met Ala Trp Gly Val Val Glu Xaa Lys Gln Thr Tyr	
145 150 155 160	
ggg tcg tgt aga aag caa cgg cat tat gct tca cat act gga ggg gca	528
Gly Ser Cys Arg Lys Gln Arg His Tyr Ala Ser His Thr Gly Gly Ala	
165 170 175	
gtg ggt gcc agt agt gtc ctg ctg gtc ctt cct gaa gaa ctg gat aca	576
Val Gly Ala Ser Ser Val Leu Leu Val Leu Pro Glu Glu Leu Asp Thr	
180 185 190	
gag act ata aat aac aag gtt ccc cca aga gga atc att gtt tct atc	624
Glu Thr Ile Asn Asn Lys Val Pro Pro Arg Gly Ile Ile Val Ser Ile	
195 200 205	
ata tgt aac atg caa tct gtt ggc ctc aat agc acc gct ttg aag att	672
Ile Cys Asn Met Gln Ser Val Gly Leu Asn Ser Thr Ala Leu Lys Ile	
210 215 220	
gcc ctt gaa ttt gat aaa gac aga tca gac tga	705
Ala Leu Glu Phe Asp Lys Asp Arg Ser Asp *	
225 230	

<210> 200

<211> 234

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

281

<222> (1)...(234)

<223> Xaa = Any Amino Acid

<400> 200

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Met Met Ser Gln Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr
 1           5           10           15
Leu Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
      20           25           30
Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val Gln
      35           40           45
Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg Phe Tyr Val Tyr
      50           55           60
Asn Lys Lys Lys Arg Leu Val Asn Thr Pro Tyr Val Asp Asn Ser Tyr
      65           70           75           80
Lys Trp Ala Gly Gly Gly Phe Leu Ser Thr Val Gly Asp Leu Leu Lys
      85           90           95
Phe Gly Asn Ala Met Leu Tyr Gly Tyr Gln Val Gly Leu Phe Lys Asn
      100           105           110
Ser Asn Glu Asn Leu Leu Pro Gly Tyr Leu Lys Pro Glu Thr Met Val
      115           120           125
Met Met Trp Thr Pro Val Pro Asn Thr Glu Met Ser Trp Asp Lys Glu
      130           135           140
Gly Lys Tyr Ala Met Ala Trp Gly Val Val Glu Xaa Lys Gln Thr Tyr
      145           150           155           160
Gly Ser Cys Arg Lys Gln Arg His Tyr Ala Ser His Thr Gly Gly Ala
      165           170           175
Val Gly Ala Ser Ser Val Leu Leu Val Leu Pro Glu Glu Leu Asp Thr
      180           185           190
Glu Thr Ile Asn Asn Lys Val Pro Pro Arg Gly Ile Ile Val Ser Ile
      195           200           205
Ile Cys Asn Met Gln Ser Val Gly Leu Asn Ser Thr Ala Leu Lys Ile
      210           215           220
Ala Leu Glu Phe Asp Lys Asp Arg Ser Asp
      225           230

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<210> 201

<211> 885

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(885)

282

<221> misc_feature

<222> (1)...(885)

<223> n = A,T,C or G

<400> 201

atg	ctg	gct	gtg	tca	gtg	ctg	gcc	gca	gtc	cgc	ggc	ggc	gac	gag	gtg	48
Met	Leu	Ala	Val	Ser	Val	Leu	Ala	Ala	Val	Arg	Gly	Gly	Asp	Glu	Val	
1				5					10					15		

agg	cgc	gtc	cgc	gag	agc	aac	gtc	ctc	cac	gag	aag	tcc	aag	ggg	aag	96
Arg	Arg	Val	Arg	Glu	Ser	Asn	Val	Leu	His	Glu	Lys	Ser	Lys	Gly	Lys	
			20					25					30			

acg	cgc	gag	gga	gcc	gag	gac	aag	atg	acc	agc	ggc	gac	gtg	ctg	tcc	144
Thr	Arg	Glu	Gly	Ala	Glu	Asp	Lys	Met	Thr	Ser	Gly	Asp	Val	Leu	Ser	
		35					40					45				

aac	cgc	aag	atg	ttc	tac	ctg	ctc	aag	acc	gcc	ttc	ccc	agc	gtc	cag	192
Asn	Arg	Lys	Met	Phe	Tyr	Leu	Leu	Lys	Thr	Ala	Phe	Pro	Ser	Val	Gln	
	50					55					60					

att	aat	act	gag	gaa	cac	gtg	gat	gca	gct	gat	cag	gag	gtt	atc	ttg	240
Ile	Asn	Thr	Glu	Glu	His	Val	Asp	Ala	Ala	Asp	Gln	Glu	Val	Ile	Leu	
65					70					75				80		

tgg	gat	cat	aag	att	cct	gag	gat	atc	cta	aag	gaa	gta	act	act	cct	288
Trp	Asp	His	Lys	Ile	Pro	Glu	Asp	Ile	Leu	Lys	Glu	Val	Thr	Thr	Pro	
			85					90						95		

aaa	gag	gta	cca	gca	gaa	agt	gtt	act	gtc	tgg	att	gac	cca	ctt	gat	336
Lys	Glu	Val	Pro	Ala	Glu	Ser	Val	Thr	Val	Trp	Ile	Asp	Pro	Leu	Asp	
		100						105					110			

gct	aca	cag	gaa	tat	aca	gag	gat	ctt	cga	aag	tac	gtc	act	act	atg	384
Ala	Thr	Gln	Glu	Tyr	Thr	Glu	Asp	Leu	Arg	Lys	Tyr	Val	Thr	Thr	Met	
		115					120					125				

gtg	tgt	gtg	gct	gta	aat	ggt	aaa	ccc	atg	cta	gga	gtt	ata	cat	aag	432
Val	Cys	Val	Ala	Val	Asn	Gly	Lys	Pro	Met	Leu	Gly	Val	Ile	His	Lys	
	130					135					140					

cca	ttt	tcc	gaa	tat	aca	gct	tgg	gca	atg	gta	gat	ggt	ggt	tca	aat	480
Pro	Phe	Ser	Glu	Tyr	Thr	Ala	Trp	Ala	Met	Val	Asp	Gly	Gly	Ser	Asn	
145					150				155					160		

283

gtg aaa gcc cgc tct tcc tac aat gag aag acc cca agg ntc gtt gtg	528
Val Lys Ala Arg Ser Ser Tyr Asn Glu Lys Thr Pro Arg Xaa Val Val	
165 170 175	
tct cgt tcc cat tca ggg atg gtc aaa cag gtc gct ctt cag act ttt	576
Ser Arg Ser His Ser Gly Met Val Lys Gln Val Ala Leu Gln Thr Phe	
180 185 190	
gga aac cag act aca att atc cca gct ggt ggt gct ggt tat aaa gtt	624
Gly Asn Gln Thr Thr Ile Ile Pro Ala Gly Gly Ala Gly Tyr Lys Val	
195 200 205	
tta gca ctt ttg gat gtg cct gat aag agt caa gaa aaa gct gat tta	672
Leu Ala Leu Leu Asp Val Pro Asp Lys Ser Gln Glu Lys Ala Asp Leu	
210 215 220	
tac atc cat gtg aca tac atc aaa aag tgg gat ata tgt gct ggt aat	720
Tyr Ile His Val Thr Tyr Ile Lys Lys Trp Asp Ile Cys Ala Gly Asn	
225 230 235 240	
gcc atc tta aaa gcc cta ggg ggg cat atg act acc ctg agt ggt gaa	768
Ala Ile Leu Lys Ala Leu Gly Gly His Met Thr Thr Leu Ser Gly Glu	
245 250 255	
gaa atc agt tac act ggt tca gac ggc att gaa ggg gga ctc ctt gct	816
Glu Ile Ser Tyr Thr Gly Ser Asp Gly Ile Glu Gly Gly Leu Leu Ala	
260 265 270	
agc atc aga atg aac cac cag gcc ctg gtc aga aaa ctc cca gat cta	864
Ser Ile Arg Met Asn His Gln Ala Leu Val Arg Lys Leu Pro Asp Leu	
275 280 285	
gaa aag aca gga cat aaa tga	885
Glu Lys Thr Gly His Lys *	
290	

<210> 202

<211> 294

<212> PRT

<213> Homo sapiens

<220>

284

<221> VARIANT

<222> (1)...(294)

<223> Xaa = Any Amino Acid

<400> 202

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Met Leu Ala Val Ser Val Leu Ala Ala Val Arg Gly Gly Asp Glu Val
 1           5           10           15
Arg Arg Val Arg Glu Ser Asn Val Leu His Glu Lys Ser Lys Gly Lys
      20           25           30
Thr Arg Glu Gly Ala Glu Asp Lys Met Thr Ser Gly Asp Val Leu Ser
      35           40           45
Asn Arg Lys Met Phe Tyr Leu Leu Lys Thr Ala Phe Pro Ser Val Gln
      50           55           60
Ile Asn Thr Glu Glu His Val Asp Ala Ala Asp Gln Glu Val Ile Leu
65           70           75           80
Trp Asp His Lys Ile Pro Glu Asp Ile Leu Lys Glu Val Thr Thr Pro
      85           90           95
Lys Glu Val Pro Ala Glu Ser Val Thr Val Trp Ile Asp Pro Leu Asp
      100           105           110
Ala Thr Gln Glu Tyr Thr Glu Asp Leu Arg Lys Tyr Val Thr Thr Met
      115           120           125
Val Cys Val Ala Val Asn Gly Lys Pro Met Leu Gly Val Ile His Lys
      130           135           140
Pro Phe Ser Glu Tyr Thr Ala Trp Ala Met Val Asp Gly Gly Ser Asn
145           150           155           160
Val Lys Ala Arg Ser Ser Tyr Asn Glu Lys Thr Pro Arg Xaa Val Val
      165           170           175
Ser Arg Ser His Ser Gly Met Val Lys Gln Val Ala Leu Gln Thr Phe
      180           185           190
Gly Asn Gln Thr Thr Ile Ile Pro Ala Gly Gly Ala Gly Tyr Lys Val
      195           200           205
Leu Ala Leu Leu Asp Val Pro Asp Lys Ser Gln Glu Lys Ala Asp Leu
      210           215           220
Tyr Ile His Val Thr Tyr Ile Lys Lys Trp Asp Ile Cys Ala Gly Asn
225           230           235           240
Ala Ile Leu Lys Ala Leu Gly Gly His Met Thr Thr Leu Ser Gly Glu
      245           250           255
Glu Ile Ser Tyr Thr Gly Ser Asp Gly Ile Glu Gly Gly Leu Leu Ala
      260           265           270
Ser Ile Arg Met Asn His Gln Ala Leu Val Arg Lys Leu Pro Asp Leu
      275           280           285
Glu Lys Thr Gly His Lys
      290

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285

<210> 203
 <211> 861
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(861)

<400> 203

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Met Glu Glu Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala	
1 5 10 15	
cct gtt aaa agc cag gcc att gct cag cca gct acc act gct aag agc	96
Pro Val Lys Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser	
20 25 30	
cat ctc cac cag aag cct ggc cag acc tgg aag aac aaa gag cat cat	144
His Leu His Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His	
35 40 45	
ctc tct gac aga gag ttt gtg ttc aaa gaa cct cag cag gta gta cgt	192
Leu Ser Asp Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg	
50 55 60	
aga gct cct gag cca cga gtg att gac aga gag ggt gtg tat gaa atc	240
Arg Ala Pro Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile	
65 70 75 80	
agc ctg tca ccc aca ggt gta tct agg gtc tgt ttg tat cct ggc ttt	288
Ser Leu Ser Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe	
85 90 95	
gtt gac gtg aaa gaa gct gac tgg ata ttg gaa cag ctt tgt caa gat	336
Val Asp Val Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp	
100 105 110	
gtt ccc tgg aaa cag agg acc ggc atc aga gag gat ata act tat cag	384
Val Pro Trp Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln	
115 120 125	
caa cca aga ctt aca gca tgg tat gga gaa ctt cct tac act tat tca	432
Gln Pro Arg Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser	

286

130	135	140	
aga atc act atg gaa cca aat cct cac tgg cac cct gtg ctg cgc aca			480
Arg Ile Thr Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr			
145	150	155	160
cta aag aac cgc att gaa gag aac act ggc cac acc ttc aac tcc tta			528
Leu Lys Asn Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu			
	165	170	175
ctc tgc aat ctt tat cgc aat gag aag gac agc gtg gac tgg cac agt			576
Leu Cys Asn Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser			
	180	185	190
gat gat gaa ccc tca cta ggg agg tgc ccc att att gct tca cta agt			624
Asp Asp Glu Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser			
	195	200	205
ttt ggt gcc aca cgc aca ttt gag atg aga aag aag cca cca cca gaa			672
Phe Gly Ala Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu			
	210	215	220
gag aat gga gac tac aca tat gtg gaa aga gtg aag ata ccc ttg gat			720
Glu Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp			
	225	230	235
cat ggt acc ttg tta atc atg gaa gga gcg aca caa gct gac tgg cag			768
His Gly Thr Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln			
	245	250	255
cat cga gtg ccc aaa gaa tac cac tct aga gaa ccg aga gtg aac ctg			816
His Arg Val Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu			
	260	265	270
acc ttt cgg aca gtc tat cca gac cct cga ggg gca ccc tgg tga			861
Thr Phe Arg Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp *			
	275	280	285

<210> 204

<211> 286

<212> PRT

<213> Homo sapiens

287

<400> 204

Met Glu Glu Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala
 1 5 10 15
 Pro Val Lys Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser
 20 25 30
 His Leu His Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His
 35 40 45
 Leu Ser Asp Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg
 50 55 60
 Arg Ala Pro Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile
 65 70 75 80
 Ser Leu Ser Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe
 85 90 95
 Val Asp Val Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp
 100 105 110
 Val Pro Trp Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln
 115 120 125
 Gln Pro Arg Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser
 130 135 140
 Arg Ile Thr Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr
 145 150 155 160
 Leu Lys Asn Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu
 165 170 175
 Leu Cys Asn Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser
 180 185 190
 Asp Asp Glu Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser
 195 200 205
 Phe Gly Ala Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu
 210 215 220
 Glu Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp
 225 230 235 240
 His Gly Thr Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln
 245 250 255
 His Arg Val Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu
 260 265 270
 Thr Phe Arg Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp
 275 280 285

<210> 205

<211> 561

<212> DNA

<213> Homo sapiens

<220>

288

<221> CDS

<222> (1)...(561)

<400> 205

atg	att	cac	tgg	cat	tct	gag	aaa	gca	act	ctt	ctt	tta	aat	gct	cca	48
Met	Ile	His	Trp	His	Ser	Glu	Lys	Ala	Thr	Leu	Leu	Leu	Asn	Ala	Pro	
1			5					10					15			

tca	ttt	tca	gat	caa	ctt	cct	ggc	aca	atg	gcc	acc	ctt	tct	ctg	gtg	96
Ser	Phe	Ser	Asp	Gln	Leu	Pro	Gly	Thr	Met	Ala	Thr	Leu	Ser	Leu	Val	
			20				25					30				

aat	gag	gca	cag	tat	ctg	ctg	atc	aac	aca	tcc	agt	att	ttg	gaa	ctt	144
Asn	Glu	Ala	Gln	Tyr	Leu	Leu	Ile	Asn	Thr	Ser	Ser	Ile	Leu	Glu	Leu	
		35					40					45				

cac	cgg	caa	cta	aac	acc	agt	gat	gag	aat	gga	aag	gag	gaa	tta	ttc	192
His	Arg	Gln	Leu	Asn	Thr	Ser	Asp	Glu	Asn	Gly	Lys	Glu	Glu	Leu	Phe	
	50					55				60						

tca	ctg	aag	gat	ctc	agc	ttg	cgt	ttt	cgt	gcc	aat	att	att	atc	aat	240
Ser	Leu	Lys	Asp	Leu	Ser	Leu	Arg	Phe	Arg	Ala	Asn	Ile	Ile	Ile	Asn	
65					70				75					80		

gga	aaa	agg	gct	ttt	gaa	gaa	gag	aaa	tgg	gat	gag	att	tca	att	ggc	288
Gly	Lys	Arg	Ala	Phe	Glu	Glu	Glu	Lys	Trp	Asp	Glu	Ile	Ser	Ile	Gly	
			85					90					95			

tct	ttg	cgt	ttc	cag	gtt	ttg	ggg	cct	tgt	cac	aga	tgc	cag	atg	att	336
Ser	Leu	Arg	Phe	Gln	Val	Leu	Gly	Pro	Cys	His	Arg	Cys	Gln	Met	Ile	
			100				105						110			

tgc	atc	gac	cag	caa	act	ggg	caa	cga	aac	cag	cat	gtt	ttc	caa	aaa	384
Cys	Ile	Asp	Gln	Gln	Thr	Gly	Gln	Arg	Asn	Gln	His	Val	Phe	Gln	Lys	
		115				120						125				

ctt	tct	gag	agt	cgt	gaa	aca	aag	gtg	aac	ttt	ggc	atg	tac	ctg	atg	432
Leu	Ser	Glu	Ser	Arg	Glu	Thr	Lys	Val	Asn	Phe	Gly	Met	Tyr	Leu	Met	
	130					135					140					

cat	gca	tca	ttg	gat	tta	tcc	tcc	cca	tgt	ttc	ctg	tct	gta	gga	tct	480
His	Ala	Ser	Leu	Asp	Leu	Ser	Ser	Pro	Cys	Phe	Leu	Ser	Val	Gly	Ser	
145					150				155					160		

289

cag gtg ctc cct gtg ttg aaa gag aat gtg gaa ggt cat gat tta cct 528
 Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly His Asp Leu Pro
 165 170 175

gca tct gag aaa cac cag gat gtt acc tcc taa 561
 Ala Ser Glu Lys His Gln Asp Val Thr Ser *
 180 185

<210> 206
 <211> 186
 <212> PRT
 <213> Homo sapiens

<400> 206
 Met Ile His Trp His Ser Glu Lys Ala Thr Leu Leu Leu Asn Ala Pro
 1 5 10 15
 Ser Phe Ser Asp Gln Leu Pro Gly Thr Met Ala Thr Leu Ser Leu Val
 20 25 30
 Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser Ile Leu Glu Leu
 35 40 45
 His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys Glu Glu Leu Phe
 50 55 60
 Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn Ile Ile Ile Asn
 65 70 75 80
 Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu Ile Ser Ile Gly
 85 90 95
 Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg Cys Gln Met Ile
 100 105 110
 Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His Val Phe Gln Lys
 115 120 125
 Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly Met Tyr Leu Met
 130 135 140
 His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu Ser Val Gly Ser
 145 150 155 160
 Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly His Asp Leu Pro
 165 170 175
 Ala Ser Glu Lys His Gln Asp Val Thr Ser
 180 185

<210> 207
 <211> 1272
 <212> DNA
 <213> Homo sapiens

290

<220>

<221> CDS

<222> (1)...(1272)

<221> misc_feature

<222> (1)...(1272)

<223> n = A,T,C or G

<400> 207

atg	cac	aat	tac	tgc	ttt	gtg	ttt	gct	ctg	gga	tac	ctc	aca	gtg	tgc	48
Met	His	Asn	Tyr	Cys	Phe	Val	Phe	Ala	Leu	Gly	Tyr	Leu	Thr	Val	Cys	
1				5					10					15		

caa	gtt	act	cga	gtc	tat	atc	ttt	gac	tat	gga	caa	tat	tct	gct	gat	96
Gln	Val	Thr	Arg	Val	Tyr	Ile	Phe	Asp	Tyr	Gly	Gln	Tyr	Ser	Ala	Asp	
			20					25					30			

ttt	tca	ggc	cca	atg	atg	atc	att	act	cag	aag	atc	act	agt	ttg	gct	144
Phe	Ser	Gly	Pro	Met	Met	Ile	Ile	Thr	Gln	Lys	Ile	Thr	Ser	Leu	Ala	
		35				40						45				

tgc	gaa	att	cat	gat	ggg	atg	ttt	cgg	aag	gat	gaa	gaa	ctg	act	tcc	192
Cys	Glu	Ile	His	Asp	Gly	Met	Phe	Arg	Lys	Asp	Glu	Glu	Leu	Thr	Ser	
	50					55					60					

tca	cag	agg	gat	tta	gct	gta	agg	cgc	atg	cca	agc	tta	ctg	gag	tat	240
Ser	Gln	Arg	Asp	Leu	Ala	Val	Arg	Arg	Met	Pro	Ser	Leu	Leu	Glu	Tyr	
	65				70					75				80		

ttg	agt	tac	aac	tgt	aac	ttc	atg	ggg	atc	ctg	gca	ngc	cca	ntt	tgc	288
Leu	Ser	Tyr	Asn	Cys	Asn	Phe	Met	Gly	Ile	Leu	Ala	Xaa	Pro	Xaa	Cys	
			85					90						95		

tct	tac	aaa	gac	tac	att	act	ttc	att	gaa	ggc	aga	tca	tac	cat	atc	336
Ser	Tyr	Lys	Asp	Tyr	Ile	Thr	Phe	Ile	Glu	Gly	Arg	Ser	Tyr	His	Ile	
			100					105					110			

aca	caa	tct	ggt	gaa	aat	gga	aaa	gaa	gag	aca	cag	tat	gaa	aga	aca	384
Thr	Gln	Ser	Gly	Glu	Asn	Gly	Lys	Glu	Glu	Thr	Gln	Tyr	Glu	Arg	Thr	
		115					120					125				

gag	cca	tct	cca	aat	act	gcg	gtt	gtt	cag	aag	ctc	tta	gtt	tgt	ggg	432
Glu	Pro	Ser	Pro	Asn	Thr	Ala	Val	Val	Gln	Lys	Leu	Leu	Val	Cys	Gly	

291

130	135	140	
ctg tcc ttg tta ttt cac ttg acc atc tgt aca aca tta cct gtg gag			480
Leu Ser Leu Leu Phe His Leu Thr Ile Cys Thr Thr Leu Pro Val Glu			
145	150	155	160
tac aac att gat gag cat ttt caa gct aca gct tcg tgg cca aca aag			528
Tyr Asn Ile Asp Glu His Phe Gln Ala Thr Ala Ser Trp Pro Thr Lys			
	165	170	175
att atc tat ctg tat atc tct ctt ttg gct gcc aga ccc aaa tac tat			576
Ile Ile Tyr Leu Tyr Ile Ser Leu Leu Ala Ala Arg Pro Lys Tyr Tyr			
	180	185	190
ttt gca tgg acg cta gct gat gcc att aat aat gct gca ggc ttt ggt			624
Phe Ala Trp Thr Leu Ala Asp Ala Ile Asn Asn Ala Ala Gly Phe Gly			
	195	200	205
ttc aga ggg tat gac gaa aat gga gca gct cgc tgg gac tta att tcc			672
Phe Arg Gly Tyr Asp Glu Asn Gly Ala Ala Arg Trp Asp Leu Ile Ser			
	210	215	220
aat ttg aga att caa caa ata gag atg tca aca agt ttc aag atg ttt			720
Asn Leu Arg Ile Gln Gln Ile Glu Met Ser Thr Ser Phe Lys Met Phe			
	225	230	235
ctt gat aat tgg aat att cag aca gct ctt tgg ctc aaa agg gtg tgt			768
Leu Asp Asn Trp Asn Ile Gln Thr Ala Leu Trp Leu Lys Arg Val Cys			
	245	250	255
tat gaa cga acc tcc ttc agt cca act atc cag acg ttc att ctc tct			816
Tyr Glu Arg Thr Ser Phe Ser Pro Thr Ile Gln Thr Phe Ile Leu Ser			
	260	265	270
gcc att tgg cac ggg gta tac cca gga tat tat cta acg ttt cta aca			864
Ala Ile Trp His Gly Val Tyr Pro Gly Tyr Tyr Leu Thr Phe Leu Thr			
	275	280	285
ggg gtg tta atg aca tta gca gca aga gct atg aga aat aac ttt aga			912
Gly Val Leu Met Thr Leu Ala Ala Arg Ala Met Arg Asn Asn Phe Arg			
	290	295	300
cat tat ttc att gaa cct tcc caa ctg aaa tta ttt tat gat gtt ata			960
His Tyr Phe Ile Glu Pro Ser Gln Leu Lys Leu Phe Tyr Asp Val Ile			

292

305	310	315	320	
aca tgg ata gta act caa gta gca ata agt tac aca gtt gtg cca ttt				1008
Thr Trp Ile Val Thr Gln Val Ala Ile Ser Tyr Thr Val Val Pro Phe				
	325	330	335	
gtg ctt ctt tct ata aaa cca tca ctc acg ttt tac agc tcc tgg tat				1056
Val Leu Leu Ser Ile Lys Pro Ser Leu Thr Phe Tyr Ser Ser Trp Tyr				
	340	345	350	
tat tgc ctg cac att ctt ggt atc tta gta tta ttg ttg ttg cca gtg				1104
Tyr Cys Leu His Ile Leu Gly Ile Leu Val Leu Leu Leu Leu Pro Val				
	355	360	365	
aaa aaa act caa aga aga aag aat aca cat gaa aac att cag ctc tca				1152
Lys Lys Thr Gln Arg Arg Lys Asn Thr His Glu Asn Ile Gln Leu Ser				
	370	375	380	
caa tcc aaa aag ttt gat gaa gga gaa aat tct ttg gga cag aac agt				1200
Gln Ser Lys Lys Phe Asp Glu Gly Glu Asn Ser Leu Gly Gln Asn Ser				
	385	390	395	400
ttt tct aca aca aac aat gtt tgc aat cag aat caa gaa ata gcc tcg				1248
Phe Ser Thr Thr Asn Asn Val Cys Asn Gln Asn Gln Glu Ile Ala Ser				
	405	410	415	
aga cat tca tca cta aag cag tga				1272
Arg His Ser Ser Leu Lys Gln *				
	420			

<210> 208

<211> 423

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(423)

<223> Xaa = Any Amino Acid

<400> 208

Met	His	Asn	Tyr	Cys	Phe	Val	Phe	Ala	Leu	Gly	Tyr	Leu	Thr	Val	Cys
1						5				10				15	

293

Gln Val Thr Arg Val Tyr Ile Phe Asp Tyr Gly Gln Tyr Ser Ala Asp
 20 25 30
 Phe Ser Gly Pro Met Met Ile Ile Thr Gln Lys Ile Thr Ser Leu Ala
 35 40 45
 Cys Glu Ile His Asp Gly Met Phe Arg Lys Asp Glu Glu Leu Thr Ser
 50 55 60
 Ser Gln Arg Asp Leu Ala Val Arg Arg Met Pro Ser Leu Leu Glu Tyr
 65 70 75 80
 Leu Ser Tyr Asn Cys Asn Phe Met Gly Ile Leu Ala Xaa Pro Xaa Cys
 85 90 95
 Ser Tyr Lys Asp Tyr Ile Thr Phe Ile Glu Gly Arg Ser Tyr His Ile
 100 105 110
 Thr Gln Ser Gly Glu Asn Gly Lys Glu Glu Thr Gln Tyr Glu Arg Thr
 115 120 125
 Glu Pro Ser Pro Asn Thr Ala Val Val Gln Lys Leu Leu Val Cys Gly
 130 135 140
 Leu Ser Leu Leu Phe His Leu Thr Ile Cys Thr Thr Leu Pro Val Glu
 145 150 155 160
 Tyr Asn Ile Asp Glu His Phe Gln Ala Thr Ala Ser Trp Pro Thr Lys
 165 170 175
 Ile Ile Tyr Leu Tyr Ile Ser Leu Leu Ala Ala Arg Pro Lys Tyr Tyr
 180 185 190
 Phe Ala Trp Thr Leu Ala Asp Ala Ile Asn Asn Ala Ala Gly Phe Gly
 195 200 205
 Phe Arg Gly Tyr Asp Glu Asn Gly Ala Ala Arg Trp Asp Leu Ile Ser
 210 215 220
 Asn Leu Arg Ile Gln Gln Ile Glu Met Ser Thr Ser Phe Lys Met Phe
 225 230 235 240
 Leu Asp Asn Trp Asn Ile Gln Thr Ala Leu Trp Leu Lys Arg Val Cys
 245 250 255
 Tyr Glu Arg Thr Ser Phe Ser Pro Thr Ile Gln Thr Phe Ile Leu Ser
 260 265 270
 Ala Ile Trp His Gly Val Tyr Pro Gly Tyr Tyr Leu Thr Phe Leu Thr
 275 280 285
 Gly Val Leu Met Thr Leu Ala Ala Arg Ala Met Arg Asn Asn Phe Arg
 290 295 300
 His Tyr Phe Ile Glu Pro Ser Gln Leu Lys Leu Phe Tyr Asp Val Ile
 305 310 315 320
 Thr Trp Ile Val Thr Gln Val Ala Ile Ser Tyr Thr Val Val Pro Phe
 325 330 335
 Val Leu Leu Ser Ile Lys Pro Ser Leu Thr Phe Tyr Ser Ser Trp Tyr
 340 345 350
 Tyr Cys Leu His Ile Leu Gly Ile Leu Val Leu Leu Leu Leu Pro Val
 355 360 365

294

Lys Lys Thr Gln Arg Arg Lys Asn Thr His Glu Asn Ile Gln Leu Ser
 370 375 380
 Gln Ser Lys Lys Phe Asp Glu Gly Glu Asn Ser Leu Gly Gln Asn Ser
 385 390 395 400
 Phe Ser Thr Thr Asn Asn Val Cys Asn Gln Asn Gln Glu Ile Ala Ser
 405 410 415
 Arg His Ser Ser Leu Lys Gln
 420

<210> 209
 <211> 1413
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1413)

<400> 209

atg tct aga ctg gga gcc ctg ggt ggt gcc cgt gcc ggg ctg gga ctg	48
Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu	
1 5 10 15	
ttg ctg ggt acc gcc gcc ggc ctt gga ttc ctg tgc ctc ctt tac agc	96
Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser	
20 25 30	
cag cga tgg aaa cgg acc cag cgt cat ggc cgc agc cag agc ctg ccc	144
Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro	
35 40 45	
aac tcc ctg gac tat acg cag act tca gat ccc gga cgc cac gtg atg	192
Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met	
50 55 60	
ctc ctg cgg gct gtc cca ggt ggg gct gga gat gcc tca gtg ctg ccc	240
Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro	
65 70 75 80	
agc ctt cca cgg gaa gga cag gag aag gtg ctg gac cgc ctg gac ttt	288
Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe	
85 90 95	
gtg ctg acc agc ctt gtg gcg ctg cgg cgg gag gtg gag gag ctg aga	336

295

Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg	
100 105 110	
agc agc ctg cga ggg ctt gcg ggg gag att gtt ggg gag gtc cga tgc	384
Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys	
115 120 125	
cac atg gaa gag aac cag aga gtg gct cgg cgg cga agg ttt ccg ttt	432
His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe	
130 135 140	
gtc cgg gag agg agt gac tcc act ggc tcc agc tct gtc tac ttc acg	480
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr	
145 150 155 160	
gcc tcc tcg gga gcc acg ttc aca gat gct gag agt gaa ggg ggt tac	528
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr	
165 170 175	
aca aca gcc aat gcg gag tct gac aat gag cgg gac tct gac aaa gaa	576
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu	
180 185 190	
agt gag gac ggg gaa gat gaa gtg agc tgt gag act gtg aag atg ggg	624
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly	
195 200 205	
aga aag gat tct ctt gac ttg gag gaa gag gca gct tca ggt gcc tcc	672
Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser	
210 215 220	
agt gcc ctg gag gct gga ggt tcc tca ggc ttg gag gat gtg ctg ccc	720
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro	
225 230 235 240	
ctc ctg cag cag gcc gac gag ctg cac agg ggt gat gag caa ggc aag	768
Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys	
245 250 255	
cgg gag ggc ttc cag ctg ctg ctc aac aac aag ctg gtg tat gga agc	816
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser	
260 265 270	
cgg cag gac ttt ctc tgg cgc ctg gcc cga gcc tac agt gac atg tgt	864

296

Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys	
275 280 285	
gag ctc act gag gag gtg agc gag aag aag tca tat gcc cta gat gga	912
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly	
290 295 300	
aaa gaa gaa gca gag gct gct ctg gag aag ggg gat gag agt gct gac	960
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp	
305 310 315 320	
tgt cac ctg tgg tat gcg gtg ctt tgt ggt cag ctg gct gag cat gag	1008
Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu	
325 330 335	
agc atc cag agg cgc atc cag agt ggc ttt agc ttc aag gag cat gtg	1056
Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val	
340 345 350	
gac aaa gcc att gct ctc cag cca gaa aac ccc atg gct cac ttt ctt	1104
Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu	
355 360 365	
ctt ggc agg tgg tgc tat cag gtc tct cac ctg agc tgg cta gaa aaa	1152
Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys	
370 375 380	
aaa act gct aca gcc ttg ctt gaa agc cct ctc agt gcc act gtg gaa	1200
Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu	
385 390 395 400	
gat gcc ctc cag agc ttc cta aag gct gaa gaa cta cag cca gga ttt	1248
Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe	
405 410 415	
tcc aaa gca gga agg gta tat att tcc aag tgc tac aga gaa cta ggg	1296
Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly	
420 425 430	
aaa aac tct gaa gct aga tgg tgg atg aag ttg gcc ctg gag ctg cca	1344
Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro	
435 440 445	
gat gtc acg aag gag gat ttg gct atc cag aag gac ctg gaa gaa ctg	1392

297

Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu
 450 455 460

gaa gtc att tta cga gac taa
 Glu Val Ile Leu Arg Asp *
 465 470

1413

<210> 210
 <211> 470
 <212> PRT
 <213> Homo sapiens

<400> 210

Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu
 1 5 10 15
 Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser
 20 25 30
 Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro
 35 40 45
 Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met
 50 55 60
 Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro
 65 70 75 80
 Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe
 85 90 95
 Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg
 100 105 110
 Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys
 115 120 125
 His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe
 130 135 140
 Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr
 145 150 155 160
 Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr
 165 170 175
 Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu
 180 185 190
 Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly
 195 200 205
 Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser
 210 215 220
 Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro
 225 230 235 240

298

[illegible]

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<210> 211
<211> 1137
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(1137)

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 Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
 1 5 10 15

299

ttc tgc tac gtc ttt att gcc tca ggg cta atc atc aac acc att cag Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln 20 25 30	96
ctc ttc act ctc ctc ctc tgg ccc att aac aag cag ctc ttc cgg aag Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys 35 40 45	144
atc aac tgc aga ctg tcc tat tgc atc tca agc cag ctg gtg atg ctg Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu 50 55 60	192
ctg gag tgg tgg tgc ggc acg gaa tgc acc atc ttc acg gac ccg cgc Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg 65 70 75 80	240
gcc tac ctc aag tat ggg aag gaa aat gcc atc gtg gtt ctc aac cac Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His 85 90 95	288
aag ttt gaa att gac ttt ctg tgt ggc tgg agc ctg tcc gaa cgc ttt Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe 100 105 110	336
ggg ctg tta ggg ggc tcc aag gtc ctg gcc aag aaa gag ctg gcc tat Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu Ala Tyr 115 120 125	384
gtc cca att atc ggc tgg atg tgg tac ttc acc gag atg gtc ttc tgt Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met Val Phe Cys 130 135 140	432
tcg cgc aag tgg gag cag gat cgc aag acg gtt gcc acc agt ttg cag Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala Thr Ser Leu Gln 145 150 155 160	480
cac ctc cgg gac tac ccc gag aag tat ttt ttc ctg att cac tgt gag His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu 165 170 175	528
ggc aca cgg ttc acg gag aag aag cat gag atc agc atg cag gtg gcc Gly Thr Arg Phe Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala 180 185 190	576

300

cgg gcc aag ggg ctg cct cgc ctc aag cat cac ctg ttg cca cga acc	624
Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr	
195 200 205	
aag ggc ttc gcc atc acc gtg agg agc ttg aga aat gta gtt tca gct	672
Lys Gly Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala	
210 215 220	
gta tat gac tgt aca ctc aat ttc aga aat aat gaa aat cca aca ctg	720
Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu	
225 230 235 240	
ctg gga gtc cta aac gga aag aaa tac cat gca gat ttg tat gtt agg	768
Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg	
245 250 255	
agg atc cca ctg gaa gac atc cct gaa gac gat gac gag tgc tcg gcc	816
Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala	
260 265 270	
tgg ctg cac aag ctc tac cag gag aag gat gcc ttt cag gag gag tac	864
Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr	
275 280 285	
tac agg acg ggc acc ttc cca gag acg ccc atg gtg ccc ccc cgg cgg	912
Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg	
290 295 300	
ccc tgg acc ctc gtg aac tgg ctg ttt tgg gcc tcg ctg gtg ctc tac	960
Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr	
305 310 315 320	
cct ttc ttc cag ttc ctg gtc agc atg atc agg agc ggg tct tcc ctg	1008
Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu	
325 330 335	
acg ctg gcc agc ttc atc ctc gtc ttc ttt gtg gcc tct gtg gga gtt	1056
Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val	
340 345 350	
cga tgg atg att ggt gtg acg gaa att gac aag ggc tct gcc tac ggc	1104
Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly	
355 360 365	

301

aac tct gac agc aag cag aaa ctg aat gac tga
 Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp *
 370 375

1137

<210> 212
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 212
 Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
 1 5 10 15
 Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln
 20 25 30
 Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys
 35 40 45
 Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu
 50 55 60
 Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg
 65 70 75 80
 Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His
 85 90 95
 Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe
 100 105 110
 Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu Ala Tyr
 115 120 125
 Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met Val Phe Cys
 130 135 140
 Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala Thr Ser Leu Gln
 145 150 155 160
 His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu
 165 170 175
 Gly Thr Arg Phe Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala
 180 185 190
 Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr
 195 200 205
 Lys Gly Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala
 210 215 220
 Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu
 225 230 235 240
 Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg
 245 250 255

302

Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala
 260 265 270
 Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr
 275 280 285
 Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg
 290 295 300
 Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr
 305 310 315 320
 Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu
 325 330 335
 Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val
 340 345 350
 Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly
 355 360 365
 Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp
 370 375

<210> 213

<211> 495

<212> DNA

<213> Homo sapiens

<220> ..

<221> CDS

<222> (1)...(495)

<400> 213

atg tcg gtg aac atg gac gag ctg cgg cac cag gtc atg atc aac cag	48
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1 5 10 15	
ttc gtg ctg gcc gcg ggc tgc gcg gcc gac cag gcg aag cag ttg ctg	96
Phe Val Leu Ala Ala Gly Cys Ala Ala Asp Gln Ala Lys Gln Leu Leu	
20 25 30	
cag gcg gcc cac tgg cag ttc gag acc gcg ctg agc acg ttc ttc caa	144
Gln Ala Ala His Trp Gln Phe Glu Thr Ala Leu Ser Thr Phe Phe Gln	
35 40 45	
gaa acc aac att ccc aac agc cac cac cac cag atg atg tgc act	192
Glu Thr Asn Ile Pro Asn Ser His His His His Gln Met Met Cys Thr	
50 55 60	
ccc agc aac acc cct gcc acg ccg ccc aac ttc ccc gat gcg ctg gcc	240

303

Pro Ser Asn Thr Pro Ala Thr Pro Pro Asn Phe Pro Asp Ala Leu Ala
 65 70 75 80
 atg ttc tcc aag ctc cgc gcc tcc gag ggc ctg cag agc agc aac agc 288
 Met Phe Ser Lys Leu Arg Ala Ser Glu Gly Leu Gln Ser Ser Asn Ser
 85 90 95
 ccc atg aca gcc gca gcc tgc tcc cca cct gca aac ttc agc ccc ttc 336
 Pro Met Thr Ala Ala Ala Cys Ser Pro Pro Ala Asn Phe Ser Pro Phe
 100 105 110
 tgg gcc tcg tcc ccg ccc agc cac cag gcg ccc tgg atc ccg ccc tcc 384
 Trp Ala Ser Ser Pro Pro Ser His Gln Ala Pro Trp Ile Pro Pro Ser
 115 120 125
 tcc ccc acc acc ttc cac cac ctc cac cgc cca cag ccc acg tgg ccc 432
 Ser Pro Thr Thr Phe His His Leu His Arg Pro Gln Pro Thr Trp Pro
 130 135 140
 cca gga gca cag cag ggg ggc gcc cag cag aaa gcc atg gcg gcc atg 480
 Pro Gly Ala Gln Gln Gly Gly Ala Gln Gln Lys Ala Met Ala Ala Met
 145 150 155 160
 gac ggc cag aga tga 495
 Asp Gly Gln Arg *

<210> 214

<211> 164

<212> PRT

<213> Homo sapiens

<400> 214

Met Ser Val Asn Met Asp Glu Leu Arg His Gln Val Met Ile Asn Gln
 1 5 10 15
 Phe Val Leu Ala Ala Gly Cys Ala Ala Asp Gln Ala Lys Gln Leu Leu
 20 25 30
 Gln Ala Ala His Trp Gln Phe Glu Thr Ala Leu Ser Thr Phe Phe Gln
 35 40 45
 Glu Thr Asn Ile Pro Asn Ser His His His His Gln Met Met Cys Thr
 50 55 60
 Pro Ser Asn Thr Pro Ala Thr Pro Pro Asn Phe Pro Asp Ala Leu Ala
 65 70 75 80

304

Met Phe Ser Lys Leu Arg Ala Ser Glu Gly Leu Gln Ser Ser Asn Ser
 85 90 95
 Pro Met Thr Ala Ala Ala Cys Ser Pro Pro Ala Asn Phe Ser Pro Phe
 100 105 110
 Trp Ala Ser Ser Pro Pro Ser His Gln Ala Pro Trp Ile Pro Pro Ser
 115 120 125
 Ser Pro Thr Thr Phe His His Leu His Arg Pro Gln Pro Thr Trp Pro
 130 135 140
 Pro Gly Ala Gln Gln Gly Gly Ala Gln Gln Lys Ala Met Ala Ala Met
 145 150 155 160
 Asp Gly Gln Arg

<210> 215
 <211> 3105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(3105)

<400> 215
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 Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser Gly Gln
 1 5 10 15
 gcg gaa ggt aaa aag atc acc gat ctg cgg gtc atc gat ctg aag tcc 96
 Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu Lys Ser
 20 25 30
 gag ctg aag cgg cgg aac tta gac atc acc gga gtc aag acc gtg ctc 144
 Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr Val Leu
 35 40 45
 atc tcc cga ctc aag cag gct att gaa gag gaa gga ggc gat cca gat 192
 Ile Ser Arg Leu Lys Gln Ala Ile Glu Glu Glu Gly Gly Asp Pro Asp
 50 55 60
 aat att gaa tta act gtt tca act gat act cca aac aag aaa cca act 240
 Asn Ile Glu Leu Thr Val Ser Thr Asp Thr Pro Asn Lys Lys Pro Thr
 65 70 75 80
 aaa ggc aaa ggt aaa aaa cat gaa gca gat gag ttg agt gga gat gct 288

305

Lys Gly Lys Gly Lys Lys His Glu Ala Asp Glu Leu Ser Gly Asp Ala	
85 90 95	
tct gtg gaa gat gat gct ttt atc aag gac tgt gaa ttg gag aat caa	336
Ser Val Glu Asp Asp Ala Phe Ile Lys Asp Cys Glu Leu Glu Asn Gln	
100 105 110	
gag gca cat gag caa gat gga aat gat gaa cta aag gac tct gaa gaa	384
Glu Ala His Glu Gln Asp Gly Asn Asp Glu Leu Lys Asp Ser Glu Glu	
115 120 125	
ttt ggt gaa aat gaa gaa gaa aat gtg cat tcc aag gag tta ctc tct	432
Phe Gly Glu Asn Glu Glu Glu Asn Val His Ser Lys Glu Leu Leu Ser	
130 135 140	
gca gaa gaa aac aag aga gct cat gaa tta ata gag gca gaa gga ata	480
Ala Glu Glu Asn Lys Arg Ala His Glu Leu Ile Glu Ala Glu Gly Ile	
145 150 155 160	
gaa gat ata gaa aaa gag gac atc gaa agt cag gaa att gaa gct caa	528
Glu Asp Ile Glu Lys Glu Asp Ile Glu Ser Gln Glu Ile Glu Ala Gln	
165 170 175	
gaa ggt gaa gat gat acc ttt cta aca gcc caa gat ggt gag gaa gaa	576
Glu Gly Glu Asp Asp Thr Phe Leu Thr Ala Gln Asp Gly Glu Glu Glu	
180 185 190	
gaa aat gag aaa gat ata gca ggt tct ggt gat ggt aca caa gaa gta	624
Glu Asn Glu Lys Asp Ile Ala Gly Ser Gly Asp Gly Thr Gln Glu Val	
195 200 205	
tct aaa cct ctt cct tca gaa ggg agc cta gct gag gct gat cac aca	672
Ser Lys Pro Leu Pro Ser Glu Gly Ser Leu Ala Glu Ala Asp His Thr	
210 215 220	
gct cat gaa gag atg gaa gct cat acg act gtg aaa gaa gct gag gat	720
Ala His Glu Glu Met Glu Ala His Thr Thr Val Lys Glu Ala Glu Asp	
225 230 235 240	
gac aac atc tcg gtc aca atc cag gct gaa gat gcc atc act ctg gat	768
Asp Asn Ile Ser Val Thr Ile Gln Ala Glu Asp Ala Ile Thr Leu Asp	
245 250 255	
ttt gat ggt gat gac ctc cta gaa aca ggt aaa aat gtg aaa att aca	816

306

Phe	Asp	Gly	Asp	Asp	Leu	Leu	Glu	Thr	Gly	Lys	Asn	Val	Lys	Ile	Thr		
			260					265					270				
gat	tct	gaa	gca	agt	aag	cca	aaa	gat	ggg	cag	gac	gcc	att	gca	cag	864	
Asp	Ser	Glu	Ala	Ser	Lys	Pro	Lys	Asp	Gly	Gln	Asp	Ala	Ile	Ala	Gln		
		275					280				285						
agc	ccg	gag	aag	gaa	agc	aag	gat	tat	gag	atg	aat	gcg	aac	cat	aaa	912	
Ser	Pro	Glu	Lys	Glu	Ser	Lys	Asp	Tyr	Glu	Met	Asn	Ala	Asn	His	Lys		
	290					295				300							
gat	ggt	aag	aag	gaa	gac	tgc	gtg	aag	ggt	gac	cct	gtc	gag	aag	gaa	960	
Asp	Gly	Lys	Lys	Glu	Asp	Cys	Val	Lys	Gly	Asp	Pro	Val	Glu	Lys	Glu		
305					310				315				320				
gcc	aga	gaa	agt	tct	aag	aaa	gca	gaa	tct	gga	gac	aaa	gaa	aag	gat	1008	
Ala	Arg	Glu	Ser	Ser	Lys	Lys	Ala	Glu	Ser	Gly	Asp	Lys	Glu	Lys	Asp		
			325					330				335					
act	ttg	aag	aaa	ggg	ccc	tcg	tct	act	ggg	gcc	tct	ggt	caa	gca	aag	1056	
Thr	Leu	Lys	Lys	Gly	Pro	Ser	Ser	Thr	Gly	Ala	Ser	Gly	Gln	Ala	Lys		
		340					345					350					
agc	tct	tca	aag	gaa	tct	aaa	gac	agc	aag	aca	tca	tct	aaa	gat	gac	1104	
Ser	Ser	Ser	Lys	Glu	Ser	Lys	Asp	Ser	Lys	Thr	Ser	Ser	Lys	Asp	Asp		
	355					360					365						
aaa	gga	agt	aca	agt	agt	act	agt	ggt	agc	agt	gga	agc	tca	act	aaa	1152	
Lys	Gly	Ser	Thr	Ser	Ser	Thr	Ser	Gly	Ser	Ser	Gly	Ser	Ser	Thr	Lys		
	370					375					380						
aat	atc	tgg	gtt	agt	gga	ctt	tca	tct	aat	acc	aaa	gct	gct	gat	ttg	1200	
Asn	Ile	Trp	Val	Ser	Gly	Leu	Ser	Ser	Asn	Thr	Lys	Ala	Ala	Asp	Leu		
385					390				395					400			
aag	aac	ctc	ttt	ggc	aaa	tat	gga	aag	gtt	ctg	agt	gca	aaa	gta	gtt	1248	
Lys	Asn	Leu	Phe	Gly	Lys	Tyr	Gly	Lys	Val	Leu	Ser	Ala	Lys	Val	Val		
		405					410					415					
aca	aat	gct	cga	agt	cct	ggg	gca	aaa	tgc	tat	ggc	att	gta	act	atg	1296	
Thr	Asn	Ala	Arg	Ser	Pro	Gly	Ala	Lys	Cys	Tyr	Gly	Ile	Val	Thr	Met		
		420				425					430						
tct	tca	agc	aca	gag	gtg	tcc	agg	tgt	att	gca	cat	ctt	cat	cgc	act	1344	

307

Ser	Ser	Ser	Thr	Glu	Val	Ser	Arg	Cys	Ile	Ala	His	Leu	His	Arg	Thr		
			435				440					445					
gag ctg cat gga cag ctg att tct gtt gaa aaa gta aaa ggt gat ccc 1392																	
Glu	Leu	His	Gly	Gln	Leu	Ile	Ser	Val	Glu	Lys	Val	Lys	Gly	Asp	Pro		
			450			455					460						
tct aag aaa gaa atg aag aaa gaa aat gat gaa aag agt agt tca aga 1440																	
Ser	Lys	Lys	Glu	Met	Lys	Lys	Glu	Asn	Asp	Glu	Lys	Ser	Ser	Ser	Arg		
			465		470				475					480			
agt tct gga gat aaa aaa aat acg agt gat aga agt agc aag aca caa 1488																	
Ser	Ser	Gly	Asp	Lys	Lys	Asn	Thr	Ser	Asp	Arg	Ser	Ser	Lys	Thr	Gln		
			485			490							495				
gcc tct gtc aaa aaa gaa gag aaa aga tcg tct gag aaa tct gaa aaa 1536																	
Ala	Ser	Val	Lys	Lys	Glu	Glu	Lys	Arg	Ser	Ser	Glu	Lys	Ser	Glu	Lys		
			500				505					510					
aaa gaa agc aag gat act aag aaa ata gaa ggt aaa gat gag aag aat 1584																	
Lys	Glu	Ser	Lys	Asp	Thr	Lys	Lys	Ile	Glu	Gly	Lys	Asp	Glu	Lys	Asn		
			515			520					525						
gat aat gga gca agt ggc caa aca tca gaa tcg att aaa aaa agt gaa 1632																	
Asp	Asn	Gly	Ala	Ser	Gly	Gln	Thr	Ser	Glu	Ser	Ile	Lys	Lys	Ser	Glu		
			530			535					540						
gaa aag aag cga ata agt tcc aag agt cca gga cat atg gta ata cta 1680																	
Glu	Lys	Lys	Arg	Ile	Ser	Ser	Lys	Ser	Pro	Gly	His	Met	Val	Ile	Leu		
			545		550				555				560				
gac caa act aaa gga gat cat tgt aga cca tca aga aga gga aga tat 1728																	
Asp	Gln	Thr	Lys	Gly	Asp	His	Cys	Arg	Pro	Ser	Arg	Arg	Gly	Arg	Tyr		
			565				570						575				
gag aaa att cat gga aga agt aag gaa aag gag aga gct agt cta gat 1776																	
Glu	Lys	Ile	His	Gly	Arg	Ser	Lys	Glu	Lys	Glu	Arg	Ala	Ser	Leu	Asp		
			580				585					590					
aaa aaa aga gat aaa gac tac aga agg aaa gag atc ttg cct ttt gaa 1824																	
Lys	Lys	Arg	Asp	Lys	Asp	Tyr	Arg	Arg	Lys	Glu	Ile	Leu	Pro	Phe	Glu		
			595			600					605						
aag atg aag gaa caa agg ttg aga gaa cat tta gtt cgt ttt gaa agg 1872																	

308

Lys Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg	
610 615 620	
ctg cga cga gca atg gaa ctt cga aga cga aga gag att gca gag aga	1920
Leu Arg Arg Ala Met Glu Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg	
625 630 635 640	
gag cgt cga gag cga gaa cgc att aga ata att cgt gaa cgg gaa gaa	1968
Glu Arg Arg Glu Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu	
645 650 655	
cgg gaa cgc tta cag aga gag aga gag cgc cta gaa att gaa agg caa	2016
Arg Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln	
660 665 670	
aaa cta gag aga gag aga atg gaa cgc gaa cgc ttg gaa agg gaa cgc	2064
Lys Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg	
675 680 685	
att cgt att gaa cag gaa cgt cgt aag gaa gct gaa cgg att gct cga	2112
Ile Arg Ile Glu Gln Glu Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg	
690 695 700	
gaa aga gag gaa ctc aga agg caa caa cag cag ctt cgt tat gaa caa	2160
Glu Arg Glu Glu Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln	
705 710 715 720	
gaa aaa agg aat tcc ttg aaa cgc cca cgt gat gta gat cat agg cga	2208
Glu Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg	
725 730 735	
gat gat cct tac tgg agc gag aat aaa aag ttg tct cta gat aca gat	2256
Asp Asp Pro Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp	
740 745 750	
gca cga ttt ggc cat gga tcc gac tac tct cgc caa cag aac aga ttt	2304
Ala Arg Phe Gly His Gly Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe	
755 760 765	
aat gac ttt gat cac cga gag agg ggc agg ttt cct gag agt tca gca	2352
Asn Asp Phe Asp His Arg Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala	
770 775 780	
gta cag tct tca tct ttt gaa agg cgg gat cgc ttt gtt ggt caa agt	2400

309

Val Gln Ser Ser Ser Phe Glu Arg Arg Asp Arg Phe Val Gly Gln Ser	
785 790 795 800	
gag ggg aaa aaa gca cga cct act gca cga agg gaa gat cca agc ttc	2448
Glu Gly Lys Lys Ala Arg Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe	
805 810 815	
gaa aga tat ccc aaa aat ttc agt gac tcc aga aga aat gag cct cca	2496
Glu Arg Tyr Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro	
820 825 830	
cca cca aga aat gaa ctt aga gaa tca gac agg cga gaa gta cga ggg	2544
Pro Pro Arg Asn Glu Leu Arg Glu Ser Asp Arg Arg Glu Val Arg Gly	
835 840 845	
gag cga gac gaa agg aga acg gtg att att cat gac agg cct gat atc	2592
Glu Arg Asp Glu Arg Arg Thr Val Ile Ile His Asp Arg Pro Asp Ile	
850 855 860	
act cat cct aga cat cct cga gag gca ggg ccc aat cct tcc aga ccc	2640
Thr His Pro Arg His Pro Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro	
865 870 875 880	
acc agc tgg aaa agt gaa gga agc atg tcc act gac aaa cgg gaa aca	2688
Thr Ser Trp Lys Ser Glu Gly Ser Met Ser Thr Asp Lys Arg Glu Thr	
885 890 895	
aga gtt gaa agg cca gaa cga tct ggg aga gaa gta tca ggg cac agt	2736
Arg Val Glu Arg Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His Ser	
900 905 910	
gtg aga ggc gct ccc cct ggg aat cgt agc agc gct tcg ggg tac ggg	2784
Val Arg Gly Ala Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly	
915 920 925	
agc aga gag gga gac aga gga gtc atc aca gac cga gga ggt gga tca	2832
Ser Arg Glu Gly Asp Arg Gly Val Ile Thr Asp Arg Gly Gly Gly Ser	
930 935 940	
cag cac tat cct gag gag cga cat gtg gtt gaa cgc cat gga cgg gac	2880
Gln His Tyr Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp	
945 950 955 960	
aca agc gga cca agg aaa gag tgg cat ggt cca ccc tct caa ggg cct	2928

310

Thr	Ser	Gly	Pro	Arg	Lys	Glu	Trp	His	Gly	Pro	Pro	Ser	Gln	Gly	Pro		
				965					970					975			
agc	tat	cat	gat	acg	agg	cga	atg	ggg	gac	ggc	cgg	gca	gga	gca	ggc		2976
Ser	Tyr	His	Asp	Thr	Arg	Arg	Met	Gly	Asp	Gly	Arg	Ala	Gly	Ala	Gly		
			980					985					990				
atg	ata	acc	caa	cat	tca	agt	aac	gca	tcc	cca	att	aat	aga	att	gta		3024
Met	Ile	Thr	Gln	His	Ser	Ser	Asn	Ala	Ser	Pro	Ile	Asn	Arg	Ile	Val		
			995					1000					1005				
caa	atc	agt	ggc	aat	tcc	atg	cca	aga	gga	agt	ggc	tcc	gga	ttt	aag		3072
Gln	Ile	Ser	Gly	Asn	Ser	Met	Pro	Arg	Gly	Ser	Gly	Ser	Gly	Phe	Lys		
			1010					1015					1020				
cca	ttt	aag	ggg	gga	cct	ccg	cga	cga	ttc	tga							3105
Pro	Phe	Lys	Gly	Gly	Pro	Pro	Arg	Arg	Phe	*							
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<210> 216

<211> 1034

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ala	Ala	Ala	Thr	Gly	Ala	Val	Ala	Ala	Ser	Ala	Ala	Ser	Gly	Gln		
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Ala	Glu	Gly	Lys	Lys	Ile	Thr	Asp	Leu	Arg	Val	Ile	Asp	Leu	Lys	Ser		
			20					25					30				
Glu	Leu	Lys	Arg	Arg	Asn	Leu	Asp	Ile	Thr	Gly	Val	Lys	Thr	Val	Leu		
			35				40						45				
Ile	Ser	Arg	Leu	Lys	Gln	Ala	Ile	Glu	Glu	Glu	Gly	Gly	Asp	Pro	Asp		
			50			55					60						
Asn	Ile	Glu	Leu	Thr	Val	Ser	Thr	Asp	Thr	Pro	Asn	Lys	Lys	Pro	Thr		
			65			70				75				80			
Lys	Gly	Lys	Gly	Lys	Lys	His	Glu	Ala	Asp	Glu	Leu	Ser	Gly	Asp	Ala		
				85					90					95			
Ser	Val	Glu	Asp	Asp	Ala	Phe	Ile	Lys	Asp	Cys	Glu	Leu	Glu	Asn	Gln		
			100					105						110			
Glu	Ala	His	Glu	Gln	Asp	Gly	Asn	Asp	Glu	Leu	Lys	Asp	Ser	Glu	Glu		
			115				120							125			
Phe	Gly	Glu	Asn	Glu	Glu	Glu	Asn	Val	His	Ser	Lys	Glu	Leu	Leu	Ser		
			130				135							140			

311

Ala Glu Glu Asn Lys Arg Ala His Glu Leu Ile Glu Ala Glu Gly Ile
 145 150 155 160
 Glu Asp Ile Glu Lys Glu Asp Ile Glu Ser Gln Glu Ile Glu Ala Gln
 165 170 175
 Glu Gly Glu Asp Asp Thr Phe Leu Thr Ala Gln Asp Gly Glu Glu Glu
 180 185 190
 Glu Asn Glu Lys Asp Ile Ala Gly Ser Gly Asp Gly Thr Gln Glu Val
 195 200 205
 Ser Lys Pro Leu Pro Ser Glu Gly Ser Leu Ala Glu Ala Asp His Thr
 210 215 220
 Ala His Glu Glu Met Glu Ala His Thr Thr Val Lys Glu Ala Glu Asp
 225 230 235 240
 Asp Asn Ile Ser Val Thr Ile Gln Ala Glu Asp Ala Ile Thr Leu Asp
 245 250 255
 Phe Asp Gly Asp Asp Leu Leu Glu Thr Gly Lys Asn Val Lys Ile Thr
 260 265 270
 Asp Ser Glu Ala Ser Lys Pro Lys Asp Gly Gln Asp Ala Ile Ala Gln
 275 280 285
 Ser Pro Glu Lys Glu Ser Lys Asp Tyr Glu Met Asn Ala Asn His Lys
 290 295 300
 Asp Gly Lys Lys Glu Asp Cys Val Lys Gly Asp Pro Val Glu Lys Glu
 305 310 315 320
 Ala Arg Glu Ser Ser Lys Lys Ala Glu Ser Gly Asp Lys Glu Lys Asp
 325 330 335
 Thr Leu Lys Lys Gly Pro Ser Ser Thr Gly Ala Ser Gly Gln Ala Lys
 340 345 350
 Ser Ser Ser Lys Glu Ser Lys Asp Ser Lys Thr Ser Ser Lys Asp Asp
 355 360 365
 Lys Gly Ser Thr Ser Ser Thr Ser Gly Ser Ser Gly Ser Ser Thr Lys
 370 375 380
 Asn Ile Trp Val Ser Gly Leu Ser Ser Asn Thr Lys Ala Ala Asp Leu
 385 390 395 400
 Lys Asn Leu Phe Gly Lys Tyr Gly Lys Val Leu Ser Ala Lys Val Val
 405 410 415
 Thr Asn Ala Arg Ser Pro Gly Ala Lys Cys Tyr Gly Ile Val Thr Met
 420 425 430
 Ser Ser Ser Thr Glu Val Ser Arg Cys Ile Ala His Leu His Arg Thr
 435 440 445
 Glu Leu His Gly Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp Pro
 450 455 460
 Ser Lys Lys Glu Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser Arg
 465 470 475 480
 Ser Ser Gly Asp Lys Lys Asn Thr Ser Asp Arg Ser Ser Lys Thr Gln
 485 490 495

312

Ala Ser Val Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu Lys
 500 505 510
 Lys Glu Ser Lys Asp Thr Lys Lys Ile Glu Gly Lys Asp Glu Lys Asn
 515 520 525
 Asp Asn Gly Ala Ser Gly Gln Thr Ser Glu Ser Ile Lys Lys Ser Glu
 530 535 540
 Glu Lys Lys Arg Ile Ser Ser Lys Ser Pro Gly His Met Val Ile Leu
 545 550 555 560
 Asp Gln Thr Lys Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr
 565 570 575
 Glu Lys Ile His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp
 580 585 590
 Lys Lys Arg Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu
 595 600 605
 Lys Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg
 610 615 620
 Leu Arg Arg Ala Met Glu Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg
 625 630 635 640
 Glu Arg Arg Glu Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu
 645 650 655
 Arg Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln
 660 665 670
 Lys Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg
 675 680 685
 Ile Arg Ile Glu Gln Glu Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg
 690 695 700
 Glu Arg Glu Glu Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln
 705 710 715 720
 Glu Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg
 725 730 735
 Asp Asp Pro Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp
 740 745 750
 Ala Arg Phe Gly His Gly Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe
 755 760 765
 Asn Asp Phe Asp His Arg Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala
 770 775 780
 Val Gln Ser Ser Ser Phe Glu Arg Arg Asp Arg Phe Val Gly Gln Ser
 785 790 795 800
 Glu Gly Lys Lys Ala Arg Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe
 805 810 815
 Glu Arg Tyr Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro
 820 825 830
 Pro Pro Arg Asn Glu Leu Arg Glu Ser Asp Arg Arg Glu Val Arg Gly
 835 840 845

313

Glu Arg Asp Glu Arg Arg Thr Val Ile Ile His Asp Arg Pro Asp Ile
 850 855 860
 Thr His Pro Arg His Pro Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro
 865 870 875 880
 Thr Ser Trp Lys Ser Glu Gly Ser Met Ser Thr Asp Lys Arg Glu Thr
 885 890 895
 Arg Val Glu Arg Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His Ser
 900 905 910
 Val Arg Gly Ala Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly
 915 920 925
 Ser Arg Glu Gly Asp Arg Gly Val Ile Thr Asp Arg Gly Gly Gly Ser
 930 935 940
 Gln His Tyr Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp
 945 950 955 960
 Thr Ser Gly Pro Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro
 965 970 975
 Ser Tyr His Asp Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly
 980 985 990
 Met Ile Thr Gln His Ser Ser Asn Ala Ser Pro Ile Asn Arg Ile Val
 995 1000 1005
 Gln Ile Ser Gly Asn Ser Met Pro Arg Gly Ser Gly Ser Gly Phe Lys
 1010 1015 1020
 Pro Phe Lys Gly Gly Pro Pro Arg Arg Phe
 1025 1030

<210> 217
 <211> 1428
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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<400> 217
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 Met Pro His Arg Lys Lys Lys Pro Phe Ile Glu Lys Lys Lys Ala Val
 1 5 10 15
 tct ttt cac ttg gtc cac cgg agc caa cga gat cct tta gca gca gat 96
 Ser Phe His Leu Val His Arg Ser Gln Arg Asp Pro Leu Ala Ala Asp
 20 25 30
 gag agt gca ccc cag agg gtt cta ttg ccc aca caa aaa ata gac aat 144

314

Glu Ser Ala Pro Gln Arg Val Leu Leu Pro Thr Gln Lys Ile Asp Asn	
35 40 45	
gaa gaa agg cga gca gaa cag agg aag tat gga gtg ttc ttt gat gac	192
Glu Glu Arg Arg Ala Glu Gln Arg Lys Tyr Gly Val Phe Phe Asp Asp	
50 55 60	
gac tat gac tac ctg cag cac ctg aag gaa cca tct ggg cct tca gag	240
Asp Tyr Asp Tyr Leu Gln His Leu Lys Glu Pro Ser Gly Pro Ser Glu	
65 70 75 80	
ctt att ccc tca agt acc ttc agt gca cac aac agg aga gag gag aaa	288
Leu Ile Pro Ser Ser Thr Phe Ser Ala His Asn Arg Arg Glu Glu Lys	
85 90 95	
gaa gaa acg cta gta att cca agc act gga att aag ttg cct tca tca	336
Glu Glu Thr Leu Val Ile Pro Ser Thr Gly Ile Lys Leu Pro Ser Ser	
100 105 110	
gtg ttt gct tca gag ttt gag gaa gat gtt gga ttg tta aat aaa gca	384
Val Phe Ala Ser Glu Phe Glu Glu Asp Val Gly Leu Leu Asn Lys Ala	
115 120 125	
gct cca gtt tca gga cct cga ctg gat ttt gat cct gac att gtt gca	432
Ala Pro Val Ser Gly Pro Arg Leu Asp Phe Asp Pro Asp Ile Val Ala	
130 135 140	
gct ctt gat gat gat ttt gac ttt gat gat cca gat aat ctg ctt gag	480
Ala Leu Asp Asp Asp Phe Asp Phe Asp Asp Pro Asp Asn Leu Leu Glu	
145 150 155 160	
gat gac ttt att ctt cag gcc aat aag gca aca gga gag gaa gag gga	528
Asp Asp Phe Ile Leu Gln Ala Asn Lys Ala Thr Gly Glu Glu Glu Gly	
165 170 175	
atg gat ata cag aaa tct gag aat gaa gat gac agc gag tgg gaa gat	576
Met Asp Ile Gln Lys Ser Glu Asn Glu Asp Asp Ser Glu Trp Glu Asp	
180 185 190	
gtg gat gat gag aag gga gat agc aat gat gac tat gac tct gca ggc	624
Val Asp Asp Glu Lys Gly Asp Ser Asn Asp Asp Tyr Asp Ser Ala Gly	
195 200 205	
cta ttg tca gat gaa gac tgt atg tct gtg ccc gga aaa act cac aga	672

315

Leu	Leu	Ser	Asp	Glu	Asp	Cys	Met	Ser	Val	Pro	Gly	Lys	Thr	His	Arg	
210						215					220					
gct ata gca gat cac ttg ttc tgg agt gag gaa aca aag agt cgc ttc																720
Ala	Ile	Ala	Asp	His	Leu	Phe	Trp	Ser	Glu	Glu	Thr	Lys	Ser	Arg	Phe	
225					230					235					240	
acg gag tat tcg atg act tcc tca gtc atg agg aga aat gaa cag ctg																768
Thr	Glu	Tyr	Ser	Met	Thr	Ser	Ser	Val	Met	Arg	Arg	Asn	Glu	Gln	Leu	
				245					250					255		
acc cta cat gat gag agg ttt gag aag ttt tat gag caa tat gat gat																816
Thr	Leu	His	Asp	Glu	Arg	Phe	Glu	Lys	Phe	Tyr	Glu	Gln	Tyr	Asp	Asp	
			260					265					270			
gat gaa att gga gct ctg gat aat gca gaa ttg gaa ggt tct att caa																864
Asp	Glu	Ile	Gly	Ala	Leu	Asp	Asn	Ala	Glu	Leu	Glu	Gly	Ser	Ile	Gln	
		275					280					285				
gtg gac agc aat cgc tta cag gaa gtt ttg aat gac tac tat aaa gag																912
Val	Asp	Ser	Asn	Arg	Leu	Gln	Glu	Val	Leu	Asn	Asp	Tyr	Tyr	Lys	Glu	
	290					295					300					
aag gca gag aat tgt gta aaa ttg aat acc ctt gaa ccc ttg gag gat																960
Lys	Ala	Glu	Asn	Cys	Val	Lys	Leu	Asn	Thr	Leu	Glu	Pro	Leu	Glu	Asp	
305					310					315					320	
caa gac ctg cca atg aat gag ctt gat gag tct gag gag gaa gaa atg																1008
Gln	Asp	Leu	Pro	Met	Asn	Glu	Leu	Asp	Glu	Ser	Glu	Glu	Glu	Glu	Met	
				325					330					335		
att act gta gtc ctt gaa gaa gcc aaa gag aag tgg gat tgt gaa tct																1056
Ile	Thr	Val	Val	Leu	Glu	Glu	Ala	Lys	Glu	Lys	Trp	Asp	Cys	Glu	Ser	
				340				345					350			
att tgt agt aca tac tca aat tta tat aac cat cca cag ctt atc aag																1104
Ile	Cys	Ser	Thr	Tyr	Ser	Asn	Leu	Tyr	Asn	His	Pro	Gln	Leu	Ile	Lys	
		355					360					365				
tat caa cca aag ccc aaa caa att cga ata tct tct aaa aca gga ata																1152
Tyr	Gln	Pro	Lys	Pro	Lys	Gln	Ile	Arg	Ile	Ser	Ser	Lys	Thr	Gly	Ile	
	370					375					380					
cct ctc aat gtc tta cca aag aaa gga ctc aca gca aag caa act gaa																1200

316

Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr Ala Lys Gln Thr Glu
 385 390 395 400

aga ata cag atg att aat ggc agt gat ctt cct aaa gta tca act cag 1248
 Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro Lys Val Ser Thr Gln
 405 410 415

cca cgt tct aaa aat gaa agc aaa gaa gat aaa aga gca aga aag caa 1296
 Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys Arg Ala Arg Lys Gln
 420 425 430

gct ata aaa gaa gag cgc aag gaa cga aga gtg gag aag aaa gct aac 1344
 Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val Glu Lys Lys Ala Asn
 435 440 445

aaa tta gca ttt aaa ctg gag aaa aga agg caa gaa aaa gag ctg ctg 1392
 Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln Glu Lys Glu Leu Leu
 450 455 460

aac ttg aag aag aat gtt gag ggt cta aag cta tag 1428
 Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu *
 465 470 475

<210> 218

<211> 475

<212> PRT

<213> Homo sapiens

<400> 218

Met Pro His Arg Lys Lys Lys Pro Phe Ile Glu Lys Lys Lys Ala Val
 1 5 10 15

Ser Phe His Leu Val His Arg Ser Gln Arg Asp Pro Leu Ala Ala Asp
 20 25 30

Glu Ser Ala Pro Gln Arg Val Leu Leu Pro Thr Gln Lys Ile Asp Asn
 35 40 45

Glu Glu Arg Arg Ala Glu Gln Arg Lys Tyr Gly Val Phe Phe Asp Asp
 50 55 60

Asp Tyr Asp Tyr Leu Gln His Leu Lys Glu Pro Ser Gly Pro Ser Glu
 65 70 75 80

Leu Ile Pro Ser Ser Thr Phe Ser Ala His Asn Arg Arg Glu Glu Lys
 85 90 95

Glu Glu Thr Leu Val Ile Pro Ser Thr Gly Ile Lys Leu Pro Ser Ser
 100 105 110

317

Val Phe Ala Ser Glu Phe Glu Glu Asp Val Gly Leu Leu Asn Lys Ala
 115 120 125
 Ala Pro Val Ser Gly Pro Arg Leu Asp Phe Asp Pro Asp Ile Val Ala
 130 135 140
 Ala Leu Asp Asp Asp Phe Asp Phe Asp Asp Pro Asp Asn Leu Leu Glu
 145 150 155 160
 Asp Asp Phe Ile Leu Gln Ala Asn Lys Ala Thr Gly Glu Glu Glu Gly
 165 170 175
 Met Asp Ile Gln Lys Ser Glu Asn Glu Asp Asp Ser Glu Trp Glu Asp
 180 185 190
 Val Asp Asp Glu Lys Gly Asp Ser Asn Asp Asp Tyr Asp Ser Ala Gly
 195 200 205
 Leu Leu Ser Asp Glu Asp Cys Met Ser Val Pro Gly Lys Thr His Arg
 210 215 220
 Ala Ile Ala Asp His Leu Phe Trp Ser Glu Glu Thr Lys Ser Arg Phe
 225 230 235 240
 Thr Glu Tyr Ser Met Thr Ser Ser Val Met Arg Arg Asn Glu Gln Leu
 245 250 255
 Thr Leu His Asp Glu Arg Phe Glu Lys Phe Tyr Glu Gln Tyr Asp Asp
 260 265 270
 Asp Glu Ile Gly Ala Leu Asp Asn Ala Glu Leu Glu Gly Ser Ile Gln
 275 280 285
 Val Asp Ser Asn Arg Leu Gln Glu Val Leu Asn Asp Tyr Tyr Lys Glu
 290 295 300
 Lys Ala Glu Asn Cys Val Lys Leu Asn Thr Leu Glu Pro Leu Glu Asp
 305 310 315 320
 Gln Asp Leu Pro Met Asn Glu Leu Asp Glu Ser Glu Glu Glu Glu Met
 325 330 335
 Ile Thr Val Val Leu Glu Glu Ala Lys Glu Lys Trp Asp Cys Glu Ser
 340 345 350
 Ile Cys Ser Thr Tyr Ser Asn Leu Tyr Asn His Pro Gln Leu Ile Lys
 355 360 365
 Tyr Gln Pro Lys Pro Lys Gln Ile Arg Ile Ser Ser Lys Thr Gly Ile
 370 375 380
 Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr Ala Lys Gln Thr Glu
 385 390 395 400
 Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro Lys Val Ser Thr Gln
 405 410 415
 Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys Arg Ala Arg Lys Gln
 420 425 430
 Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val Glu Lys Lys Ala Asn
 435 440 445
 Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln Glu Lys Glu Leu Leu
 450 455 460

318

Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu
 465 470 475

<210> 219
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(300)

<400> 219
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 Met Ala Phe Ser Ala Cys Phe Gly Gly Ile Ile Phe Asn Ile Leu Val
 1 5 10 15
 ggt gtg ggg ctg ggc tgc ctg ctc cag atc tcc cga agc cac aca gaa 96
 Gly Val Gly Leu Gly Cys Leu Leu Gln Ile Ser Arg Ser His Thr Glu
 20 25 30
 gtg aag ctg gag cca gac gga ctg ctg gtg tgg gtc ctg gca ggc gcc 144
 Val Lys Leu Glu Pro Asp Gly Leu Leu Val Trp Val Leu Ala Gly Ala
 35 40 45
 ctg ggg ctc agc ctc gtc ttc tcc ctg gtc tca gtc cca ttg cag tgc 192
 Leu Gly Leu Ser Leu Val Phe Ser Leu Val Ser Val Pro Leu Gln Cys
 50 55 60
 ttc cag ctc agc aga gtc tat ggc ttc tgc ctg ctc ctc ttc tac ctg 240
 Phe Gln Leu Ser Arg Val Tyr Gly Phe Cys Leu Leu Leu Phe Tyr Leu
 65 70 75 80
 aac ttc ctt gtc gtg gcc ctc ctc act gaa ttt gga gtg att cac ctg 288
 Asn Phe Leu Val Val Ala Leu Leu Thr Glu Phe Gly Val Ile His Leu
 85 90 95
 aaa agc atg tga 300
 Lys Ser Met *

<210> 220
 <211> 99

319

<212> PRT

<213> Homo sapiens

<400> 220

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Met Ala Phe Ser Ala Cys Phe Gly Gly Ile Ile Phe Asn Ile Leu Val
 1      5      10      15
Gly Val Gly Leu Gly Cys Leu Leu Gln Ile Ser Arg Ser His Thr Glu
      20      25      30
Val Lys Leu Glu Pro Asp Gly Leu Leu Val Trp Val Leu Ala Gly Ala
      35      40      45
Leu Gly Leu Ser Leu Val Phe Ser Leu Val Ser Val Pro Leu Gln Cys
      50      55      60
Phe Gln Leu Ser Arg Val Tyr Gly Phe Cys Leu Leu Leu Phe Tyr Leu
      65      70      75      80
Asn Phe Leu Val Val Ala Leu Leu Thr Glu Phe Gly Val Ile His Leu
      85      90      95
Lys Ser Met

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<210> 221

<211> 1113

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1113)

<400> 221

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atg agt gcc tct gcg gcc acc ggg gtc ttc gtg ctg tcc ctc tcg gcc      48
Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
 1      5      10      15

atc ccg gtc acc tat gtc ttc aac cac ctg gcg gcc cag cat gat tcc      96
Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
      20      25      30

tgg act att gta ggg gtt gct gcc ctc atc ctg ttc ctg gta gca ctg      144
Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
      35      40      45

ctg gct cgt gtc ctc gtc aaa aga aaa cca ccc cgg gac cca ctg ttc      192
Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
      50      55      60

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320

tat gtg tat gca gtt ttt gga ttt acc agc gtg gtg aac ctc atc ata	240
Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile	
65 70 75 80	
gga ctg gag caa gat gga atc att gac ggg ttc atg aca cac tac ttg	288
Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu	
85 90 95	
aga gag ggt gaa ccg tat ctg aac acc gca tat ggg cac atg atc tgc	336
Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys	
100 105 110	
tac tgg gat ggc tct gct cat tat ctg atg tac ctg gtg atg gtg gca	384
Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala	
115 120 125	
gcc ata gca tgg gag gaa act tat aga acc att ggc cta tat tgg gtt	432
Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val	
130 135 140	
gga tct att att atg agt gtt gtt gtt ttt gtg cca gga aac att gta	480
Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val	
145 150 155 160	
ggg aag tat gga aca cga att tgc cct gct ttt ttc tta agc ata cca	528
Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro	
165 170 175	
tat act tgt ctt cct gtc tgg gct ggt ttc aga atc tat aat cag cca	576
Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro	
180 185 190	
tca gaa aat tat aat tac ccc tca aag gtt att caa gaa gcc caa gcg	624
Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala	
195 200 205	
aaa gac ctg ctg aga aga cca ttt gat tta atg ttg gtt gtg tgt ctc	672
Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu	
210 215 220	
ctc ctg gca act gga ttt tgc ctg ttc aga ggt ttg att gct ttg gat	720
Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp	
225 230 235 240	

321

tgc cca tct gag ctc tgc cga tta tat acg caa ttt caa gag ccc tat	768
Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr	
245 250 255	
cta aag gat cct gct gct tat cct aaa att cag atg ctg gca tat atg	816
Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met	
260 265 270	
ttc tat tct gtt cct tac ttt gtg act gca ctg tat ggc tta gtg gtt	864
Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val	
275 280 285	
cct gga tgt tcc tgg atg cct gac atc aca ttg ata cat gct gga ggt	912
Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly	
290 295 300	
ctg gct cag gct cag ttt tct cac att ggt gca tct ctt cat gct aga	960
Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg	
305 310 315 320	
act gct tat gtc tac aga gtc cct gaa gaa gcaaaa atc ctt ttt tta	1008
Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu	
325 330 335	
gca tta aac ata gca tat gga gtt ctt cct cag ctc ttg gcc tat cgt	1056
Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg	
340 345 350	
tgt atc tac aaa cca gag ttc ttc ata aaa aca aag gca gaa gaa aaa	1104
Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys	
355 360 365	
gtg gaa taa	1113
Val Glu *	
370	

<210> 222

<211> 370

<212> PRT

<213> Homo sapiens

<400> 222

322

Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
 1 5 10 15
 Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
 20 25 30
 Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
 35 40 45
 Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
 50 55 60
 Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile
 65 70 75 80
 Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu
 85 90 95
 Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys
 100 105 110
 Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala
 115 120 125
 Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val
 130 135 140
 Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val
 145 150 155 160
 Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro
 165 170 175
 Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro
 180 185 190
 Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala
 195 200 205
 Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu
 210 215 220
 Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp
 225 230 235 240
 Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr
 245 250 255
 Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met
 260 265 270
 Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val
 275 280 285
 Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly
 290 295 300
 Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg
 305 310 315 320
 Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu
 325 330 335
 Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg
 340 345 350

323

Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys
 355 360 365
 Val Glu
 370

<210> 223
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(357)

<400> 223

atg gag cgt ctc ggt gtg ctg tgg acg ctg ctg gtg tcc cgc tgg ttc 48
 Met Glu Arg Leu Gly Val Leu Trp Thr Leu Leu Val Ser Arg Trp Phe
 1 5 10 15

atc tgc ctg ttt gtg gac atc ttg ccc gtg gag aca gtg ctt cgg atc 96
 Ile Cys Leu Phe Val Asp Ile Leu Pro Val Glu Thr Val Leu Arg Ile
 20 25 30

tgg gac tgt ttg ttt aac gaa ggc tcg aag att atc ttc cgg gtg gcc 144
 Trp Asp Cys Leu Phe Asn Glu Gly Ser Lys Ile Ile Phe Arg Val Ala
 35 40 45

ctg acc tta att aag cag cac cag gag ttg att ttg gaa gcc acc agc 192
 Leu Thr Leu Ile Lys Gln His Gln Glu Leu Ile Leu Glu Ala Thr Ser
 50 55 60

gtt cca gac att tgc gat aag ttt aag cag ata acc aaa ggg agt ttc 240
 Val Pro Asp Ile Cys Asp Lys Phe Lys Gln Ile Thr Lys Gly Ser Phe
 65 70 75 80

gtg atg gag tgt cac acg ttt atg cag aaa ata ttt tca gaa cct gga 288
 Val Met Glu Cys His Thr Phe Met Gln Lys Ile Phe Ser Glu Pro Gly
 85 90 95

agc tta tcc atg gcc acc gtc gcc aag ctc cgc gag agc tgc agg gcc 336
 Ser Leu Ser Met Ala Thr Val Ala Lys Leu Arg Glu Ser Cys Arg Ala
 100 105 110

cgg ctg ctg gca cag ggg tga 357

324

Arg Leu Leu Ala Gln Gly *
115

<210> 224
<211> 118
<212> PRT
<213> Homo sapiens

<400> 224
Met Glu Arg Leu Gly Val Leu Trp Thr Leu Leu Val Ser Arg Trp Phe
1 5 10 15
Ile Cys Leu Phe Val Asp Ile Leu Pro Val Glu Thr Val Leu Arg Ile
20 25 30
Trp Asp Cys Leu Phe Asn Glu Gly Ser Lys Ile Ile Phe Arg Val Ala
35 40 45
Leu Thr Leu Ile Lys Gln His Gln Glu Leu Ile Leu Glu Ala Thr Ser
50 55 60
Val Pro Asp Ile Cys Asp Lys Phe Lys Gln Ile Thr Lys Gly Ser Phe
65 70 75 80
Val Met Glu Cys His Thr Phe Met Gln Lys Ile Phe Ser Glu Pro Gly
85 90 95
Ser Leu Ser Met Ala Thr Val Ala Lys Leu Arg Glu Ser Cys Arg Ala
100 105 110
Arg Leu Leu Ala Gln Gly
115

<210> 225
<211> 1764
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1764)

<400> 225
atg agg ccg cga ggt ctc ccg ccg ctc ctg gtg gtg ctc ctg ggc tgc 48
Met Arg Pro Arg Gly Leu Pro Pro Leu Leu Val Val Leu Leu Gly Cys
1 5 10 15
tgg gcc tcc gtg agc gcc cag acc gat gcc acc ccg gcg gtg acg aca 96
Trp Ala Ser Val Ser Ala Gln Thr Asp Ala Thr Pro Ala Val Thr Thr
20 25 30

325

gag ggc ctc aac tcc acc gag gca gcc ctg gcc acc ttc gga act ttc	144
Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu Ala Thr Phe Gly Thr Phe	
35 40 45	
ccg tcg acc agg ccc ccc ggg act ccc agg gct cca ggg ccc tcc tcc	192
Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg Ala Pro Gly Pro Ser Ser	
50 55 60	
ggc ccc agg cct acc cca gtc acg gac gtt gct gtt ctc tgt gtc tgt	240
Gly Pro Arg Pro Thr Pro Val Thr Asp Val Ala Val Leu Cys Val Cys	
65 70 75 80	
gac tta tcc cca gca cag tgt gac atc aac tgc tgc tgt gat ccc gac	288
Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn Cys Cys Cys Asp Pro Asp	
85 90 95	
tgc agc tcc gtg gat ttc agt gtc ttt tct gcc tgc tca gtt cca gtt	336
Cys Ser Ser Val Asp Phe Ser Val Phe Ser Ala Cys Ser Val Pro Val	
100 105 110	
gtc acg ggc gac agc cag ttt tgt agt caa aaa gca gtc atc tat tca	384
Val Thr Gly Asp Ser Gln Phe Cys Ser Gln Lys Ala Val Ile Tyr Ser	
115 120 125	
ttg aat ttt aca gca aac cca cct caa aga gta ttt gaa ctt gtt gac	432
Leu Asn Phe Thr Ala Asn Pro Pro Gln Arg Val Phe Glu Leu Val Asp	
130 135 140	
cag att aat cca tct att ttc tgc att cat att aca aac tat aaa cct	480
Gln Ile Asn Pro Ser Ile Phe Cys Ile His Ile Thr Asn Tyr Lys Pro	
145 150 155 160	
gca tta tcc ttt att aat cca gaa gta cct gat gaa aac aat ttt gat	528
Ala Leu Ser Phe Ile Asn Pro Glu Val Pro Asp Glu Asn Asn Phe Asp	
165 170 175	
aca ttg atg aaa aca tct gat ggt ttt aca ttg aat gct gaa tca tat	576
Thr Leu Met Lys Thr Ser Asp Gly Phe Thr Leu Asn Ala Glu Ser Tyr	
180 185 190	
gtt tcc ttc aca acc aaa ctg gat att cct act gct gct aaa tat gag	624
Val Ser Phe Thr Thr Lys Leu Asp Ile Pro Thr Ala Ala Lys Tyr Glu	
195 200 205	

326

tat ggg gtt cct ctg cag act tca gat tcg ttt ctg aga ttt cct tcg Tyr Gly Val Pro Leu Gln Thr Ser Asp Ser Phe Leu Arg Phe Pro Ser 210 215 220	672
tcc ctg aca tca tct ctg tgc act gat aat aac cct gca gcg ttt ctg Ser Leu Thr Ser Ser Leu Cys Thr Asp Asn Asn Pro Ala Ala Phe Leu 225 230 235 240	720
gtg aac cag gct gtt aag tgc acc aga aaa ata aat tta gaa cag tgt Val Asn Gln Ala Val Lys Cys Thr Arg Lys Ile Asn Leu Glu Gln Cys 245 250 255	768
gaa gaa att gaa gcc ctc agc atg gct ttt tac agc agc ccg gaa att Glu Glu Ile Glu Ala Leu Ser Met Ala Phe Tyr Ser Ser Pro Glu Ile 260 265 270	816
ctg agg gta cct gat tca aga aaa aag gtc cct atc act gtt cag tcc Leu Arg Val Pro Asp Ser Arg Lys Lys Val Pro Ile Thr Val Gln Ser 275 280 285	864
atc gtc att cag tct cta aat aaa acg ctc acc cga cgg gag gac act Ile Val Ile Gln Ser Leu Asn Lys Thr Leu Thr Arg Arg Glu Asp Thr 290 295 300	912
gat gtg ctg cag ccg act ctc gtc aac gct gga cac ttt agc ctt tgc Asp Val Leu Gln Pro Thr Leu Val Asn Ala Gly His Phe Ser Leu Cys 305 310 315 320	960
gtg aat gtt gtt ctt gag gta aag tac agc ctc aca tac aca gat gca Val Asn Val Val Leu Glu Val Lys Tyr Ser Leu Thr Tyr Thr Asp Ala 325 330 335	1008
ggt gaa gtc acc aaa gct gat ctc tca ttc gtt ctg ggg aca gtt agc Gly Glu Val Thr Lys Ala Asp Leu Ser Phe Val Leu Gly Thr Val Ser 340 345 350	1056
agc gta gtg gtc cca ctg cag caa aag ttt gaa att cat ttt ctt cag Ser Val Val Val Pro Leu Gln Gln Lys Phe Glu Ile His Phe Leu Gln 355 360 365	1104
gaa aat acc cag cca gtc cct ctc agt gga aac cct ggt tat gtc gtg Glu Asn Thr Gln Pro Val Pro Leu Ser Gly Asn Pro Gly Tyr Val Val 370 375 380	1152

327

ggg ctc cca tta gct gct gga ttc cag cct cat aag ggg tct ggg att Gly Leu Pro Leu Ala Ala Gly Phe Gln Pro His Lys Gly Ser Gly Ile 385 390 395 400	1200
att cag acc aca aat aga tat gga cag ctt act att ctt cat agc aca Ile Gln Thr Thr Asn Arg Tyr Gly Gln Leu Thr Ile Leu His Ser Thr 405 410 415	1248
act gag caa gac tgc tta gca ctg gag ggg gtc cgg acc cca gta tta Thr Glu Gln Asp Cys Leu Ala Leu Glu Gly Val Arg Thr Pro Val Leu 420 425 430	1296
ttt ggt tac act atg caa tct ggc tgt aaa cta aga ctg act gga gct Phe Gly Tyr Thr Met Gln Ser Gly Cys Lys Leu Arg Leu Thr Gly Ala 435 440 445	1344
ctc ccg tgt cag ctc gta gca cag aag gtg aag agc ctg ctg tgg ggc Leu Pro Cys Gln Leu Val Ala Gln Lys Val Lys Ser Leu Leu Trp Gly 450 455 460	1392
cag ggc ttc cca gat tac gtg gcc cct ttt gga aat tcc cag gcc cag Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe Gly Asn Ser Gln Ala Gln 465 470 475 480	1440
gac atg ctg gac tgg gtg ccc atc cac ttc atc acc cag tca ttc aac Asp Met Leu Asp Trp Val Pro Ile His Phe Ile Thr Gln Ser Phe Asn 485 490 495	1488
agg aag gat tcc tgc cag ctc cca ggg gct ttg gtt ata gaa gtg aag Arg Lys Asp Ser Cys Gln Leu Pro Gly Ala Leu Val Ile Glu Val Lys 500 505 510	1536
tgg act aaa tac gga tcc ctg ctg aat cca cag gcc aaa ata gtc aat Trp Thr Lys Tyr Gly Ser Leu Leu Asn Pro Gln Ala Lys Ile Val Asn 515 520 525	1584
gta act gca aat cta att tca tcc tcc ttt cct gag gcc aac tca gga Val Thr Ala Asn Leu Ile Ser Ser Ser Phe Pro Glu Ala Asn Ser Gly 530 535 540	1632
aat gaa agg acg att ctt att tcc act gcg gtt act ttt gtg gat gtg Asn Glu Arg Thr Ile Leu Ile Ser Thr Ala Val Thr Phe Val Asp Val 545 550 555 560	1680

328

tct gca cct gca gag gca ggc ttc aga gct cca cca gcc atc aat gcc 1728
 Ser Ala Pro Ala Glu Ala Gly Phe Arg Ala Pro Pro Ala Ile Asn Ala
 565 570 575

agg ctg ccc ttt aac ttc ttc ttc ccg ttt gtt tga 1764
 Arg Leu Pro Phe Asn Phe Phe Phe Pro Phe Val *
 580 585

<210> 226
 <211> 587
 <212> PRT
 <213> Homo sapiens

<400> 226
 Met Arg Pro Arg Gly Leu Pro Pro Leu Leu Val Val Leu Leu Gly Cys
 1 5 10 15
 Trp Ala Ser Val Ser Ala Gln Thr Asp Ala Thr Pro Ala Val Thr Thr
 20 25 30
 Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu Ala Thr Phe Gly Thr Phe
 35 40 45
 Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg Ala Pro Gly Pro Ser Ser
 50 55 60
 Gly Pro Arg Pro Thr Pro Val Thr Asp Val Ala Val Leu Cys Val Cys
 65 70 75 80
 Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn Cys Cys Cys Asp Pro Asp
 85 90 95
 Cys Ser Ser Val Asp Phe Ser Val Phe Ser Ala Cys Ser Val Pro Val
 100 105 110
 Val Thr Gly Asp Ser Gln Phe Cys Ser Gln Lys Ala Val Ile Tyr Ser
 115 120 125
 Leu Asn Phe Thr Ala Asn Pro Pro Gln Arg Val Phe Glu Leu Val Asp
 130 135 140
 Gln Ile Asn Pro Ser Ile Phe Cys Ile His Ile Thr Asn Tyr Lys Pro
 145 150 155 160
 Ala Leu Ser Phe Ile Asn Pro Glu Val Pro Asp Glu Asn Asn Phe Asp
 165 170 175
 Thr Leu Met Lys Thr Ser Asp Gly Phe Thr Leu Asn Ala Glu Ser Tyr
 180 185 190
 Val Ser Phe Thr Thr Lys Leu Asp Ile Pro Thr Ala Ala Lys Tyr Glu
 195 200 205
 Tyr Gly Val Pro Leu Gln Thr Ser Asp Ser Phe Leu Arg Phe Pro Ser
 210 215 220

329

Ser Leu Thr Ser Ser Leu Cys Thr Asp Asn Asn Pro Ala Ala Phe Leu
 225 230 235 240
 Val Asn Gln Ala Val Lys Cys Thr Arg Lys Ile Asn Leu Glu Gln Cys
 245 250 255
 Glu Glu Ile Glu Ala Leu Ser Met Ala Phe Tyr Ser Ser Pro Glu Ile
 260 265 270
 Leu Arg Val Pro Asp Ser Arg Lys Lys Val Pro Ile Thr Val Gln Ser
 275 280 285
 Ile Val Ile Gln Ser Leu Asn Lys Thr Leu Thr Arg Arg Glu Asp Thr
 290 295 300
 Asp Val Leu Gln Pro Thr Leu Val Asn Ala Gly His Phe Ser Leu Cys
 305 310 315 320
 Val Asn Val Val Leu Glu Val Lys Tyr Ser Leu Thr Tyr Thr Asp Ala
 325 330 335
 Gly Glu Val Thr Lys Ala Asp Leu Ser Phe Val Leu Gly Thr Val Ser
 340 345 350
 Ser Val Val Val Pro Leu Gln Gln Lys Phe Glu Ile His Phe Leu Gln
 355 360 365
 Glu Asn Thr Gln Pro Val Pro Leu Ser Gly Asn Pro Gly Tyr Val Val
 370 375 380
 Gly Leu Pro Leu Ala Ala Gly Phe Gln Pro His Lys Gly Ser Gly Ile
 385 390 395 400
 Ile Gln Thr Thr Asn Arg Tyr Gly Gln Leu Thr Ile Leu His Ser Thr
 405 410 415
 Thr Glu Gln Asp Cys Leu Ala Leu Glu Gly Val Arg Thr Pro Val Leu
 420 425 430
 Phe Gly Tyr Thr Met Gln Ser Gly Cys Lys Leu Arg Leu Thr Gly Ala
 435 440 445
 Leu Pro Cys Gln Leu Val Ala Gln Lys Val Lys Ser Leu Leu Trp Gly
 450 455 460
 Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe Gly Asn Ser Gln Ala Gln
 465 470 475 480
 Asp Met Leu Asp Trp Val Pro Ile His Phe Ile Thr Gln Ser Phe Asn
 485 490 495
 Arg Lys Asp Ser Cys Gln Leu Pro Gly Ala Leu Val Ile Glu Val Lys
 500 505 510
 Trp Thr Lys Tyr Gly Ser Leu Leu Asn Pro Gln Ala Lys Ile Val Asn
 515 520 525
 Val Thr Ala Asn Leu Ile Ser Ser Phe Pro Glu Ala Asn Ser Gly
 530 535 540
 Asn Glu Arg Thr Ile Leu Ile Ser Thr Ala Val Thr Phe Val Asp Val
 545 550 555 560
 Ser Ala Pro Ala Glu Ala Gly Phe Arg Ala Pro Pro Ala Ile Asn Ala
 565 570 575

330

Arg Leu Pro Phe Asn Phe Phe Phe Pro Phe Val
 580 585

<210> 227
 <211> 963
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(963)

<400> 227
 atg gcc ggc ctg gcg gcg cgg ttg gtc ctg cta gct ggg gca gcg gcg 48
 Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala Ala
 1 5 10 15
 ctg gcg agc ggc tcc cag ggc gac cgt gag ccg gtg tac cgc gac tgc 96
 Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg Asp Cys
 20 25 30
 gta ctg cag tgc gaa gag cag aac tgc tct ggg ggc gct ctg aat cac 144
 Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala Leu Asn His
 35 40 45
 ttc cgc tcc cgc cag cca atc tac atg agt cta gca ggc tgg acc tgt 192
 Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala Gly Trp Thr Cys
 50 55 60
 cgg gac gac tgt aag tat gag tgt atg tgg gtc acc gtt ggg ctc tac 240
 Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val Thr Val Gly Leu Tyr
 65 70 75 80
 ctc cag gaa ggt cac aaa gtg cct cag ttc cat ggc aag tgg ccc ttc 288
 Leu Gln Glu Gly His Lys Val Pro Gln Phe His Gly Lys Trp Pro Phe
 85 90 95
 tcc cgg ttc ctg ttc ttt caa gag ccg gca tcg gcc gtg gcc tcg ttt 336
 Ser Arg Phe Leu Phe Phe Gln Glu Pro Ala Ser Ala Val Ala Ser Phe
 100 105 110
 ctc aat ggc ctg gcc agc ctg gtg atg ctc tgc cgc tac cgc acc ttc 384
 Leu Asn Gly Leu Ala Ser Leu Val Met Leu Cys Arg Tyr Arg Thr Phe
 115 120 125

331

gtg cca gcc tcc tcc ccc atg tac cac acc tgt gtg gcc ttc gcc tgg Val Pro Ala Ser Ser Pro Met Tyr His Thr Cys Val Ala Phe Ala Trp 130 135 140	432
gtg tcc ctc aat gca tgg ttc tgg tcc aca gtc ttc cac acc agg gac Val Ser Leu Asn Ala Trp Phe Trp Ser Thr Val Phe His Thr Arg Asp 145 150 155 160	480
act gac ctc aca gag aaa atg gac tac ttc tgt gcc tcc act gtc atc Thr Asp Leu Thr Glu Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile 165 170 175	528
cta cac tca atc tac ctg tgc tgc gtc agg acc gtg ggg ctg cag cac Leu His Ser Ile Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His 180 185 190	576
cca gct gtg gtc agt gcc ttc cgg gct ctc ctg ctg ctc atg ctg acc Pro Ala Val Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr 195 200 205	624
gtg cac gtc tcc tac ctg agc ctc atc cgc ttc gac tat ggc tac aac Val His Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn 210 215 220	672
ctg gtg gcc aac gtg gct att ggc ctg gtc aac gtg gtg tgg tgg ctg Leu Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu 225 230 235 240	720
gcc tgg tgc ctg tgg aac cag cgg cgg ctg cct cac gtg cgc aag tgc Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys Cys 245 250 255	768
gtg gtg gtg gtc ttg ctg ctg cag ggg ctg tcc ctg ctc gag ctg ctt Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu Leu Leu 260 265 270	816
gac ttc cca ccg ctc ttc tgg gtc ctg gat gcc cat gcc atc tgg cac Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala Ile Trp His 275 280 285	864
atc agc acc atc cct gtc cac gtc ctc ttt ttc agc ttt ctg gaa gat Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser Phe Leu Glu Asp 290 295 300	912

332

gac agc ctg tac ctg ctg aag gaa tca gag gac aag ttc aag ctg gac 960
 Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp Lys Phe Lys Leu Asp
 305 310 315 320

tga 963
 *

<210> 228
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 228
 Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala Ala
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 Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg Asp Cys
 20 25 30
 Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala Leu Asn His
 35 40 45
 Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala Gly Trp Thr Cys
 50 55 60
 Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val Thr Val Gly Leu Tyr
 65 70 75 80
 Leu Gln Glu Gly His Lys Val Pro Gln Phe His Gly Lys Trp Pro Phe
 85 90 95
 Ser Arg Phe Leu Phe Phe Gln Glu Pro Ala Ser Ala Val Ala Ser Phe
 100 105 110
 Leu Asn Gly Leu Ala Ser Leu Val Met Leu Cys Arg Tyr Arg Thr Phe
 115 120 125
 Val Pro Ala Ser Ser Pro Met Tyr His Thr Cys Val Ala Phe Ala Trp
 130 135 140
 Val Ser Leu Asn Ala Trp Phe Trp Ser Thr Val Phe His Thr Arg Asp
 145 150 155 160
 Thr Asp Leu Thr Glu Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile
 165 170 175
 Leu His Ser Ile Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His
 180 185 190
 Pro Ala Val Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr
 195 200 205
 Val His Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn
 210 215 220

333

Leu Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu
 225 230 235 240
 Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys Cys
 245 250 255
 Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu Leu Leu
 260 265 270
 Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala Ile Trp His
 275 280 285
 Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser Phe Leu Glu Asp
 290 295 300
 Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp Lys Phe Lys Leu Asp
 305 310 315 320

<210> 229

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(657)

<221> misc_feature

<222> (1)...(657)

<223> n = A,T,C or G

<400> 229

atg gcg cgg aag aag gtg cgt ccg cgg ctg atc gcg gan ctg gcc cgc	48
Met Ala Arg Lys Lys Val Arg Pro Arg Leu Ile Ala Xaa Leu Ala Arg	
1 5 10 15	
cgc gtg cgc gcc ctg cgg gag caa ctg aac agg ccg cgc gac tcc cag	96
Arg Val Arg Ala Leu Arg Glu Gln Leu Asn Arg Pro Arg Asp Ser Gln	
20 25 30	
ctc tac gcg gtg gac tac gag acc ttg acg cgg ccg ttc tct gga cgc	144
Leu Tyr Ala Val Asp Tyr Glu Thr Leu Thr Arg Pro Phe Ser Gly Arg	
35 40 45	
cgg ctg ccg gtc cgg gcc tgg gcc gac gtg cgc cgc gag anc cgc ctc	192
Arg Leu Pro Val Arg Ala Trp Ala Asp Val Arg Arg Glu Xaa Arg Leu	
50 55 60	
ttg cag ctg ctc ggc cgc ctc ccg ctc ttc ggc ctg ggc cgc ctg gtc	240

334

Leu	Gln	Leu	Leu	Gly	Arg	Leu	Pro	Leu	Phe	Gly	Leu	Gly	Arg	Leu	Val	
65					70					75					80	
acg	cgc	aag	tcc	tgg	ctg	tgg	cag	cac	gac	gag	ccg	tgc	tac	tgg	cgc	288
Thr	Arg	Lys	Ser	Trp	Leu	Trp	Gln	His	Asp	Glu	Pro	Cys	Tyr	Trp	Arg	
				85					90					95		
ctc	acg	cgg	gtg	cgg	ccc	gac	tac	acg	gcg	cag	aac	ttg	gac	cac	ggg	336
Leu	Thr	Arg	Val	Arg	Pro	Asp	Tyr	Thr	Ala	Gln	Asn	Leu	Asp	His	Gly	
			100					105					110			
aag	gcc	tgg	ggc	atc	ctg	acc	ttc	aaa	ggg	aag	act	gag	agc	gag	gcg	384
Lys	Ala	Trp	Gly	Ile	Leu	Thr	Phe	Lys	Gly	Lys	Thr	Glu	Ser	Glu	Ala	
		115					120					125				
cgg	gag	atc	gaa	cac	gtc	atg	tac	cat	gac	tgg	cgg	ctg	gtg	ccc	aag	432
Arg	Glu	Ile	Glu	His	Val	Met	Tyr	His	Asp	Trp	Arg	Leu	Val	Pro	Lys	
	130					135					140					
cac	gag	gag	gag	gcc	ttc	acc	gcg	ttc	acg	ccg	gcg	ccg	gaa	gac	agc	480
His	Glu	Glu	Glu	Ala	Phe	Thr	Ala	Phe	Thr	Pro	Ala	Pro	Glu	Asp	Ser	
145					150					155				160		
ctg	gcc	tcc	gtg	ccg	tac	ccg	cct	ctc	ctc	cgg	gcc	atg	att	atc	gca	528
Leu	Ala	Ser	Val	Pro	Tyr	Pro	Pro	Leu	Leu	Arg	Ala	Met	Ile	Ile	Ala	
				165				170						175		
gaa	cga	cag	aaa	aat	gga	gac	aca	agc	acc	gag	gag	ccc	atg	ctg	aat	576
Glu	Arg	Gln	Lys	Asn	Gly	Asp	Thr	Ser	Thr	Glu	Glu	Pro	Met	Leu	Asn	
			180					185					190			
gtg	cag	agg	ata	cgc	atg	gaa	ccc	tgg	gat	tac	cct	gca	aaa	cag	gaa	624
Val	Gln	Arg	Ile	Arg	Met	Glu	Pro	Trp	Asp	Tyr	Pro	Ala	Lys	Gln	Glu	
		195					200					205				
gac	aaa	gga	agg	gcc	aag	ggc	acc	ccc	gtc	tag						657
Asp	Lys	Gly	Arg	Ala	Lys	Gly	Thr	Pro	Val	*						
	210					215										

<210> 230

<211> 218

<212> PRT

<213> Homo sapiens

335

<220>

<221> VARIANT

<222> (1)...(218)

<223> Xaa = Any Amino Acid

<400> 230

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Met Ala Arg Lys Lys Val Arg Pro Arg Leu Ile Ala Xaa Leu Ala Arg
 1          5          10          15
Arg Val Arg Ala Leu Arg Glu Gln Leu Asn Arg Pro Arg Asp Ser Gln
          20          25          30
Leu Tyr Ala Val Asp Tyr Glu Thr Leu Thr Arg Pro Phe Ser Gly Arg
          35          40          45
Arg Leu Pro Val Arg Ala Trp Ala Asp Val Arg Arg Glu Xaa Arg Leu
          50          55          60
Leu Gln Leu Leu Gly Arg Leu Pro Leu Phe Gly Leu Gly Arg Leu Val
65          70          75          80
Thr Arg Lys Ser Trp Leu Trp Gln His Asp Glu Pro Cys Tyr Trp Arg
          85          90          95
Leu Thr Arg Val Arg Pro Asp Tyr Thr Ala Gln Asn Leu Asp His Gly
          100          105          110
Lys Ala Trp Gly Ile Leu Thr Phe Lys Gly Lys Thr Glu Ser Glu Ala
          115          120          125
Arg Glu Ile Glu His Val Met Tyr His Asp Trp Arg Leu Val Pro Lys
          130          135          140
His Glu Glu Glu Ala Phe Thr Ala Phe Thr Pro Ala Pro Glu Asp Ser
145          150          155          160
Leu Ala Ser Val Pro Tyr Pro Pro Leu Leu Arg Ala Met Ile Ile Ala
          165          170          175
Glu Arg Gln Lys Asn Gly Asp Thr Ser Thr Glu Glu Pro Met Leu Asn
          180          185          190
Val Gln Arg Ile Arg Met Glu Pro Trp Asp Tyr Pro Ala Lys Gln Glu
          195          200          205
Asp Lys Gly Arg Ala Lys Gly Thr Pro Val
          210          215

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<210> 231

<211> 1116

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1116)

336

<221> misc_feature

<222> (1)...(1116)

<223> n = A,T,C or G

<400> 231

atg tct gtg gcc cac tgt ttc tcc atc aaa ggc caa ggc act gtg atg	48
Met Ser Val Ala His Cys Phe Ser Ile Lys Gly Gln Gly Thr Val Met	
1 5 10 15	

aca ggg acc atc ctt tca ggc tcc atc agc ctc ggt gac agt gtg gag	96
Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val Glu	
20 25 30	

atc cct gcc ctc aag gtg gtg aag aag gtg aag tcc atg cag atg ttc	144
Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met Phe	
35 40 45	

cac atg ccc atc act tca gcc atg caa gga gac cgg ctg ggc atc tgc	192
His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile Cys	
50 55 60	

gtc acc cag ttt gac cct aag ctg ctg gag cgc ggg ttg gtg tgt gcc	240
Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys Ala	
65 70 75 80	

ccc gag tcc ctg cac act gtc cat gcg gcc ctc atc tct gtg gaa aag	288
Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu Lys	
85 90 95	

ata ccg tat ttc cgg ggg ccc ctg caa acc aag gcc aag ttc cac att	336
Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His Ile	
100 105 110	

aca gtg ggc cat gaa aca gtc atg ggc cgg ttg atg ttc ttc agt cct	384
Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser Pro	
115 120 125	

gct cca gat aac ttt gac cag gag cct ata ctg gac tct ttc aac ttc	432
Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn Phe	
130 135 140	

tct caa gaa tac ctt ttc cag gag cag tac ctg tcc aag gat ttg aca	480
Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu Thr	

337

145	150	155	160	
cca gca gtg aca gac aat gat gag gcc gac aag aag gcc ggc cag gcc				528
Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln Ala				
	165	170	175	
aca gag ggc cat tgt cct cgg cag cag tgg gcc ctg gtg gag ttt gag				576
Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe Glu				
	180	185	190	
aag ccc gtc acc tgc cct cgg ctg tgc ctg gtg att ggc tcc agg cta				624
Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg Leu				
	195	200	205	
gat gcg gac att cac acc aac acg tgc cgg cta gcc ttc cat ggc atc				672
Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly Ile				
	210	215	220	
ctg ctc cac ggg cta gag gac agg aac tac gcc gac agc ttc ctg ccc				720
Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu Pro				
	225	230	235	240
agg ctg aag gtg tac aag ctg aag cac aag cat ggc ctt gtg gag cgg				768
Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu Arg				
	245	250	255	
gcg atg gat gac tac agt gtg atc ggc cgc tcc ctg ttc aaa aag gaa				816
Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys Glu				
	260	265	270	
acc aac atc cag ctc ttc gtg ggg ctc aag gtg cac ttg tcc act ggg				864
Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr Gly				
	275	280	285	
gaa ctg ggc atc atc gac agt gcc ttc ggc cag agc ggc aag ttc aag				912
Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe Lys				
	290	295	300	
atc cac atc cca ggt ggc ctc agc ccc gag tcc aag aag atc ctg aca				960
Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu Thr				
	310	315	320	
ccc gcc ctc aag aag cgg gcc cgg gct ggc cgt ggg gag gcc acc agg				1008
Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr Arg				

338

325	330	335	
cag gag gag agc gcc gag cgg agn agg ccc tca cag cat gtg gtg ctc			1056
Gln Glu Glu Ser Ala Glu Arg Xaa Arg Pro Ser Gln His Val Val Leu			
340	345	350	
agc ctg act ttc aag cgt tat gtc ttc gac acc cac aag cgc atg gtt			1104
Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met Val			
355	360	365	
cag tct ccc tga			1116
Gln Ser Pro *			
370			

<210> 232

<211> 371

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(371)

<223> Xaa = Any Amino Acid

<400> 232

Met Ser Val Ala His Cys Phe Ser Ile Lys Gly Gln Gly Thr Val Met			
1	5	10	15
Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val Glu			
20	25	30	
Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met Phe			
35	40	45	
His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile Cys			
50	55	60	
Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys Ala			
65	70	75	80
Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu Lys			
85	90	95	
Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His Ile			
100	105	110	
Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser Pro			
115	120	125	
Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn Phe			
130	135	140	

339

Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu Thr
 145 150 155 160
 Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln Ala
 165 170 175
 Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe Glu
 180 185 190
 Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg Leu
 195 200 205
 Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly Ile
 210 215 220
 Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu Pro
 225 230 235 240
 Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu Arg
 245 250 255
 Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys Glu
 260 265 270
 Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr Gly
 275 280 285
 Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe Lys
 290 295 300
 Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu Thr
 305 310 315 320
 Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr Arg
 325 330 335
 Gln Glu Glu Ser Ala Glu Arg Xaa Arg Pro Ser Gln His Val Val Leu
 340 345 350
 Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met Val
 355 360 365
 Gln Ser Pro
 370

<210> 233

<211> 1275

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1275)

<221> misc_feature

<222> (1)...(1275)

<223> n = A,T,C or G

340

<400> 233

atg gcg gca gtg gca acc tgc ggt agt gtt gcc gcg agt act ggg tct	48
Met Ala Ala Val Ala Thr Cys Gly Ser Val Ala Ala Ser Thr Gly Ser	
1 5 10 15	
gca gtg gcg aca gca gnc aag agc aac gtc acc agt ttc cag agg agg	96
Ala Val Ala Thr Ala Xaa Lys Ser Asn Val Thr Ser Phe Gln Arg Arg	
20 25 30	
ggt cct aga gcc agc gtg acc aac gac agc ggc cct cga ctg gtg tcc	144
Gly Pro Arg Ala Ser Val Thr Asn Asp Ser Gly Pro Arg Leu Val Ser	
35 40 45	
att gcg ggc acg cga ccg tcg gtg cgg aat gga cag ctg ctg gta tca	192
Ile Ala Gly Thr Arg Pro Ser Val Arg Asn Gly Gln Leu Leu Val Ser	
50 55 60	
acc ggg ctc cca gcc cta gac cag ctc tta ggt gga ggt tta gcc gtt	240
Thr Gly Leu Pro Ala Leu Asp Gln Leu Leu Gly Gly Gly Leu Ala Val	
65 70 75 80	
gga aca gtt ctt cta att gag gag gat aaa tat aat att tac tca cct	288
Gly Thr Val Leu Leu Ile Glu Glu Asp Lys Tyr Asn Ile Tyr Ser Pro	
85 90 95	
ttg ctc ttc aag tat ttc ctg gca gaa gga att gtc aat ggg cat act	336
Leu Leu Phe Lys Tyr Phe Leu Ala Glu Gly Ile Val Asn Gly His Thr	
100 105 110	
ttg ttg gtt gca tct gct aaa gag gat cct gcc aac att tta cag gaa	384
Leu Leu Val Ala Ser Ala Lys Glu Asp Pro Ala Asn Ile Leu Gln Glu	
115 120 125	
ctt cca gca cca tta ctt gat gat aaa tgt aaa aag gaa ttt gat gaa	432
Leu Pro Ala Pro Leu Leu Asp Asp Lys Cys Lys Lys Glu Phe Asp Glu	
130 135 140	
gat gta tac aat cat aaa aca cca gaa tct aat att aag atg aaa ata	480
Asp Val Tyr Asn His Lys Thr Pro Glu Ser Asn Ile Lys Met Lys Ile	
145 150 155 160	
gct tgg cgt tac cag tta tta ccc aag atg gag att gga cca gta tca	528
Ala Trp Arg Tyr Gln Leu Leu Pro Lys Met Glu Ile Gly Pro Val Ser	
165 170 175	

341

tct tca aga ttt ggt cac tat tat gat gca tca aaa aga atg cca caa Ser Ser Arg Phe Gly His Tyr Tyr Asp Ala Ser Lys Arg Met Pro Gln 180 185 190	576
gaa cta att gag gct tca aat tgg cat gga ttt ttt ctt cca gag aaa Glu Leu Ile Glu Ala Ser Asn Trp His Gly Phe Phe Leu Pro Glu Lys 195 200 205	624
ata tct tca act ctc aaa gta gaa ccc tgt tct ttg acc cct ggc tac Ile Ser Ser Thr Leu Lys Val Glu Pro Cys Ser Leu Thr Pro Gly Tyr 210 215 220	672
aca aag ctg ctt cag ttt atc cag aac atc att tat gag gaa gga ttt Thr Lys Leu Leu Gln Phe Ile Gln Asn Ile Ile Tyr Glu Glu Gly Phe 225 230 235 240	720
gat gga tcc aat cct cag aaa aaa cag aga aac att tta aga ata gga Asp Gly Ser Asn Pro Gln Lys Lys Gln Arg Asn Ile Leu Arg Ile Gly 245 250 255	768
att cag aat ctt ggc tca cct tta tgg gga gac gat att tgc tgt gca Ile Gln Asn Leu Gly Ser Pro Leu Trp Gly Asp Asp Ile Cys Cys Ala 260 265 270	816
gaa aat ggt ggc aac agt cac agc ctt acc aag ttc ctc tat gtt ctc Glu Asn Gly Gly Asn Ser His Ser Leu Thr Lys Phe Leu Tyr Val Leu 275 280 285	864
cgt ggt ctt ctg aga acc tct ctt tca gcc tgc atc atc aca atg cca Arg Gly Leu Leu Arg Thr Ser Leu Ser Ala Cys Ile Ile Thr Met Pro 290 295 300	912
aca cat ctg atc cag aat aaa gcc att att gcc cgt gtc aca acc ttg Thr His Leu Ile Gln Asn Lys Ala Ile Ile Ala Arg Val Thr Thr Leu 305 310 315 320	960
tca gat gta gta gtt ggt ctg gaa tca ttt att ggt tct gag aga gaa Ser Asp Val Val Val Gly Leu Glu Ser Phe Ile Gly Ser Glu Arg Glu 325 330 335	1008
act aac cca ttg tat aag gat tat cat gga ttg att cat ata cgg cag Thr Asn Pro Leu Tyr Lys Asp Tyr His Gly Leu Ile His Ile Arg Gln 340 345 350	1056

342

att cct cgg ctt aat aac ttg atc tgt gat gaa tca gat gtc aaa gac 1104
 Ile Pro Arg Leu Asn Asn Leu Ile Cys Asp Glu Ser Asp Val Lys Asp
 355 360 365

tta gct ttt aaa tta aaa agg aag cta ttc acc att gag cga ctg cat 1152
 Leu Ala Phe Lys Leu Lys Arg Lys Leu Phe Thr Ile Glu Arg Leu His
 370 375 380

ttg cct cca gac ttg tca gac aca gtg agc cgc tca agc aaa atg gat 1200
 Leu Pro Pro Asp Leu Ser Asp Thr Val Ser Arg Ser Ser Lys Met Asp
 385 390 395 400

ctg gca gaa tcc gcc aag cgg ctg ggc cca ggc tgt ggc atg atg gcc 1248
 Leu Ala Glu Ser Ala Lys Arg Leu Gly Pro Gly Cys Gly Met Met Ala
 405 410 415

gga ggc aag aag cac ctg gac ttc tag 1275
 Gly Gly Lys Lys His Leu Asp Phe *
 420

<210> 234

<211> 424

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(424)

<223> Xaa = Any Amino Acid

<400> 234

Met Ala Ala Val Ala Thr Cys Gly Ser Val Ala Ala Ser Thr Gly Ser
 1 5 10 15
 Ala Val Ala Thr Ala Xaa Lys Ser Asn Val Thr Ser Phe Gln Arg Arg
 20 25 30
 Gly Pro Arg Ala Ser Val Thr Asn Asp Ser Gly Pro Arg Leu Val Ser
 35 40 45
 Ile Ala Gly Thr Arg Pro Ser Val Arg Asn Gly Gln Leu Leu Val Ser
 50 55 60
 Thr Gly Leu Pro Ala Leu Asp Gln Leu Leu Gly Gly Gly Leu Ala Val
 65 70 75 80
 Gly Thr Val Leu Leu Ile Glu Glu Asp Lys Tyr Asn Ile Tyr Ser Pro

85															90					95				
Leu	Leu	Phe	Lys	Tyr	Phe	Leu	Ala	Glu	Gly	Ile	Val	Asn	Gly	His	Thr									
			100				105						110											
Leu	Leu	Val	Ala	Ser	Ala	Lys	Glu	Asp	Pro	Ala	Asn	Ile	Leu	Gln	Glu									
			115				120						125											
Leu	Pro	Ala	Pro	Leu	Leu	Asp	Asp	Lys	Cys	Lys	Lys	Glu	Phe	Asp	Glu									
			130				135						140											
Asp	Val	Tyr	Asn	His	Lys	Thr	Pro	Glu	Ser	Asn	Ile	Lys	Met	Lys	Ile									
145				150						155			160											
Ala	Trp	Arg	Tyr	Gln	Leu	Leu	Pro	Lys	Met	Glu	Ile	Gly	Pro	Val	Ser									
			165						170			175												
Ser	Ser	Arg	Phe	Gly	His	Tyr	Tyr	Asp	Ala	Ser	Lys	Arg	Met	Pro	Gln									
			180						185			190												
Glu	Leu	Ile	Glu	Ala	Ser	Asn	Trp	His	Gly	Phe	Phe	Leu	Pro	Glu	Lys									
			195						200			205												
Ile	Ser	Ser	Thr	Leu	Lys	Val	Glu	Pro	Cys	Ser	Leu	Thr	Pro	Gly	Tyr									
210				215						220			225											
Thr	Lys	Leu	Leu	Gln	Phe	Ile	Gln	Asn	Ile	Ile	Tyr	Glu	Glu	Gly	Phe									
225				230						235			240											
Asp	Gly	Ser	Asn	Pro	Gln	Lys	Lys	Gln	Arg	Asn	Ile	Leu	Arg	Ile	Gly									
			245						250			255												
Ile	Gln	Asn	Leu	Gly	Ser	Pro	Leu	Trp	Gly	Asp	Asp	Ile	Cys	Cys	Ala									
			260						265			270												
Glu	Asn	Gly	Gly	Asn	Ser	His	Ser	Leu	Thr	Lys	Phe	Leu	Tyr	Val	Leu									
			275						280			285												
Arg	Gly	Leu	Leu	Arg	Thr	Ser	Leu	Ser	Ala	Cys	Ile	Ile	Thr	Met	Pro									
290				295						300			305											
Thr	His	Leu	Ile	Gln	Asn	Lys	Ala	Ile	Ile	Ala	Arg	Val	Thr	Thr	Leu									
305				310						315			320											
Ser	Asp	Val	Val	Val	Gly	Leu	Glu	Ser	Phe	Ile	Gly	Ser	Glu	Arg	Glu									
			325						330			335												
Thr	Asn	Pro	Leu	Tyr	Lys	Asp	Tyr	His	Gly	Leu	Ile	His	Ile	Arg	Gln									
			340						345			350												
Ile	Pro	Arg	Leu	Asn	Asn	Leu	Ile	Cys	Asp	Glu	Ser	Asp	Val	Lys	Asp									
			355						360			365												
Leu	Ala	Phe	Lys	Leu	Lys	Arg	Lys	Leu	Phe	Thr	Ile	Glu	Arg	Leu	His									
			370						375			380												
Leu	Pro	Pro	Asp	Leu	Ser	Asp	Thr	Val	Ser	Arg	Ser	Ser	Lys	Met	Asp									
385																								

344

<210> 235
 <211> 1188
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1188)

<400> 235

atg	gag	gag	ctc	cca	ggc	tat	gaa	gag	acc	ctg	acc	cgc	ctg	gct	gcc	48
Met	Glu	Glu	Leu	Pro	Gly	Tyr	Glu	Glu	Thr	Leu	Thr	Arg	Leu	Ala	Ala	
1				5					10					15		

att	ctc	gcc	aaa	cac	ttt	gcc	gac	gca	cgc	att	gtg	ggc	act	gac	atc	96
Ile	Leu	Ala	Lys	His	Phe	Ala	Asp	Ala	Arg	Ile	Val	Gly	Thr	Asp	Ile	
			20						25				30			

cga	gac	tca	ctg	atg	cag	gcc	ctg	gcc	agc	tac	gtg	tgc	tac	cca	cac	144
Arg	Asp	Ser	Leu	Met	Gln	Ala	Leu	Ala	Ser	Tyr	Val	Cys	Tyr	Pro	His	
			35				40					45				

tcc	ctg	cgg	gct	gtg	gag	cga	atc	ccc	gag	gag	cag	cgt	atc	gcc	atg	192
Ser	Leu	Arg	Ala	Val	Glu	Arg	Ile	Pro	Glu	Glu	Gln	Arg	Ile	Ala	Met	
			50				55					60				

gtg	agg	aac	ctc	ctg	gcg	ccc	tat	gag	cag	cgg	ccc	tgg	gcc	cag	acc	240
Val	Arg	Asn	Leu	Leu	Ala	Pro	Tyr	Glu	Gln	Arg	Pro	Trp	Ala	Gln	Thr	
			65			70				75				80		

aac	tgg	atc	ctg	gtg	cgg	ctc	tgg	agg	ggc	tgt	ggc	ttc	ggg	tac	cgc	288
Asn	Trp	Ile	Leu	Val	Arg	Leu	Trp	Arg	Gly	Cys	Gly	Phe	Gly	Tyr	Arg	
				85					90					95		

tat	aca	cgg	ctg	cca	cat	ctg	ctg	aaa	acc	aaa	ctt	gag	gac	gcc	aat	336
Tyr	Thr	Arg	Leu	Pro	His	Leu	Leu	Lys	Thr	Lys	Leu	Glu	Asp	Ala	Asn	
			100					105						110		

ttg	ccc	agc	ctc	cag	aag	ccc	tgc	cct	tcc	acc	ctg	ctg	cag	cag	cac	384
Leu	Pro	Ser	Leu	Gln	Lys	Pro	Cys	Pro	Ser	Thr	Leu	Leu	Gln	Gln	His	
			115				120						125			

atg	gcg	gac	ctc	cta	cag	cag	ggc	cct	gat	gtg	gca	ccc	agc	ttc	ctc	432
Met	Ala	Asp	Leu	Leu	Gln	Gln	Gly	Pro	Asp	Val	Ala	Pro	Ser	Phe	Leu	

345

130	135	140	
aac agc gtc ctc aat cag ctc aac tgg gcc ttc tct gaa ttc att ggc			480
Asn Ser Val Leu Asn Gln Leu Asn Trp Ala Phe Ser Glu Phe Ile Gly			
145	150	155	160
atg atc caa gag atc cag cag gct gct gag cgc ctg gag cgg aac ttt			528
Met Ile Gln Glu Ile Gln Gln Ala Ala Glu Arg Leu Glu Arg Asn Phe			
	165	170	175
gtg gac agc cgg cag ctc aag gta tgt gcc acc tgc ttt gac ctc tcg			576
Val Asp Ser Arg Gln Leu Lys Val Cys Ala Thr Cys Phe Asp Leu Ser			
	180	185	190
gtc agc ctg ctg cgt gtc ttg gag atg act atc aca ctg gtg cct gag			624
Val Ser Leu Leu Arg Val Leu Glu Met Thr Ile Thr Leu Val Pro Glu			
	195	200	205
ata ttc ctt gac tgg acc cgg cct acc tct gag atg ctg ctg cgg cgt			672
Ile Phe Leu Asp Trp Thr Arg Pro Thr Ser Glu Met Leu Leu Arg Arg			
210	215	220	
ctt gca cag ctg cta aac cag gtg ctg aac cgg gtg aca gct gag agg			720
Leu Ala Gln Leu Leu Asn Gln Val Leu Asn Arg Val Thr Ala Glu Arg			
225	230	235	240
aac ctg ttt gat cgt gtg gtc acc cta cgg ctg cct ggc cta gag agc			768
Asn Leu Phe Asp Arg Val Val Thr Leu Arg Leu Pro Gly Leu Glu Ser			
	245	250	255
gtg gac cac tat ccc att ctg gtg gca gtg acg ggc atc ctg gtg cag			816
Val Asp His Tyr Pro Ile Leu Val Ala Val Thr Gly Ile Leu Val Gln			
	260	265	270
ctc ctg gtg cgt ggc cca gcc tca gag aga gag caa gcc aca tca gtg			864
Leu Leu Val Arg Gly Pro Ala Ser Glu Arg Glu Gln Ala Thr Ser Val			
	275	280	285
ctc ctg gca gat ccc tgc ttc cag cta cgc tca ata tgc tat ctc ctg			912
Leu Leu Ala Asp Pro Cys Phe Gln Leu Arg Ser Ile Cys Tyr Leu Leu			
290	295	300	
gga cag cca gag ccc cca gca cct ggc act gct ctg cca gcc cct gac			960
Gly Gln Pro Glu Pro Pro Ala Pro Gly Thr Ala Leu Pro Ala Pro Asp			

346

305	310	315	320	
cgg aag cgc ttc tcc ctg cag agc tat gcg gat tat atc agt gcc gat				1008
Arg Lys Arg Phe Ser Leu Gln Ser Tyr Ala Asp Tyr Ile Ser Ala Asp				
	325	330	335	
gag ctg gcc caa gtg gaa cag atg ctg gcg cac ctg acc tct gca tct				1056
Glu Leu Ala Gln Val Glu Gln Met Leu Ala His Leu Thr Ser Ala Ser				
	340	345	350	
gcc cag gca gca gct gcc tcc ctg ccc acc agt gag gag gac tct gcc				1104
Ala Gln Ala Ala Ala Ala Ser Leu Pro Thr Ser Glu Glu Asp Ser Ala				
	355	360	365	
cca tct gct atg ccc acc cca tct ctg ctg tgt tcc agc cct gtg gcc				1152
Pro Ser Ala Met Pro Thr Pro Ser Leu Leu Cys Ser Ser Pro Val Ala				
	370	375	380	
aca agt cct gca aag cct gta tca acc agc acc tga				1188
Thr Ser Pro Ala Lys Pro Val Ser Thr Ser *				
385	390	395		

<210> 236

<211> 395

<212> PRT

<213> Homo sapiens

<400> 236

Met Glu Glu Leu Pro Gly Tyr Glu Glu Thr Leu Thr Arg Leu Ala Ala	
1 5 10 15	
Ile Leu Ala Lys His Phe Ala Asp Ala Arg Ile Val Gly Thr Asp Ile	
20 25 30	
Arg Asp Ser Leu Met Gln Ala Leu Ala Ser Tyr Val Cys Tyr Pro His	
35 40 45	
Ser Leu Arg Ala Val Glu Arg Ile Pro Glu Glu Gln Arg Ile Ala Met	
50 55 60	
Val Arg Asn Leu Leu Ala Pro Tyr Glu Gln Arg Pro Trp Ala Gln Thr	
65 70 75 80	
Asn Trp Ile Leu Val Arg Leu Trp Arg Gly Cys Gly Phe Gly Tyr Arg	
85 90 95	
Tyr Thr Arg Leu Pro His Leu Leu Lys Thr Lys Leu Glu Asp Ala Asn	
100 105 110	
Leu Pro Ser Leu Gln Lys Pro Cys Pro Ser Thr Leu Leu Gln Gln His	

347

	115		120		125	
Met	Ala	Asp	Leu	Leu	Gln	Gln
	130				135	
Asn	Ser	Val	Leu	Asn	Gln	Leu
145					150	
Met	Ile	Gln	Glu	Ile	Gln	Gln
					165	
Val	Asp	Ser	Arg	Gln	Leu	Lys
					180	
Val	Ser	Leu	Leu	Arg	Val	Leu
					195	
Ile	Phe	Leu	Asp	Trp	Thr	Arg
210					215	
Leu	Ala	Gln	Leu	Leu	Asn	Gln
225					230	
Asn	Leu	Phe	Asp	Arg	Val	Val
					245	
Val	Asp	His	Tyr	Pro	Ile	Leu
					260	
Leu	Leu	Val	Arg	Gly	Pro	Ala
					275	
Leu	Leu	Ala	Asp	Pro	Cys	Phe
290					295	
Gly	Gln	Pro	Glu	Pro	Pro	Ala
305					310	
Arg	Lys	Arg	Phe	Ser	Leu	Gln
					325	
Glu	Leu	Ala	Gln	Val	Glu	Gln
					340	
Ala	Gln	Ala	Ala	Ala	Ala	Ser
					355	
Pro	Ser	Ala	Met	Pro	Thr	Pro
					370	
Thr	Ser	Pro	Ala	Lys	Pro	Val
385					390	

<210> 237
 <211> 1278
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1278)

348

<221> misc_feature

<222> (1)...(1278)

<223> n = A,T,C or G

<400> 237

atg	gat	gac	ttg	caa	aag	ttg	gga	gtc	ata	ttg	cac	agt	gct	att	tca	48
Met	Asp	Asp	Leu	Gln	Lys	Leu	Gly	Val	Ile	Leu	His	Ser	Ala	Ile	Ser	
1			5					10					15			

gtc	cca	ata	agt	tca	gat	gca	tcc	cct	ttt	att	ctt	cca	tct	tat	acc	96
Val	Pro	Ile	Ser	Ser	Asp	Ala	Ser	Pro	Phe	Ile	Leu	Pro	Ser	Tyr	Thr	
		20					25					30				

gaa	gca	gtt	ttg	aca	agt	tta	cag	gaa	gct	gta	ctt	aca	gct	tta	gat	144
Glu	Ala	Val	Leu	Thr	Ser	Leu	Gln	Glu	Ala	Val	Leu	Thr	Ala	Leu	Asp	
	35						40				45					

gtt	ctc	caa	aag	gcc	att	tgt	gta	gga	cca	gaa	aac	atg	cag	ata	atg	192
Val	Leu	Gln	Lys	Ala	Ile	Cys	Val	Gly	Pro	Glu	Asn	Met	Gln	Ile	Met	
	50					55				60						

tat	cca	gct	ata	ttt	gac	cag	ttg	ttg	gca	ttt	gta	gaa	ttt	tcc	tgt	240
Tyr	Pro	Ala	Ile	Phe	Asp	Gln	Leu	Leu	Ala	Phe	Val	Glu	Phe	Ser	Cys	
	65				70				75					80		

aaa	cct	cca	cag	tat	gga	cag	ctn	gaa	aca	aag	cac	att	gca	aat	gca	288
Lys	Pro	Pro	Gln	Tyr	Gly	Gln	Xaa	Glu	Thr	Lys	His	Ile	Ala	Asn	Ala	
			85					90					95			

aaa	tat	aat	cag	atc	caa	cta	ttt	gca	ccg	gcg	gaa	tgg	gta	gcc	ttg	336
Lys	Tyr	Asn	Gln	Ile	Gln	Leu	Phe	Ala	Pro	Ala	Glu	Trp	Val	Ala	Leu	
		100					105					110				

aat	tat	gtg	ccg	ttt	gct	gaa	agg	tct	tta	gaa	gta	gtt	gtg	gat	tta	384
Asn	Tyr	Val	Pro	Phe	Ala	Glu	Arg	Ser	Leu	Glu	Val	Val	Val	Asp	Leu	
		115				120					125					

tac	caa	aaa	aca	gcg	tgt	cac	aaa	gca	gtg	gtg	aat	gag	aaa	gtg	ctc	432
Tyr	Gln	Lys	Thr	Ala	Cys	His	Lys	Ala	Val	Val	Asn	Glu	Lys	Val	Leu	
	130				135				140							

cag	aat	att	att	aag	act	ctt	agg	gtt	cct	ctc	agt	ttg	aag	tat	tcc	480
Gln	Asn	Ile	Ile	Lys	Thr	Leu	Arg	Val	Pro	Leu	Ser	Leu	Lys	Tyr	Ser	

349

145	150	155	160	
tgc cct tct gaa agc	aca tgg aaa cta gca gta tcc tct ctc ctc aga			528
Cys Pro Ser Glu Ser	Thr Trp Lys Leu Ala Val Ser Ser Leu Leu Arg			
	165	170	175	
gtt ctt tct att ggg	cta cct gtt gcc cgg cag cat gct tct tct gga		576	
Val Leu Ser Ile Gly	Leu Pro Val Ala Arg Gln His Ala Ser Ser Gly			
	180	185	190	
aaa ttt gac agt atg	tgg cca gaa cta gcc aat act ttt gaa gat ttt		624	
Lys Phe Asp Ser Met	Trp Pro Glu Leu Ala Asn Thr Phe Glu Asp Phe			
	195	200	205	
ctc ttt act aaa agc	ata cct cca gat aat ctc tct att caa gag ttt		672	
Leu Phe Thr Lys Ser	Ile Pro Pro Asp Asn Leu Ser Ile Gln Glu Phe			
	210	215	220	
caa aga aat gaa aat	att gat gtc gag gta gtt caa ctt atc agc aat		720	
Gln Arg Asn Glu Asn	Ile Asp Val Glu Val Val Gln Leu Ile Ser Asn			
	225	230	235	240
gag ata cta cct tat	gcc aat ttt att cct aag gaa ttt gtt ggt caa		768	
Glu Ile Leu Pro Tyr	Ala Asn Phe Ile Pro Lys Glu Phe Val Gly Gln			
	245	250	255	
ata atg aca atg ctt	aac aag ggc tca ata cat tct cag tca tct tca		816	
Ile Met Thr Met Leu	Asn Lys Gly Ser Ile His Ser Gln Ser Ser Ser			
	260	265	270	
ttt aca gaa gca gag	att gat att cgt ttg aga gag gaa ttt tct aaa		864	
Phe Thr Glu Ala Glu	Ile Asp Ile Arg Leu Arg Glu Glu Phe Ser Lys			
	275	280	285	
atg tgt ttt gaa aca	tta ctc cag ttt tcc ttc agt aat aaa gtc aca		912	
Met Cys Phe Glu Thr	Leu Leu Gln Phe Ser Phe Ser Asn Lys Val Thr			
	290	295	300	
aca cct caa gaa ggc	tac atc tca cga atg gca ctc tca gtg ctt tta		960	
Thr Pro Gln Glu Gly	Tyr Ile Ser Arg Met Ala Leu Ser Val Leu Leu			
	305	310	315	320
aag agg tcc caa gat	gta cta cat cgc tat ata gag gat gaa aga tta		1008	
Lys Arg Ser Gln Asp	Val Leu His Arg Tyr Ile Glu Asp Glu Arg Leu			

350

325

330

335

agt ggt aaa tgc cct ctt cca agg caa caa gta aca gaa att ata ttt 1056
 Ser Gly Lys Cys Pro Leu Pro Arg Gln Gln Val Thr Glu Ile Ile Phe
 340 345 350

gtt tta aaa gca gtc agt act ctt att gat tca ctt aag aaa act cag 1104
 Val Leu Lys Ala Val Ser Thr Leu Ile Asp Ser Leu Lys Lys Thr Gln
 355 360 365

cct gag aat gtt gat gga aat acc tgg gca caa gta att gcc tta tac 1152
 Pro Glu Asn Val Asp Gly Asn Thr Trp Ala Gln Val Ile Ala Leu Tyr
 370 375 380

cca act tta gta gaa tgc atc acc tgt tct tct tca gaa gtc tgt tct 1200
 Pro Thr Leu Val Glu Cys Ile Thr Cys Ser Ser Ser Glu Val Cys Ser
 385 390 395 400

gca ctt aaa gag gca cta gtt cct ttt aag gat ttc atg cag cca cca 1248
 Ala Leu Lys Glu Ala Leu Val Pro Phe Lys Asp Phe Met Gln Pro Pro
 405 410 415

gca tcc aga gtt caa aat gga gaa tct tga 1278
 Ala Ser Arg Val Gln Asn Gly Glu Ser *
 420 425

<210> 238

<211> 425

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(425)

<223> Xaa = Any Amino Acid

<400> 238

Met Asp Asp Leu Gln Lys Leu Gly Val Ile Leu His Ser Ala Ile Ser
 1 5 10 15
 Val Pro Ile Ser Ser Asp Ala Ser Pro Phe Ile Leu Pro Ser Tyr Thr
 20 25 30
 Glu Ala Val Leu Thr Ser Leu Gln Glu Ala Val Leu Thr Ala Leu Asp
 35 40 45

351

Val Leu Gln Lys Ala Ile Cys Val Gly Pro Glu Asn Met Gln Ile Met
 50 55 60
 Tyr Pro Ala Ile Phe Asp Gln Leu Leu Ala Phe Val Glu Phe Ser Cys
 65 70 75 80
 Lys Pro Pro Gln Tyr Gly Gln Xaa Glu Thr Lys His Ile Ala Asn Ala
 85 90 95
 Lys Tyr Asn Gln Ile Gln Leu Phe Ala Pro Ala Glu Trp Val Ala Leu
 100 105 110
 Asn Tyr Val Pro Phe Ala Glu Arg Ser Leu Glu Val Val Val Asp Leu
 115 120 125
 Tyr Gln Lys Thr Ala Cys His Lys Ala Val Val Asn Glu Lys Val Leu
 130 135 140
 Gln Asn Ile Ile Lys Thr Leu Arg Val Pro Leu Ser Leu Lys Tyr Ser
 145 150 155 160
 Cys Pro Ser Glu Ser Thr Trp Lys Leu Ala Val Ser Ser Leu Leu Arg
 165 170 175
 Val Leu Ser Ile Gly Leu Pro Val Ala Arg Gln His Ala Ser Ser Gly
 180 185 190
 Lys Phe Asp Ser Met Trp Pro Glu Leu Ala Asn Thr Phe Glu Asp Phe
 195 200 205
 Leu Phe Thr Lys Ser Ile Pro Pro Asp Asn Leu Ser Ile Gln Glu Phe
 210 215 220
 Gln Arg Asn Glu Asn Ile Asp Val Glu Val Val Gln Leu Ile Ser Asn
 225 230 235 240
 Glu Ile Leu Pro Tyr Ala Asn Phe Ile Pro Lys Glu Phe Val Gly Gln
 245 250 255
 Ile Met Thr Met Leu Asn Lys Gly Ser Ile His Ser Gln Ser Ser Ser
 260 265 270
 Phe Thr Glu Ala Glu Ile Asp Ile Arg Leu Arg Glu Glu Phe Ser Lys
 275 280 285
 Met Cys Phe Glu Thr Leu Leu Gln Phe Ser Phe Ser Asn Lys Val Thr
 290 295 300
 Thr Pro Gln Glu Gly Tyr Ile Ser Arg Met Ala Leu Ser Val Leu Leu
 305 310 315 320
 Lys Arg Ser Gln Asp Val Leu His Arg Tyr Ile Glu Asp Glu Arg Leu
 325 330 335
 Ser Gly Lys Cys Pro Leu Pro Arg Gln Gln Val Thr Glu Ile Ile Phe
 340 345 350
 Val Leu Lys Ala Val Ser Thr Leu Ile Asp Ser Leu Lys Lys Thr Gln
 355 360 365
 Pro Glu Asn Val Asp Gly Asn Thr Trp Ala Gln Val Ile Ala Leu Tyr
 370 375 380
 Pro Thr Leu Val Glu Cys Ile Thr Cys Ser Ser Ser Glu Val Cys Ser
 385 390 395 400

352

Ala Leu Lys Glu Ala Leu Val Pro Phe Lys Asp Phe Met Gln Pro Pro
 405 410 415

Ala Ser Arg Val Gln Asn Gly Glu Ser
 420 425

<210> 239

<211> 1053

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1053)

<400> 239

atg gat ttg aag gct ctc ctt tct tcc ttg aat gac ttt gca tcc ctc 48
 Met Asp Leu Lys Ala Leu Leu Ser Ser Leu Asn Asp Phe Ala Ser Leu
 1 5 10 15

tcg ttt gct gag agt tgg gac aat gtt gga tta ctg gtg gaa cca agc 96
 Ser Phe Ala Glu Ser Trp Asp Asn Val Gly Leu Leu Val Glu Pro Ser
 20 25 30

cca cca cat act gta aat aca ctc ttc ctg acc aat gac ctg act gag 144
 Pro Pro His Thr Val Asn Thr Leu Phe Leu Thr Asn Asp Leu Thr Glu
 35 40 45

gaa gtg atg gag gag gtg ctg caa aag aag gca gac ctc att ctc tcc 192
 Glu Val Met Glu Glu Val Leu Gln Lys Lys Ala Asp Leu Ile Leu Ser
 50 55 60

tac cat ccg cct atc ttc cga ccc atg aag cgc ata acc tgg aac aca 240
 Tyr His Pro Pro Ile Phe Arg Pro Met Lys Arg Ile Thr Trp Asn Thr
 65 70 75 80

tgg aag gag cgc ctg gtg atc cgg gct ctg gag aac aga gtc ggt atc 288
 Trp Lys Glu Arg Leu Val Ile Arg Ala Leu Glu Asn Arg Val Gly Ile
 85 90 95

tac tct cct cat aca gcc tat gat gct gcg ccc cag ggc gtc aac aac 336
 Tyr Ser Pro His Thr Ala Tyr Asp Ala Ala Pro Gln Gly Val Asn Asn
 100 105 110

tgg ttg gct aaa ggg ctt gga gct tgt acc tcc agg ccc ata cat cct 384

353

Trp	Leu	Ala	Lys	Gly	Leu	Gly	Ala	Cys	Thr	Ser	Arg	Pro	Ile	His	Pro		
	115						120					125					
tcc	aaa	gct	ccc	aac	tac	cct	aca	gag	gga	aac	cac	cga	gta	gaa	ttc	432	
Ser	Lys	Ala	Pro	Asn	Tyr	Pro	Thr	Glu	Gly	Asn	His	Arg	Val	Glu	Phe		
	130					135					140						
aac	gtt	aac	tac	acc	caa	gac	ctg	gac	aaa	gtc	atg	tct	gca	gtg	aaa	480	
Asn	Val	Asn	Tyr	Thr	Gln	Asp	Leu	Asp	Lys	Val	Met	Ser	Ala	Val	Lys		
145					150					155					160		
gga	att	gac	ggt	gtt	tct	gtc	act	tct	ttt	tct	gct	agg	act	ggt	aat	528	
Gly	Ile	Asp	Gly	Val	Ser	Val	Thr	Ser	Phe	Ser	Ala	Arg	Thr	Gly	Asn		
				165					170						175		
gag	gaa	caa	aca	cgg	att	aat	ctg	aat	tgt	act	cag	aag	gct	ttg	atg	576	
Glu	Glu	Gln	Thr	Arg	Ile	Asn	Leu	Asn	Cys	Thr	Gln	Lys	Ala	Leu	Met		
			180					185					190				
cag	gtg	gta	gat	ttt	ctt	tcc	cgg	aac	aaa	caa	ctt	tat	cag	aag	acg	624	
Gln	Val	Val	Asp	Phe	Leu	Ser	Arg	Asn	Lys	Gln	Leu	Tyr	Gln	Lys	Thr		
	195						200					205					
gaa	att	ctg	tca	ctg	gag	aag	cct	ttg	ctt	cta	cat	act	gga	atg	gga	672	
Glu	Ile	Leu	Ser	Leu	Glu	Lys	Pro	Leu	Leu	Leu	His	Thr	Gly	Met	Gly		
	210					215					220						
cgg	tta	tgc	aca	ctg	gat	gaa	tct	gtc	tcc	ctg	gca	acc	atg	att	gat	720	
Arg	Leu	Cys	Thr	Leu	Asp	Glu	Ser	Val	Ser	Leu	Ala	Thr	Met	Ile	Asp		
225					230					235					240		
cga	ata	aaa	aga	cac	cta	aaa	cta	tct	cat	att	cgc	tta	gcc	ctt	ggg	768	
Arg	Ile	Lys	Arg	His	Leu	Lys	Leu	Ser	His	Ile	Arg	Leu	Ala	Leu	Gly		
				245					250					255			
gtg	ggg	aga	acc	tta	gag	tct	caa	gtc	aaa	gtc	gtg	gcc	ctg	tgt	gct	816	
Val	Gly	Arg	Thr	Leu	Glu	Ser	Gln	Val	Lys	Val	Val	Ala	Leu	Cys	Ala		
			260					265					270				
ggt	tct	ggg	agc	agc	gtt	ctg	cag	ggt	gtt	gag	gct	gac	ctt	tac	ctc	864	
Gly	Ser	Gly	Ser	Ser	Val	Leu	Gln	Gly	Val	Glu	Ala	Asp	Leu	Tyr	Leu		
	275						280					285					
aca	ggt	gag	atg	tcc	cat	cat	gat	act	ttg	gat	gct	gct	tcc	caa	gga	912	

354

Thr	Gly	Glu	Met	Ser	His	His	Asp	Thr	Leu	Asp	Ala	Ala	Ser	Gln	Gly	
290						295					300					
ata	aat	gtc	atc	ctc	tgt	gaa	cac	agc	aac	act	gaa	cga	ggc	ttt	ctt	960
Ile	Asn	Val	Ile	Leu	Cys	Glu	His	Ser	Asn	Thr	Glu	Arg	Gly	Phe	Leu	
305					310					315					320	
tct	gac	ctt	cga	gat	atg	ctg	gat	tct	cac	ttg	gag	aat	aag	ata	aat	1008
Ser	Asp	Leu	Arg	Asp	Met	Leu	Asp	Ser	His	Leu	Glu	Asn	Lys	Ile	Asn	
				325					330					335		
att	atc	cta	tca	gag	act	gac	agg	gac	cct	ctt	cag	gtg	gta	taa		1053
Ile	Ile	Leu	Ser	Glu	Thr	Asp	Arg	Asp	Pro	Leu	Gln	Val	Val	*		
			340					345					350			

<210> 240

<211> 350

<212> PRT

<213> Homo sapiens

<400> 240

Met	Asp	Leu	Lys	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Asp	Phe	Ala	Ser	Leu	
1				5					10					15		
Ser	Phe	Ala	Glu	Ser	Trp	Asp	Asn	Val	Gly	Leu	Leu	Val	Glu	Pro	Ser	
			20					25					30			
Pro	Pro	His	Thr	Val	Asn	Thr	Leu	Phe	Leu	Thr	Asn	Asp	Leu	Thr	Glu	
		35				40					45					
Glu	Val	Met	Glu	Glu	Val	Leu	Gln	Lys	Lys	Ala	Asp	Leu	Ile	Leu	Ser	
	50					55				60						
Tyr	His	Pro	Pro	Ile	Phe	Arg	Pro	Met	Lys	Arg	Ile	Thr	Trp	Asn	Thr	
65				70						75				80		
Trp	Lys	Glu	Arg	Leu	Val	Ile	Arg	Ala	Leu	Glu	Asn	Arg	Val	Gly	Ile	
			85					90					95			
Tyr	Ser	Pro	His	Thr	Ala	Tyr	Asp	Ala	Ala	Pro	Gln	Gly	Val	Asn	Asn	
			100				105						110			
Trp	Leu	Ala	Lys	Gly	Leu	Gly	Ala	Cys	Thr	Ser	Arg	Pro	Ile	His	Pro	
	115						120					125				
Ser	Lys	Ala	Pro	Asn	Tyr	Pro	Thr	Glu	Gly	Asn	His	Arg	Val	Glu	Phe	
	130					135				140						
Asn	Val	Asn	Tyr	Thr	Gln	Asp	Leu	Asp	Lys	Val	Met	Ser	Ala	Val	Lys	
145					150					155				160		
Gly	Ile	Asp	Gly	Val	Ser	Val	Thr	Ser	Phe	Ser	Ala	Arg	Thr	Gly	Asn	
			165					170						175		

355

Glu Glu Gln Thr Arg Ile Asn Leu Asn Cys Thr Gln Lys Ala Leu Met
 180 185 190
 Gln Val Val Asp Phe Leu Ser Arg Asn Lys Gln Leu Tyr Gln Lys Thr
 195 200 205
 Glu Ile Leu Ser Leu Glu Lys Pro Leu Leu Leu His Thr Gly Met Gly
 210 215 220
 Arg Leu Cys Thr Leu Asp Glu Ser Val Ser Leu Ala Thr Met Ile Asp
 225 230 235 240
 Arg Ile Lys Arg His Leu Lys Leu Ser His Ile Arg Leu Ala Leu Gly
 245 250 255
 Val Gly Arg Thr Leu Glu Ser Gln Val Lys Val Val Ala Leu Cys Ala
 260 265 270
 Gly Ser Gly Ser Ser Val Leu Gln Gly Val Glu Ala Asp Leu Tyr Leu
 275 280 285
 Thr Gly Glu Met Ser His His Asp Thr Leu Asp Ala Ala Ser Gln Gly
 290 295 300
 Ile Asn Val Ile Leu Cys Glu His Ser Asn Thr Glu Arg Gly Phe Leu
 305 310 315 320
 Ser Asp Leu Arg Asp Met Leu Asp Ser His Leu Glu Asn Lys Ile Asn
 325 330 335
 Ile Ile Leu Ser Glu Thr Asp Arg Asp Pro Leu Gln Val Val
 340 345 350

<210> 241

<211> 933

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(933)

<400> 241

atg ggc gga gaa ttt tgt gtg gct gct atc ttc gga aca tcc agg tca 48
 Met Gly Gly Glu Phe Cys Val Ala Ala Ile Phe Gly Thr Ser Arg Ser
 1 5 10 15

tgg ttt gca aat aat gca ggt ctg aaa aga gaa aaa gat cag tcc aaa 96
 Trp Phe Ala Asn Asn Ala Gly Leu Lys Arg Glu Lys Asp Gln Ser Lys
 20 25 30

caa gtt gta gtt gag tcc ctg tac att atc agt tgc tat ggc acc tta 144
 Gln Val Val Val Glu Ser Leu Tyr Ile Ile Ser Cys Tyr Gly Thr Leu
 35 40 45

356

gtg gaa cac atg atg gag ccg cga ccc ctc agc act gca ccc aag att	192
Val Glu His Met Met Glu Pro Arg Pro Leu Ser Thr Ala Pro Lys Ile	
50 55 60	
agt gac gac aca cca ctg gaa atg atg aca tcg cct cga gcc agc tgg	240
Ser Asp Asp Thr Pro Leu Glu Met Met Thr Ser Pro Arg Ala Ser Trp	
65 70 75 80	
act ctg gtt aga acc cct caa tgg aat gaa ttg cag cca ccg ttt aat	288
Thr Leu Val Arg Thr Pro Gln Trp Asn Glu Leu Gln Pro Pro Phe Asn	
85 90 95	
gca aac cac cct ctg ctc ctc gct gca gat gca gta cag tat tat cag	336
Ala Asn His Pro Leu Leu Leu Ala Ala Asp Ala Val Gln Tyr Tyr Gln	
100 105 110	
ttc ctg ctt gct ggc ctg gtt ccc cct gga agt cct ggg ccc att act	384
Phe Leu Leu Ala Gly Leu Val Pro Pro Gly Ser Pro Gly Pro Ile Thr	
115 120 125	
cga cat ggg tct tac gac agt tta gct tct gac cat agt gga cag gaa	432
Arg His Gly Ser Tyr Asp Ser Leu Ala Ser Asp His Ser Gly Gln Glu	
130 135 140	
gat gaa gaa tgg ctt tcc cag gtt gaa att gta aca cac act gga ccc	480
Asp Glu Glu Trp Leu Ser Gln Val Glu Ile Val Thr His Thr Gly Pro	
145 150 155 160	
cat aga cgt ctg tgg atg ggt cca cag ttc cag ttc aaa acc atc cat	528
His Arg Arg Leu Trp Met Gly Pro Gln Phe Gln Phe Lys Thr Ile His	
165 170 175	
ccc tca ggc caa acc aca gtt atc tca tcc agt tca tct gtg ttg cag	576
Pro Ser Gly Gln Thr Thr Val Ile Ser Ser Ser Ser Ser Val Leu Gln	
180 185 190	
tct cat ggt ccg agt gac acg cca cag cct ctt ttg gat ttt gat aca	624
Ser His Gly Pro Ser Asp Thr Pro Gln Pro Leu Leu Asp Phe Asp Thr	
195 200 205	
gat gat ctt gat ctc aac agt ctc agg atc cag cca gtc cgc tct gac	672
Asp Asp Leu Asp Leu Asn Ser Leu Arg Ile Gln Pro Val Arg Ser Asp	
210 215 220	

357

ccc gtc agc atg cca ggg tca tcc cgt cca gtc tct gat cga agg gga 720
 Pro Val Ser Met Pro Gly Ser Ser Arg Pro Val Ser Asp Arg Arg Gly
 225 230 235 240

gtt tcc aca gtg att gat gct gcc tca ggt acc ttt gac agg agc gtg 768
 Val Ser Thr Val Ile Asp Ala Ala Ser Gly Thr Phe Asp Arg Ser Val
 245 250 255

acc ctg ctg gag gtg tgc ggg agc tgg cct gag ggc ttc ggg ctg cgg 816
 Thr Leu Leu Glu Val Cys Gly Ser Trp Pro Glu Gly Phe Gly Leu Arg
 260 265 270

cac atg tcc tcc atg gag cac acg gag gag ggc tcc ggg agc gac ttg 864
 His Met Ser Ser Met Glu His Thr Glu Glu Gly Ser Gly Ser Asp Leu
 275 280 285

ccg acg cca tgg ccg agt cac cta gcc ggg acg tcg tgg gat ccg gaa 912
 Pro Thr Pro Trp Pro Ser His Leu Ala Gly Thr Ser Trp Asp Pro Glu
 290 295 300

cag aca cag ccc ttg acg tag 933
 Gln Thr Gln Pro Leu Thr *
 305 310

<210> 242

<211> 310

<212> PRT

<213> Homo sapiens

<400> 242

Met Gly Gly Glu Phe Cys Val Ala Ala Ile Phe Gly Thr Ser Arg Ser
 1 5 10 15
 Trp Phe Ala Asn Asn Ala Gly Leu Lys Arg Glu Lys Asp Gln Ser Lys
 20 25 30
 Gln Val Val Val Glu Ser Leu Tyr Ile Ile Ser Cys Tyr Gly Thr Leu
 35 40 45
 Val Glu His Met Met Glu Pro Arg Pro Leu Ser Thr Ala Pro Lys Ile
 50 55 60
 Ser Asp Asp Thr Pro Leu Glu Met Met Thr Ser Pro Arg Ala Ser Trp
 65 70 75 80
 Thr Leu Val Arg Thr Pro Gln Trp Asn Glu Leu Gln Pro Pro Phe Asn
 85 90 95

358

Ala Asn His Pro Leu Leu Leu Ala Ala Asp Ala Val Gln Tyr Tyr Gln
 100 105 110
 Phe Leu Leu Ala Gly Leu Val Pro Pro Gly Ser Pro Gly Pro Ile Thr
 115 120 125
 Arg His Gly Ser Tyr Asp Ser Leu Ala Ser Asp His Ser Gly Gln Glu
 130 135 140
 Asp Glu Glu Trp Leu Ser Gln Val Glu Ile Val Thr His Thr Gly Pro
 145 150 155 160
 His Arg Arg Leu Trp Met Gly Pro Gln Phe Gln Phe Lys Thr Ile His
 165 170 175
 Pro Ser Gly Gln Thr Thr Val Ile Ser Ser Ser Ser Ser Val Leu Gln
 180 185 190
 Ser His Gly Pro Ser Asp Thr Pro Gln Pro Leu Leu Asp Phe Asp Thr
 195 200 205
 Asp Asp Leu Asp Leu Asn Ser Leu Arg Ile Gln Pro Val Arg Ser Asp
 210 215 220
 Pro Val Ser Met Pro Gly Ser Ser Arg Pro Val Ser Asp Arg Arg Gly
 225 230 235 240
 Val Ser Thr Val Ile Asp Ala Ala Ser Gly Thr Phe Asp Arg Ser Val
 245 250 255
 Thr Leu Leu Glu Val Cys Gly Ser Trp Pro Glu Gly Phe Gly Leu Arg
 260 265 270
 His Met Ser Ser Met Glu His Thr Glu Glu Gly Ser Gly Ser Asp Leu
 275 280 285
 Pro Thr Pro Trp Pro Ser His Leu Ala Gly Thr Ser Trp Asp Pro Glu
 290 295 300
 Gln Thr Gln Pro Leu Thr
 305 310

<210> 243
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(465)

<221> misc_feature
 <222> (1)...(465)
 <223> n = A,T,C or G

<400> 243

atg tnc tct ggg gcg agg aca cgg ctt ntg gct nct ggc nct gct gtc

359

Met	Xaa	Ser	Gly	Ala	Arg	Thr	Arg	Leu	Xaa	Ala	Xaa	Gly	Xaa	Ala	Val	
1				5					10					15		
tca	ctg	gcc	nct	ttg	ttg	aat	aag	gcg	gct	gat	aaa	gga	agc	agg	aag	96
Ser	Leu	Ala	Xaa	Leu	Leu	Asn	Lys	Ala	Ala	Asp	Lys	Gly	Ser	Arg	Lys	
			20					25					30			
cgc	tat	gaa	cca	tca	gac	aag	gac	agg	cag	agc	cct	cct	cca	gcc	aag	144
Arg	Tyr	Glu	Pro	Ser	Asp	Lys	Asp	Arg	Gln	Ser	Pro	Pro	Pro	Pro	Ala	Lys
			35				40					45				
cgg	ccc	aac	aca	tcc	cca	gac	cga	ggg	tct	cgg	gac	cgg	aag	tca	ggg	192
Arg	Pro	Asn	Thr	Ser	Pro	Asp	Arg	Gly	Ser	Arg	Asp	Arg	Lys	Ser	Gly	
	50					55					60					
ggg	aga	ctg	ggc	tcc	ccg	aag	cca	gag	cgg	cag	aga	ggc	cag	aac	tcc	240
Gly	Arg	Leu	Gly	Ser	Pro	Lys	Pro	Glu	Arg	Gln	Arg	Gly	Gln	Asn	Ser	
	65				70				75						80	
aaa	gcc	cct	gca	gcc	ccg	gct	gac	agg	aag	cgc	can	ntg	tca	ccc	cag	288
Lys	Ala	Pro	Ala	Ala	Pro	Ala	Asp	Arg	Lys	Arg	Xaa	Xaa	Ser	Pro	Gln	
			85					90						95		
tcc	aag	agc	tcc	agc	aag	gtc	acg	agc	gtg	ccc	ggc	aaa	gcc	tcg	gat	336
Ser	Lys	Ser	Ser	Ser	Lys	Val	Thr	Ser	Val	Pro	Gly	Lys	Ala	Ser	Asp	
			100					105					110			
ccc	ggc	gcc	gcc	agc	acc	aaa	tca	ggg	aag	gcc	agc	acg	ctg	tct	cgg	384
Pro	Gly	Ala	Ala	Ser	Thr	Lys	Ser	Gly	Lys	Ala	Ser	Thr	Leu	Ser	Arg	
		115					120					125				
cgg	gag	gag	ctg	ctg	aaa	cag	ctg	aag	gcc	gtg	gag	gat	gct	att	gca	432
Arg	Glu	Glu	Leu	Leu	Lys	Gln	Leu	Lys	Ala	Val	Glu	Asp	Ala	Ile	Ala	
	130					135				140						
cgc	aag	cgg	gcc	aag	atc	ccc	ggg	aaa	gca	tag						465
Arg	Lys	Arg	Ala	Lys	Ile	Pro	Gly	Lys	Ala	*						
145					150											

<210> 244

<211> 154

<212> PRT

<213> Homo sapiens

360

<220>

<221> VARIANT

<222> (1)...(154)

<223> Xaa = Any Amino Acid

<400> 244

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Met Xaa Ser Gly Ala Arg Thr Arg Leu Xaa Ala Xaa Gly Xaa Ala Val
 1          5          10          15
Ser Leu Ala Xaa Leu Leu Asn Lys Ala Ala Asp Lys Gly Ser Arg Lys
          20          25          30
Arg Tyr Glu Pro Ser Asp Lys Asp Arg Gln Ser Pro Pro Pro Ala Lys
          35          40          45
Arg Pro Asn Thr Ser Pro Asp Arg Gly Ser Arg Asp Arg Lys Ser Gly
          50          55          60
Gly Arg Leu Gly Ser Pro Lys Pro Glu Arg Gln Arg Gly Gln Asn Ser
65          70          75          80
Lys Ala Pro Ala Ala Pro Ala Asp Arg Lys Arg Xaa Xaa Ser Pro Gln
          85          90          95
Ser Lys Ser Ser Ser Lys Val Thr Ser Val Pro Gly Lys Ala Ser Asp
          100          105          110
Pro Gly Ala Ala Ser Thr Lys Ser Gly Lys Ala Ser Thr Leu Ser Arg
          115          120          125
Arg Glu Glu Leu Leu Lys Gln Leu Lys Ala Val Glu Asp Ala Ile Ala
          130          135          140
Arg Lys Arg Ala Lys Ile Pro Gly Lys Ala
145          150

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<210> 245

<211> 1839

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1839)

<400> 245

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atg gcg gcg gcg ggc cgg ctc ccg agc tcc tgg gcc ctc ttc tcg ccg      48
Met Ala Ala Ala Gly Arg Leu Pro Ser Ser Trp Ala Leu Phe Ser Pro
 1          5          10          15

ctc ctc gca ggg ctt gca cta ctg gga gtc ggg ccg gtc cca gcg cgg      96
Leu Leu Ala Gly Leu Ala Leu Leu Gly Val Gly Pro Val Pro Ala Arg

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361

20	25	30	
gcg ctg cac aac gtc acg gcc gag ctc ttt ggg gcc gag gcc tgg ggc Ala Leu His Asn Val Thr Ala Glu Leu Phe Gly Ala Glu Ala Trp Gly 35 40 45			144
acc ctt gcg gct ttc ggg gac ctc aac tcc gac aag cag acg gat ctc Thr Leu Ala Ala Phe Gly Asp Leu Asn Ser Asp Lys Gln Thr Asp Leu 50 55 60			192
ttc gtg ctg cgg gaa aga aat gac tta atc gtc ttt ttg gca gac cag Phe Val Leu Arg Glu Arg Asn Asp Leu Ile Val Phe Leu Ala Asp Gln 65 70 75 80			240
aat gca ccc tat ttt aaa ccc aaa gta aag gta tct ttc aag aat cac Asn Ala Pro Tyr Phe Lys Pro Lys Val Lys Val Ser Phe Lys Asn His 85 90 95			288
agt gca ttg ata aca agt gta gtc cct ggg gat tat gat gga gat tct Ser Ala Leu Ile Thr Ser Val Val Pro Gly Asp Tyr Asp Gly Asp Ser 100 105 110			336
caa atg gat gtc ctt ctg aca tat ctt ccc aaa aat tat gcc aag agt Gln Met Asp Val Leu Leu Thr Tyr Leu Pro Lys Asn Tyr Ala Lys Ser 115 120 125			384
gaa tta gga gct gtt atc ttc tgg gga caa aat caa aca tta gat cct Glu Leu Gly Ala Val Ile Phe Trp Gly Gln Asn Gln Thr Leu Asp Pro 130 135 140			432
aac aat atg acc ata ctc aat agg act ttt caa gat gag cca cta att Asn Asn Met Thr Ile Leu Asn Arg Thr Phe Gln Asp Glu Pro Leu Ile 145 150 155 160			480
atg gat ttc aat ggt gat cta att cct gat att ttt ggt atc aca aat Met Asp Phe Asn Gly Asp Leu Ile Pro Asp Ile Phe Gly Ile Thr Asn 165 170 175			528
gaa tcc aac cag cca cag ata cta tta gga ggg aat tta tca tgg cat Glu Ser Asn Gln Pro Gln Ile Leu Leu Gly Gly Asn Leu Ser Trp His 180 185 190			576
cca gca ttg acc act aca agt aaa atg cga att cca cat tct cat gca Pro Ala Leu Thr Thr Thr Ser Lys Met Arg Ile Pro His Ser His Ala			624

362

195	200	205	
ttt att gat ctg act gaa gat ttt aca gca gat tta ttc ctg acg aca Phe Ile Asp Leu Thr Glu Asp Phe Thr Ala Asp Leu Phe Leu Thr Thr 210 215 220			672
ttg aat gcc acc act agt acc ttc cag ttt gaa ata tgg gaa aat ttg Leu Asn Ala Thr Thr Ser Thr Phe Gln Phe Glu Ile Trp Glu Asn Leu 225 230 235 240			720
gat gga aac ttc tct gtc agt act ata ttg gaa aaa cct caa aat atg Asp Gly Asn Phe Ser Val Ser Thr Ile Leu Glu Lys Pro Gln Asn Met 245 250 255			768
atg gtg gtt gga cag tca gca ttt gca gac ttt gat gga gat gga cac Met Val Val Gly Gln Ser Ala Phe Ala Asp Phe Asp Gly Asp Gly His 260 265 270			816
atg gat cat tta ctg cca ggc tgt gaa gat aaa aat tgc caa aag agt Met Asp His Leu Leu Pro Gly Cys Glu Asp Lys Asn Cys Gln Lys Ser 275 280 285			864
acc atc tac tta gtg aga tct ggg atg aag cag tgg gtt cca gtc cta Thr Ile Tyr Leu Val Arg Ser Gly Met Lys Gln Trp Val Pro Val Leu 290 295 300			912
caa gat ttc agc aat aag ggc aca ctc tgg ggc ttt gtg cca ttt gtg Gln Asp Phe Ser Asn Lys Gly Thr Leu Trp Gly Phe Val Pro Phe Val 305 310 315 320			960
gat gaa cag caa cca act gaa ata cca att cca att acc ctt cat att Asp Glu Gln Gln Pro Thr Glu Ile Pro Ile Pro Ile Thr Leu His Ile 325 330 335			1008
gga gac tac aat atg gat ggc tat cca gac gct ctg gtc ata cta aag Gly Asp Tyr Asn Met Asp Gly Tyr Pro Asp Ala Leu Val Ile Leu Lys 340 345 350			1056
aac aca tct gga agc aac cag cag gcc ttt tta ctg gag aac gtc cct Asn Thr Ser Gly Ser Asn Gln Gln Ala Phe Leu Leu Glu Asn Val Pro 355 360 365			1104
tgt aat aat gca agc tgt gaa gag gcg cgt cga atg ttt aaa gtc tac Cys Asn Asn Ala Ser Cys Glu Glu Ala Arg Arg Met Phe Lys Val Tyr			1152

363

370	375	380	
tgg gag ctg aca gac cta aat caa att aag gat gcc atg gtt gcc acc			1200
Trp Glu Leu Thr Asp Leu Asn Gln Ile Lys Asp Ala Met Val Ala Thr			
385	390	395	400
ttc ttt gac att tac gaa gat gga atc ttg gac att gta gtg cta agt			1248
Phe Phe Asp Ile Tyr Glu Asp Gly Ile Leu Asp Ile Val Val Leu Ser			
	405	410	415
aaa gga tat aca aag aat gat ttt gcc att cat aca cta aaa aat aac			1296
Lys Gly Tyr Thr Lys Asn Asp Phe Ala Ile His Thr Leu Lys Asn Asn			
	420	425	430
ttt gaa gca gat gct tat ttt gtt aaa gtt att gtt ctt agt ggt ctg			1344
Phe Glu Ala Asp Ala Tyr Phe Val Lys Val Ile Val Leu Ser Gly Leu			
	435	440	445
tgt tct aat gac tgt cct cgt aag ata aca ccc ttt gga gtg aat caa			1392
Cys Ser Asn Asp Cys Pro Arg Lys Ile Thr Pro Phe Gly Val Asn Gln			
	450	455	460
cct gga cct tat atc atg tat aca act gta gat gca aat ggg tat ctg			1440
Pro Gly Pro Tyr Ile Met Tyr Thr Thr Val Asp Ala Asn Gly Tyr Leu			
	465	470	475
aaa aat gga tca gct ggc caa ctc agc caa tcc gca cat tta gct ctc			1488
Lys Asn Gly Ser Ala Gly Gln Leu Ser Gln Ser Ala His Leu Ala Leu			
	485	490	495
caa cta cca tac aac gtg ctt ggt tta ggt cgg agc gca aat ttt ctt			1536
Gln Leu Pro Tyr Asn Val Leu Gly Leu Gly Arg Ser Ala Asn Phe Leu			
	500	505	510
gac cat ctc tac gtt ggt att ccc cgt cca tct gga gaa aaa tct ata			1584
Asp His Leu Tyr Val Gly Ile Pro Arg Pro Ser Gly Glu Lys Ser Ile			
	515	520	525
cga aaa caa gag tgg act gca atc att cca aat tcc cag cta att gtc			1632
Arg Lys Gln Glu Trp Thr Ala Ile Ile Pro Asn Ser Gln Leu Ile Val			
	530	535	540
att cca tac cct cac aat gtc cct cga agt tgg agt gcc aaa ctg tat			1680
Ile Pro Tyr Pro His Asn Val Pro Arg Ser Trp Ser Ala Lys Leu Tyr			

364

545	550	555	560	
ctt aca cca agt aat att gtt ctg ctt act gct ata gct ctc atc ggt				1728
Leu Thr Pro Ser Asn Ile Val Leu Leu Thr Ala Ile Ala Leu Ile Gly				
	565	570	575	
gtc tgt gtt ttc atc ttg gca ata att ggc att tta cat tgg cag gaa				1776
Val Cys Val Phe Ile Leu Ala Ile Ile Gly Ile Leu His Trp Gln Glu				
	580	585	590	
aag aaa gca gat gat aga gaa aaa cga caa gaa gcc cac cgg ttt cat				1824
Lys Lys Ala Asp Asp Arg Glu Lys Arg Gln Glu Ala His Arg Phe His				
	595	600	605	
ttt gat gct atg tga				1839
Phe Asp Ala Met *				
610				

<210> 246

<211> 612

<212> PRT

<213> Homo sapiens

<400> 246

Met	Ala	Ala	Ala	Gly	Arg	Leu	Pro	Ser	Ser	Trp	Ala	Leu	Phe	Ser	Pro
1				5					10					15	
Leu	Leu	Ala	Gly	Leu	Ala	Leu	Leu	Gly	Val	Gly	Pro	Val	Pro	Ala	Arg
		20						25					30		
Ala	Leu	His	Asn	Val	Thr	Ala	Glu	Leu	Phe	Gly	Ala	Glu	Ala	Trp	Gly
		35					40					45			
Thr	Leu	Ala	Ala	Phe	Gly	Asp	Leu	Asn	Ser	Asp	Lys	Gln	Thr	Asp	Leu
	50					55					60				
Phe	Val	Leu	Arg	Glu	Arg	Asn	Asp	Leu	Ile	Val	Phe	Leu	Ala	Asp	Gln
65			70							75				80	
Asn	Ala	Pro	Tyr	Phe	Lys	Pro	Lys	Val	Lys	Val	Ser	Phe	Lys	Asn	His
			85					90					95		
Ser	Ala	Leu	Ile	Thr	Ser	Val	Val	Pro	Gly	Asp	Tyr	Asp	Gly	Asp	Ser
		100						105					110		
Gln	Met	Asp	Val	Leu	Leu	Thr	Tyr	Leu	Pro	Lys	Asn	Tyr	Ala	Lys	Ser
		115					120						125		
Glu	Leu	Gly	Ala	Val	Ile	Phe	Trp	Gly	Gln	Asn	Gln	Thr	Leu	Asp	Pro
	130						135				140				
Asn	Asn	Met	Thr	Ile	Leu	Asn	Arg	Thr	Phe	Gln	Asp	Glu	Pro	Leu	Ile

365

145 150 155 160
 Met Asp Phe Asn Gly Asp Leu Ile Pro Asp Ile Phe Gly Ile Thr Asn
 165 170 175
 Glu Ser Asn Gln Pro Gln Ile Leu Leu Gly Gly Asn Leu Ser Trp His
 180 185 190
 Pro Ala Leu Thr Thr Thr Ser Lys Met Arg Ile Pro His Ser His Ala
 195 200 205
 Phe Ile Asp Leu Thr Glu Asp Phe Thr Ala Asp Leu Phe Leu Thr Thr
 210 215 220
 Leu Asn Ala Thr Thr Ser Thr Phe Gln Phe Glu Ile Trp Glu Asn Leu
 225 230 235 240
 Asp Gly Asn Phe Ser Val Ser Thr Ile Leu Glu Lys Pro Gln Asn Met
 245 250 255
 Met Val Val Gly Gln Ser Ala Phe Ala Asp Phe Asp Gly Asp Gly His
 260 265 270
 Met Asp His Leu Leu Pro Gly Cys Glu Asp Lys Asn Cys Gln Lys Ser
 275 280 285
 Thr Ile Tyr Leu Val Arg Ser Gly Met Lys Gln Trp Val Pro Val Leu
 290 295 300
 Gln Asp Phe Ser Asn Lys Gly Thr Leu Trp Gly Phe Val Pro Phe Val
 305 310 315 320
 Asp Glu Gln Gln Pro Thr Glu Ile Pro Ile Pro Ile Thr Leu His Ile
 325 330 335
 Gly Asp Tyr Asn Met Asp Gly Tyr Pro Asp Ala Leu Val Ile Leu Lys
 340 345 350
 Asn Thr Ser Gly Ser Asn Gln Gln Ala Phe Leu Leu Glu Asn Val Pro
 355 360 365
 Cys Asn Asn Ala Ser Cys Glu Glu Ala Arg Arg Met Phe Lys Val Tyr
 370 375 380
 Trp Glu Leu Thr Asp Leu Asn Gln Ile Lys Asp Ala Met Val Ala Thr
 385 390 395 400
 Phe Phe Asp Ile Tyr Glu Asp Gly Ile Leu Asp Ile Val Val Leu Ser
 405 410 415
 Lys Gly Tyr Thr Lys Asn Asp Phe Ala Ile His Thr Leu Lys Asn Asn
 420 425 430
 Phe Glu Ala Asp Ala Tyr Phe Val Lys Val Ile Val Leu Ser Gly Leu
 435 440 445
 Cys Ser Asn Asp Cys Pro Arg Lys Ile Thr Pro Phe Gly Val Asn Gln
 450 455 460
 Pro Gly Pro Tyr Ile Met Tyr Thr Thr Val Asp Ala Asn Gly Tyr Leu
 465 470 475 480
 Lys Asn Gly Ser Ala Gly Gln Leu Ser Gln Ser Ala His Leu Ala Leu
 485 490 495
 Gln Leu Pro Tyr Asn Val Leu Gly Leu Gly Arg Ser Ala Asn Phe Leu

366

500 505 510
 Asp His Leu Tyr Val Gly Ile Pro Arg Pro Ser Gly Glu Lys Ser Ile
 515 520 525
 Arg Lys Gln Glu Trp Thr Ala Ile Ile Pro Asn Ser Gln Leu Ile Val
 530 535 540
 Ile Pro Tyr Pro His Asn Val Pro Arg Ser Trp Ser Ala Lys Leu Tyr
 545 550 555 560
 Leu Thr Pro Ser Asn Ile Val Leu Leu Thr Ala Ile Ala Leu Ile Gly
 565 570 575
 Val Cys Val Phe Ile Leu Ala Ile Ile Gly Ile Leu His Trp Gln Glu
 580 585 590
 Lys Lys Ala Asp Asp Arg Glu Lys Arg Gln Glu Ala His Arg Phe His
 595 600 605
 Phe Asp Ala Met
 610

<210> 247
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(462)

<400> 247
 atg ggc cgg ctc cca ttg ctc cgg cgc gtt ctc aag ggc ttg cag ctg 48
 Met Gly Arg Leu Pro Leu Leu Arg Arg Val Leu Lys Gly Leu Gln Leu
 1 5 10 15
 ttg ctg tct ctg ctg gcc ttc atc tgt gaa gaa gtt gta tca caa tgt 96
 Leu Leu Ser Leu Leu Ala Phe Ile Cys Glu Glu Val Val Ser Gln Cys
 20 25 30
 act tta tgt gga gga ctt tat ttt ttt gag ttt gta agc tgc agt gcc 144
 Thr Leu Cys Gly Gly Leu Tyr Phe Phe Glu Phe Val Ser Cys Ser Ala
 35 40 45
 ttt ctt ctg agt ctc ctt ata ctg att gtg tat tgc act cca ttt tat 192
 Phe Leu Leu Ser Leu Leu Ile Leu Ile Val Tyr Cys Thr Pro Phe Tyr
 50 55 60
 gag aga gtt gat acc aca aaa gta aaa tca tcg gat ttt tat att act 240
 Glu Arg Val Asp Thr Thr Lys Val Lys Ser Ser Asp Phe Tyr Ile Thr

367

65	70	75	80	
ttg gga aca gga tgt gtg ttt ttg ttg gca tcc atc att ttt gtt tcc	288			
Leu Gly Thr Gly Cys Val Phe Leu Leu Ala Ser Ile Ile Phe Val Ser				
85	90	95		
aca cat gac agg act tca gct gag att gct gca att gtg ttt gga ttt	336			
Thr His Asp Arg Thr Ser Ala Glu Ile Ala Ala Ile Val Phe Gly Phe				
100	105	110		
ata gca agt ttt atg ttc cta ctt gac ttt atc act atg ctg tat gaa	384			
Ile Ala Ser Phe Met Phe Leu Leu Asp Phe Ile Thr Met Leu Tyr Glu				
115	120	125		
aaa cga cag gag tcc cag ctg aga aaa cct gaa aat acc act agg gct	432			
Lys Arg Gln Glu Ser Gln Leu Arg Lys Pro Glu Asn Thr Thr Arg Ala				
130	135	140		
gaa gcc ctc act gag cca ctt aat gcc taa	462			
Glu Ala Leu Thr Glu Pro Leu Asn Ala *				
145	150			

<210> 248

<211> 153

<212> PRT

<213> Homo sapiens

<400> 248

Met Gly Arg Leu Pro Leu Leu Arg Arg Val Leu Lys Gly Leu Gln Leu	
1 5 10 15	
Leu Leu Ser Leu Leu Ala Phe Ile Cys Glu Glu Val Val Ser Gln Cys	
20 25 30	
Thr Leu Cys Gly Gly Leu Tyr Phe Phe Glu Phe Val Ser Cys Ser Ala	
35 40 45	
Phe Leu Leu Ser Leu Leu Ile Leu Ile Val Tyr Cys Thr Pro Phe Tyr	
50 55 60	
Glu Arg Val Asp Thr Thr Lys Val Lys Ser Ser Asp Phe Tyr Ile Thr	
65 70 75 80	
Leu Gly Thr Gly Cys Val Phe Leu Leu Ala Ser Ile Ile Phe Val Ser	
85 90 95	
Thr His Asp Arg Thr Ser Ala Glu Ile Ala Ala Ile Val Phe Gly Phe	
100 105 110	
Ile Ala Ser Phe Met Phe Leu Leu Asp Phe Ile Thr Met Leu Tyr Glu	

368

115 120 125
 Lys Arg Gln Glu Ser Gln Leu Arg Lys Pro Glu Asn Thr Thr Arg Ala
 130 135 140
 Glu Ala Leu Thr Glu Pro Leu Asn Ala
 145 150

<210> 249
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1071)

<221> misc_feature
 <222> (1)...(1071)
 <223> n = A,T,C or G

<400> 249
 atg aca ggg acc atc ctt tca ggc tcc atc agc ctc ggt gac agt gtg 48
 Met Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val
 1 5 10 15
 gag atc cct gcc ctc aag gtg gtg aag aag gtg aag tcc atg cag atg 96
 Glu Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met
 20 25 30
 ttc cac atg ccc atc act tca gcc atg caa gga gac cgg ctg ggc atc 144
 Phe His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile
 35 40 45
 tgc gtc acc cag ttt gac cct aag ctg ctg gag cgc ggg ttg gtg tgt 192
 Cys Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys
 50 55 60
 gcc ccc gag tcc ctg cac act gtc cat gcg gcc ctc atc tct gtg gaa 240
 Ala Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu
 65 70 75 80
 aag ata ccg tat ttc cgg ggg ccc ctg caa acc aag gcc aag ttc cac 288
 Lys Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His
 85 90 95

369

att aca gtg ggc cat gaa aca gtc atg ggc cgg ttg atg ttc ttc agt Ile Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser 100 105 110	336
cct gct cca gat aac ttt gac cag gag cct ata ctg gac tct ttc aac Pro Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn 115 120 125	384
ttc tct caa gaa tac ctt ttc cag gag cag tac ctg tcc aag gat ttg Phe Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu 130 135 140	432
aca cca gca gtg aca gac aat gat gag gcc gac aag aag gcc ggc cag Thr Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln 145 150 155 160	480
gcc aca gag ggc cat tgt cct cgg cag cag tgg gcc ctg gtg gag ttt Ala Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe 165 170 175	528
gag aag ccc gtc acc tgc cct cgg ctg tgc ctg gtg att ggc tcc agg Glu Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg 180 185 190	576
cta gat gcg gac att cac acc aac acg tgc cgg cta gcc ttc cat ggc Leu Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly 195 200 205	624
atc ctg ctc cac ggg cta gag gac agg aac tac gcc gac agc ttc ctg Ile Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu 210 215 220	672
ccc agg ctg aag gtg tac aag ctg aag cac aag cat ggc ctt gtg gag Pro Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu 225 230 235 240	720
cgg gcg atg gat gac tac agt gtg atc ggc cgc tcc ctg ttc aaa aag Arg Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys 245 250 255	768
gaa acc aac atc cag ctc ttc gtg ggg ctc aag gtg cac ttg tcc act Glu Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr 260 265 270	816

370

ggg gaa ctg ggc atc atc gac agt gcc ttc ggc cag agc ggc aag ttc 864
Gly Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe
275 280 285

aag atc cac atc cca ggt ggc ctc agc ccc gag tcc aag aag atc ctg 912
Lys Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu
290 295 300

aca ccc gcc ctc aag aag cgg gcc cgg gct ggc cgt ggg gag gcc acc 960
Thr Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr
305 310 315 320

agg cag gag gag agc gcc gag cgg agn ngg ccc tca cag cat gtg gtg 1008
Arg Gln Glu Glu Ser Ala Glu Arg Xaa Xaa Pro Ser Gln His Val Val
325 330 335

ctc agc ctg act ttc aag cgt tat gtc ttc gac acc cac aag cgc atg 1056
Leu Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met
340 345 350

gtt cag tct ccc tga 1071
Val Gln Ser Pro *
355

<210> 250

<211> 356

<212> PRT

<213> Homo sapiens

$\langle 220 \rangle$

<221> VARIANT

<222> (1)...(356)

<223> Xaa = Any Amino Acid

<400> 250

Met Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val
1 5 10 15
Glu Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met
20 25 30
Phe His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile
35 40 45
Cys Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys
50 55 60

371

Ala Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu
 65 70 75 80
 Lys Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His
 85 90 95
 Ile Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser
 100 105 110
 Pro Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn
 115 120 125
 Phe Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu
 130 135 140
 Thr Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln
 145 150 155 160
 Ala Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe
 165 170 175
 Glu Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg
 180 185 190
 Leu Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly
 195 200 205
 Ile Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu
 210 215 220
 Pro Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu
 225 230 235 240
 Arg Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys
 245 250 255
 Glu Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr
 260 265 270
 Gly Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe
 275 280 285
 Lys Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu
 290 295 300
 Thr Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr
 305 310 315 320
 Arg Gln Glu Glu Ser Ala Glu Arg Xaa Xaa Pro Ser Gln His Val Val
 325 330 335
 Leu Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met
 340 345 350
 Val Gln Ser Pro
 355

<210> 251

<211> 567

<212> DNA

<213> Homo sapiens

372

<220>

<221> CDS

<222> (1)...(567)

<400> 251

atg gct gcc tct gcc ttt gct ggt gca gtg aga gca gct tca gga atc	48
Met Ala Ala Ser Ala Phe Ala Gly Ala Val Arg Ala Ala Ser Gly Ile	
1 5 10 15	

cta cgg tcc ctg aat att ttg gca tct tca acc tac cgc aac tgt gtc	96
Leu Arg Ser Leu Asn Ile Leu Ala Ser Ser Thr Tyr Arg Asn Cys Val	
20 25 30	

aag aat gcc tct ctt att tct gca ttg tcc act gga cgt ttt agt cat	144
Lys Asn Ala Ser Leu Ile Ser Ala Leu Ser Thr Gly Arg Phe Ser His	
35 40 45	

att cag aca cca gtt gtt tcc tcc act ccc aga ctt acc aca tct gag	192
Ile Gln Thr Pro Val Val Ser Ser Thr Pro Arg Leu Thr Thr Ser Glu	
50 55 60	

aga aac ctg aca tgt ggg cat acc tca gtg atc ctt aat aga atg gcc	240
Arg Asn Leu Thr Cys Gly His Thr Ser Val Ile Leu Asn Arg Met Ala	
65 70 75 80	

ccc gtg ctt cca agt gtc ctg aag ctg cca gtc aga tct cta aca tac	288
Pro Val Leu Pro Ser Val Leu Lys Leu Pro Val Arg Ser Leu Thr Tyr	
85 90 95	

ttc agt gca aga aaa ggc aag aga aag acc gtg aaa gct gtc atc gat	336
Phe Ser Ala Arg Lys Gly Lys Arg Lys Thr Val Lys Ala Val Ile Asp	
100 105 110	

agg ttt ctt cga ctt cat tgt ggc ctt tgg gtg agg aga aag gct ggc	384
Arg Phe Leu Arg Leu His Cys Gly Leu Trp Val Arg Arg Lys Ala Gly	
115 120 125	

tat aag aaa aaa tta tgg aaa aag aca cct gca agg aag aag cga ttg	432
Tyr Lys Lys Lys Leu Trp Lys Lys Thr Pro Ala Arg Lys Lys Arg Leu	
130 135 140	

agg gaa ttt gta ttc tgc aat aaa acc cag agt aaa ctc tta gat aaa	480
Arg Glu Phe Val Phe Cys Asn Lys Thr Gln Ser Lys Leu Leu Asp Lys	
145 150 155 160	

373

atg acg acg tcc ttc tgg aag agg cga aac tgg tac gtt gat gat cct 528
 Met Thr Thr Ser Phe Trp Lys Arg Arg Asn Trp Tyr Val Asp Asp Pro
 165 170 175

tat cag aag tat cat gat cga aca aac ctg aaa gta tag 567
 Tyr Gln Lys Tyr His Asp Arg Thr Asn Leu Lys Val *
 180 185

<210> 252

<211> 188

<212> PRT

<213> Homo sapiens

<400> 252

Met Ala Ala Ser Ala Phe Ala Gly Ala Val Arg Ala Ala Ser Gly Ile
 1 5 10 15
 Leu Arg Ser Leu Asn Ile Leu Ala Ser Ser Thr Tyr Arg Asn Cys Val
 20 25 30
 Lys Asn Ala Ser Leu Ile Ser Ala Leu Ser Thr Gly Arg Phe Ser His
 35 40 45
 Ile Gln Thr Pro Val Val Ser Ser Thr Pro Arg Leu Thr Thr Ser Glu
 50 55 60
 Arg Asn Leu Thr Cys Gly His Thr Ser Val Ile Leu Asn Arg Met Ala
 65 70 75 80
 Pro Val Leu Pro Ser Val Leu Lys Leu Pro Val Arg Ser Leu Thr Tyr
 85 90 95
 Phe Ser Ala Arg Lys Gly Lys Arg Lys Thr Val Lys Ala Val Ile Asp
 100 105 110
 Arg Phe Leu Arg Leu His Cys Gly Leu Trp Val Arg Arg Lys Ala Gly
 115 120 125
 Tyr Lys Lys Lys Leu Trp Lys Lys Thr Pro Ala Arg Lys Lys Arg Leu
 130 135 140
 Arg Glu Phe Val Phe Cys Asn Lys Thr Gln Ser Lys Leu Leu Asp Lys
 145 150 155 160
 Met Thr Thr Ser Phe Trp Lys Arg Arg Asn Trp Tyr Val Asp Asp Pro
 165 170 175
 Tyr Gln Lys Tyr His Asp Arg Thr Asn Leu Lys Val
 180 185

<210> 253

<211> 453

<212> DNA

374

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(453)

<400> 253

atg gac ttc cac ata ctg atc gtc atc ggt tgt gtg gtc agc gcc tcg	48
Met Asp Phe His Ile Leu Ile Val Ile Gly Cys Val Val Ser Ala Ser	
1 5 10 15	
ctg ctc tcg ttc ctg ttc atc aac aag atc ttc cgg cgc aag act ttt	96
Leu Leu Ser Phe Leu Phe Ile Asn Lys Ile Phe Arg Arg Lys Thr Phe	
20 25 30	
gag gag gtg gta gcc gag aag cgt gcc ctg agc gcc aat ctc tac aag	144
Glu Glu Val Val Ala Glu Lys Arg Ala Leu Ser Ala Asn Leu Tyr Lys	
35 40 45	
gcg gcc ggt ggt gcc gct acc aag aag ccc aag aag aag gaa ctt aag	192
Ala Ala Gly Gly Ala Ala Thr Lys Lys Pro Lys Lys Lys Glu Leu Lys	
50 55 60	
cgc gaa aag aag caa cgt cag cgg gaa cag cag agg gat gtg aac aac	240
Arg Glu Lys Lys Gln Arg Gln Arg Glu Gln Gln Arg Asp Val Asn Asn	
65 70 75 80	
gag ccg gaa cca gag gaa gcc gaa gac tac tcc gat ggt cag tcg gag	288
Glu Pro Glu Pro Glu Glu Ala Glu Asp Tyr Ser Asp Gly Gln Ser Glu	
85 90 95	
ggt cag ggc tcc gtg gct ggc gag gaa ccc ggt ctc tcc aag cag cat	336
Gly Gln Gly Ser Val Ala Gly Glu Glu Pro Gly Leu Ser Lys Gln His	
100 105 110	
gtt gaa ttt gaa ccc gat gca gag gtc ctc act gat cag cga cga ccc	384
Val Glu Phe Glu Pro Asp Ala Glu Val Leu Thr Asp Gln Arg Arg Pro	
115 120 125	
agt agc gtg gct gag aag gag aac caa cct tct ggg gct ggc aaa aag	432
Ser Ser Val Ala Glu Lys Glu Asn Gln Pro Ser Gly Ala Gly Lys Lys	
130 135 140	
gga aag aag gat aaa cgt taa	453

375

Gly Lys Lys Asp Lys Arg *
 145 150

<210> 254
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Asp Phe His Ile Leu Ile Val Ile Gly Cys Val Val Ser Ala Ser
 1 5 10 15
 Leu Leu Ser Phe Leu Phe Ile Asn Lys Ile Phe Arg Arg Lys Thr Phe
 20 25 30
 Glu Glu Val Val Ala Glu Lys Arg Ala Leu Ser Ala Asn Leu Tyr Lys
 35 40 45
 Ala Ala Gly Gly Ala Ala Thr Lys Lys Pro Lys Lys Lys Glu Leu Lys
 50 55 60
 Arg Glu Lys Lys Gln Arg Gln Arg Glu Gln Gln Arg Asp Val Asn Asn
 65 70 75 80
 Glu Pro Glu Pro Glu Glu Ala Glu Asp Tyr Ser Asp Gly Gln Ser Glu
 85 90 95
 Gly Gln Gly Ser Val Ala Gly Glu Glu Pro Gly Leu Ser Lys Gln His
 100 105 110
 Val Glu Phe Glu Pro Asp Ala Glu Val Leu Thr Asp Gln Arg Arg Pro
 115 120 125
 Ser Ser Val Ala Glu Lys Glu Asn Gln Pro Ser Gly Ala Gly Lys Lys
 130 135 140
 Gly Lys Lys Asp Lys Arg
 145 150

<210> 255
 <211> 489
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(489)

<400> 255
 atg gca ttt ctc tca ccc ttg gtt ctc att tgc cat cca acc cat ttt
 Met Ala Phe Leu Ser Pro Leu Val Leu Ile Cys His Pro Thr His Phe
 1 5 10 15

48

376

ctt gac cca aag ctt atg aaa gaa gaa caa atg tca cag gcc cag ctc	96
Leu Asp Pro Lys Leu Met Lys Glu Glu Gln Met Ser Gln Ala Gln Leu	
20 25 30	
ttc acc aga agc ttt gat gat ggc ctg ggc ttt gaa tac gtg atg ttc	144
Phe Thr Arg Ser Phe Asp Asp Gly Leu Gly Phe Glu Tyr Val Met Phe	
35 40 45	
tac aat gac att gag aaa agg atg gtt tgc tta ttt caa gga ggc cct	192
Tyr Asn Asp Ile Glu Lys Arg Met Val Cys Leu Phe Gln Gly Gly Pro	
50 55 60	
tac ctg gaa gga cca cct gga ttc att cat gga ggt gcc att gca acc	240
Tyr Leu Glu Gly Pro Pro Gly Phe Ile His Gly Gly Ala Ile Ala Thr	
65 70 75 80	
atg att gat gct act gtt ggt atg tgt gca atg atg gct ggg gga atc	288
Met Ile Asp Ala Thr Val Gly Met Cys Ala Met Met Ala Gly Gly Ile	
85 90 95	
gtc atg act gcc aat ctc aac atc aat tat aaa aga cct atc cct ctt	336
Val Met Thr Ala Asn Leu Asn Ile Asn Tyr Lys Arg Pro Ile Pro Leu	
100 105 110	
tgt tct gtt gtt atg ata aat agc caa ctt gat aaa gtt gaa gga agg	384
Cys Ser Val Val Met Ile Asn Ser Gln Leu Asp Lys Val Glu Gly Arg	
115 120 125	
aaa ttt ttt gtt tcc tgt aat gtt cag agt gtt gat gag aag acc cta	432
Lys Phe Phe Val Ser Cys Asn Val Gln Ser Val Asp Glu Lys Thr Leu	
130 135 140	
tac tca gag gcg aca agc tta ttt ata aag ctg aat cct gct aaa agt	480
Tyr Ser Glu Ala Thr Ser Leu Phe Ile Lys Leu Asn Pro Ala Lys Ser	
145 150 155 160	
ctg aca taa	489
Leu Thr *	

<210> 256

<211> 162

377

<212> PRT

<213> Homo sapiens

<400> 256

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Met Ala Phe Leu Ser Pro Leu Val Leu Ile Cys His Pro Thr His Phe
 1             5             10             15
Leu Asp Pro Lys Leu Met Lys Glu Glu Gln Met Ser Gln Ala Gln Leu
      20             25             30
Phe Thr Arg Ser Phe Asp Asp Gly Leu Gly Phe Glu Tyr Val Met Phe
      35             40             45
Tyr Asn Asp Ile Glu Lys Arg Met Val Cys Leu Phe Gln Gly Gly Pro
 50             55             60
Tyr Leu Glu Gly Pro Pro Gly Phe Ile His Gly Gly Ala Ile Ala Thr
65             70             75             80
Met Ile Asp Ala Thr Val Gly Met Cys Ala Met Met Ala Gly Gly Ile
      85             90             95
Val Met Thr Ala Asn Leu Asn Ile Asn Tyr Lys Arg Pro Ile Pro Leu
      100            105            110
Cys Ser Val Val Met Ile Asn Ser Gln Leu Asp Lys Val Glu Gly Arg
      115            120            125
Lys Phe Phe Val Ser Cys Asn Val Gln Ser Val Asp Glu Lys Thr Leu
      130            135            140
Tyr Ser Glu Ala Thr Ser Leu Phe Ile Lys Leu Asn Pro Ala Lys Ser
145            150            155            160
Leu Thr

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<210> 257

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(480)

<400> 257

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atg tgt ctt ttg gca gtc agt cca gat ggg aat tgg cta gct gca tca      48
Met Cys Leu Leu Ala Val Ser Pro Asp Gly Asn Trp Leu Ala Ala Ser
 1             5             10             15

ggg acc agt gct gga gtc cat gtc tac aac gta aaa cag cta aag ctt      96
Gly Thr Ser Ala Gly Val His Val Tyr Asn Val Lys Gln Leu Lys Leu
      20             25             30

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378

cac tgc acg gtg cct gct tac aat ttc cca gtg act gct atg gct att 144
 His Cys Thr Val Pro Ala Tyr Asn Phe Pro Val Thr Ala Met Ala Ile
 35 40 45

gcc ccc aat acc aac aac ctt gtc atc gct cat tcg gac cag cag gta 192
 Ala Pro Asn Thr Asn Asn Leu Val Ile Ala His Ser Asp Gln Gln Val
 50 55 60

ttt gag tac agc atc cca gac aaa cag tat aca gat tgg agc cgg act 240
 Phe Glu Tyr Ser Ile Pro Asp Lys Gln Tyr Thr Asp Trp Ser Arg Thr
 65 70 75 80

gtc cag aag cag ggc ttt cac cac ctt tgg ctc caa agg gat act cct 288
 Val Gln Lys Gln Gly Phe His His Leu Trp Leu Gln Arg Asp Thr Pro
 85 90 95

atc aca cac atc agt ttt cat ccc aag aga ccg atg cac atc ctt ctc 336
 Ile Thr His Ile Ser Phe His Pro Lys Arg Pro Met His Ile Leu Leu
 100 105 110

cat gat gcc tac atg ttc tgc atc att gac aag tca ttg ccc ctt cca 384
 His Asp Ala Tyr Met Phe Cys Ile Ile Asp Lys Ser Leu Pro Leu Pro
 115 120 125

aat gac aaa acc tta ctc tac aat cca ttt cct ccc acg aat gac atc 432
 Asn Asp Lys Thr Leu Leu Tyr Asn Pro Phe Pro Pro Thr Asn Asp Ile
 130 135 140

att gct cag ctc cca cca ccc att aaa aag aag aaa ttt gga acc taa 480
 Ile Ala Gln Leu Pro Pro Pro Ile Lys Lys Lys Lys Phe Gly Thr *
 145 150 155

<210> 258

<211> 159

<212> PRT

<213> Homo sapiens

<400> 258

Met Cys Leu Leu Ala Val Ser Pro Asp Gly Asn Trp Leu Ala Ala Ser
 1 5 10 15
 Gly Thr Ser Ala Gly Val His Val Tyr Asn Val Lys Gln Leu Lys Leu
 20 25 30

379

His Cys Thr Val Pro Ala Tyr Asn Phe Pro Val Thr Ala Met Ala Ile
 35 40 45
 Ala Pro Asn Thr Asn Asn Leu Val Ile Ala His Ser Asp Gln Gln Val
 50 55 60
 Phe Glu Tyr Ser Ile Pro Asp Lys Gln Tyr Thr Asp Trp Ser Arg Thr
 65 70 75 80
 Val Gln Lys Gln Gly Phe His His Leu Trp Leu Gln Arg Asp Thr Pro
 85 90 95
 Ile Thr His Ile Ser Phe His Pro Lys Arg Pro Met His Ile Leu Leu
 100 105 110
 His Asp Ala Tyr Met Phe Cys Ile Ile Asp Lys Ser Leu Pro Leu Pro
 115 120 125
 Asn Asp Lys Thr Leu Leu Tyr Asn Pro Phe Pro Pro Thr Asn Asp Ile
 130 135 140
 Ile Ala Gln Leu Pro Pro Pro Ile Lys Lys Lys Lys Phe Gly Thr
 145 150 155

<210> 259

<211> 627

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(627)

<400> 259

atg gcg tcc tct ttg ctt gcg ggc gag cga ttg gtg cgt gct ttg ggc 48
 Met Ala Ser Ser Leu Leu Ala Gly Glu Arg Leu Val Arg Ala Leu Gly
 1 5 10 15

ccc ggc ggg gag ctg gag cca gag cgg cta ccc cga aag ctg cgg gcc 96
 Pro Gly Gly Glu Leu Glu Pro Glu Arg Leu Pro Arg Lys Leu Arg Ala
 20 25 30

gag ctt gag gcc gcg ctg ggg aag aag cac aag ggc ggt gat agc tcc 144
 Glu Leu Glu Ala Ala Leu Gly Lys Lys His Lys Gly Gly Asp Ser Ser
 35 40 45

agt ggc ccc caa cgc ttg gtt tct ttc cgt ctc atc cgg gat ctg cac 192
 Ser Gly Pro Gln Arg Leu Val Ser Phe Arg Leu Ile Arg Asp Leu His
 50 55 60

cag cat ctg aga gaa agg gat tcc aaa cta tac ctc cat gag ctc cta 240

381

<400> 260
 Met Ala Ser Ser Leu Leu Ala Gly Glu Arg Leu Val Arg Ala Leu Gly
 1 5 10 15
 Pro Gly Gly Glu Leu Glu Pro Glu Arg Leu Pro Arg Lys Leu Arg Ala
 20 25 30
 Glu Leu Glu Ala Ala Leu Gly Lys Lys His Lys Gly Gly Asp Ser Ser
 35 40 45
 Ser Gly Pro Gln Arg Leu Val Ser Phe Arg Leu Ile Arg Asp Leu His
 50 55 60
 Gln His Leu Arg Glu Arg Asp Ser Lys Leu Tyr Leu His Glu Leu Leu
 65 70 75 80
 Glu Gly Ser Glu Ile Tyr Leu Pro Glu Val Val Lys Pro Pro Arg Asn
 85 90 95
 Pro Glu Leu Val Ala Arg Leu Glu Lys Ile Lys Ile Gln Leu Ala Asn
 100 105 110
 Glu Glu Tyr Lys Arg Ile Thr Arg Asn Val Thr Cys Gln Asp Thr Arg
 115 120 125
 His Gly Gly Thr Leu Ser Asp Leu Gly Lys Gln Val Arg Ser Leu Lys
 130 135 140
 Ala Leu Val Ile Thr Ile Phe Asn Phe Ile Val Thr Val Val Ala Ala
 145 150 155 160
 Phe Val Cys Thr Tyr Leu Gly Ser Gln Tyr Ile Phe Thr Glu Met Ala
 165 170 175
 Ser Arg Val Leu Ala Ala Leu Ile Val Ala Ser Val Val Gly Leu Ala
 180 185 190
 Glu Leu Tyr Val Met Val Arg Ala Met Glu Gly Glu Leu Gly Glu Leu
 195 200 205

<210> 261
 <211> 1092
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1092)

<400> 261
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 Met Ala Ala Ala Ala Met Ala Ala Ala Ala Gly Gly Gly Ala Gly Ala
 1 5 10 15
 gcc cgc tcc ctc tcg cgc ttc cga ggc tgc ctg gct ggc gcg ctg ctc 96

382

Ala Arg Ser Leu Ser Arg Phe Arg Gly Cys Leu Ala Gly Ala Leu Leu	
20 25 30	
ggg gac tgc gtg ggc tcc ttc tac gag gcc cac gac acc gtc gac ctg	144
Gly Asp Cys Val Gly Ser Phe Tyr Glu Ala His Asp Thr Val Asp Leu	
35 40 45	
acg tca gtc ctg cgt cat gtc cag agt ctg gag ccg gac ccc ggc acg	192
Thr Ser Val Leu Arg His Val Gln Ser Leu Glu Pro Asp Pro Gly Thr	
50 55 60	
ccc ggg agt gag cgg aca gaa gcc ttg tac tac aca gat gac aca gcc	240
Pro Gly Ser Glu Arg Thr Glu Ala Leu Tyr Tyr Thr Asp Asp Thr Ala	
65 70 75 80	
atg gcc agg gcc ctg gtg cag tcc ctg cta gcc aag gag gcc ttt gac	288
Met Ala Arg Ala Leu Val Gln Ser Leu Leu Ala Lys Glu Ala Phe Asp	
85 90 95	
gag gtg gac atg gct cac aga ttt gct cag gag tac aag aaa gac cct	336
Glu Val Asp Met Ala His Arg Phe Ala Gln Glu Tyr Lys Lys Asp Pro	
100 105 110	
gac agg ggc tat ggt gct gga gta gtc act gtc ttc aag aag ctc ctg	384
Asp Arg Gly Tyr Gly Ala Gly Val Val Thr Val Phe Lys Lys Leu Leu	
115 120 125	
aac ccc aaa tgt cgc gat gtc ttt gag cct gcc cgg gcc cag ttt aac	432
Asn Pro Lys Cys Arg Asp Val Phe Glu Pro Ala Arg Ala Gln Phe Asn	
130 135 140	
ggg aaa ggc tcc tat ggc aat gga ggt gcc atg cgg gtg gct ggc atc	480
Gly Lys Gly Ser Tyr Gly Asn Gly Gly Ala Met Arg Val Ala Gly Ile	
145 150 155 160	
tcc ctg gcc tat agc agt gtc cag gat gtg cag aag ttt gcc cgg ctc	528
Ser Leu Ala Tyr Ser Ser Val Gln Asp Val Gln Lys Phe Ala Arg Leu	
165 170 175	
tcg gcc cag ctg aca cac gcc tcc tcc ctg ggt tac aat ggc gcc atc	576
Ser Ala Gln Leu Thr His Ala Ser Ser Leu Gly Tyr Asn Gly Ala Ile	
180 185 190	
ctg cag gcc ctg gct gtg cac ctg gcc ttg cag ggc gag tct tcc agc	624

Leu	Gln	Ala	Leu	Ala	Val	His	Leu	Ala	Leu	Gln	Gly	Glu	Ser	Ser	Ser		
195						200						205					
gag	cac	ttt	ctc	aag	caa	ctc	ctg	ggc	cac	atg	gag	gat	ctg	gag	ggg	672	
Glu	His	Phe	Leu	Lys	Gln	Leu	Leu	Gly	His	Met	Glu	Asp	Leu	Glu	Gly		
210						215						220					
gat	gcc	cag	tcc	gtc	ttg	gat	gcc	agg	gag	ttg	ggc	atg	gag	gag	cgt	720	
Asp	Ala	Gln	Ser	Val	Leu	Asp	Ala	Arg	Glu	Leu	Gly	Met	Glu	Glu	Arg		
225						230						235			240		
cca	tac	tcc	agc	cgc	ctg	aag	aag	att	gga	gag	ctt	cta	gac	cag	gca	768	
Pro	Tyr	Ser	Ser	Arg	Leu	Lys	Lys	Ile	Gly	Glu	Leu	Leu	Asp	Gln	Ala		
			245						250						255		
tcg	gtg	acc	agg	gag	gaa	gtg	gtg	tct	gag	cta	ggg	aat	ggc	att	gct	816	
Ser	Val	Thr	Arg	Glu	Glu	Val	Val	Ser	Glu	Leu	Gly	Asn	Gly	Ile	Ala		
			260						265						270		
gcc	ttt	gag	tcg	gta	ccc	acc	gcc	atc	tac	tgc	ttc	cta	cgc	tgc	atg	864	
Ala	Phe	Glu	Ser	Val	Pro	Thr	Ala	Ile	Tyr	Cys	Phe	Leu	Arg	Cys	Met		
275						280						285					
gag	cca	gac	cct	gag	atc	cct	tct	gcc	ttc	aat	agc	ctc	caa	agg	act	912	
Glu	Pro	Asp	Pro	Glu	Ile	Pro	Ser	Ala	Phe	Asn	Ser	Leu	Gln	Arg	Thr		
290						295						300					
ctc	att	tat	tcc	atc	tca	ctt	ggg	ggg	gac	aca	gac	acc	att	gcc	acc	960	
Leu	Ile	Tyr	Ser	Ile	Ser	Leu	Gly	Gly	Asp	Thr	Asp	Thr	Ile	Ala	Thr		
305						310						315			320		
atg	gct	ggg	gcc	att	gct	ggg	gcc	tac	tat	ggg	atg	gat	cag	gtg	cca	1008	
Met	Ala	Gly	Ala	Ile	Ala	Gly	Ala	Tyr	Tyr	Gly	Met	Asp	Gln	Val	Pro		
			325						330						335		
gag	agc	tgg	cag	caa	agc	tgt	gaa	ggc	tac	gag	gag	aca	gac	atc	ctg	1056	
Glu	Ser	Trp	Gln	Gln	Ser	Cys	Glu	Gly	Tyr	Glu	Glu	Thr	Asp	Ile	Leu		
			340						345						350		
gcc	caa	agc	ctg	cac	cgt	gtc	ttc	cag	aag	agt	tga					1092	
Ala	Gln	Ser	Leu	His	Arg	Val	Phe	Gln	Lys	Ser	*						
355						360											

384

<210> 262
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 262

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Met Ala Ala Ala Ala Met Ala Ala Ala Ala Gly Gly Gly Ala Gly Ala
 1           5           10           15
Ala Arg Ser Leu Ser Arg Phe Arg Gly Cys Leu Ala Gly Ala Leu Leu
           20           25           30
Gly Asp Cys Val Gly Ser Phe Tyr Glu Ala His Asp Thr Val Asp Leu
           35           40           45
Thr Ser Val Leu Arg His Val Gln Ser Leu Glu Pro Asp Pro Gly Thr
           50           55           60
Pro Gly Ser Glu Arg Thr Glu Ala Leu Tyr Tyr Thr Asp Asp Thr Ala
65           70           75           80
Met Ala Arg Ala Leu Val Gln Ser Leu Leu Ala Lys Glu Ala Phe Asp
           85           90           95
Glu Val Asp Met Ala His Arg Phe Ala Gln Glu Tyr Lys Lys Asp Pro
           100          105          110
Asp Arg Gly Tyr Gly Ala Gly Val Val Thr Val Phe Lys Lys Leu Leu
           115          120          125
Asn Pro Lys Cys Arg Asp Val Phe Glu Pro Ala Arg Ala Gln Phe Asn
           130          135          140
Gly Lys Gly Ser Tyr Gly Asn Gly Gly Ala Met Arg Val Ala Gly Ile
145          150          155          160
Ser Leu Ala Tyr Ser Ser Val Gln Asp Val Gln Lys Phe Ala Arg Leu
           165          170          175
Ser Ala Gln Leu Thr His Ala Ser Ser Leu Gly Tyr Asn Gly Ala Ile
           180          185          190
Leu Gln Ala Leu Ala Val His Leu Ala Leu Gln Gly Glu Ser Ser Ser
           195          200          205
Glu His Phe Leu Lys Gln Leu Leu Gly His Met Glu Asp Leu Glu Gly
           210          215          220
Asp Ala Gln Ser Val Leu Asp Ala Arg Glu Leu Gly Met Glu Glu Arg
225          230          235          240
Pro Tyr Ser Ser Arg Leu Lys Lys Ile Gly Glu Leu Leu Asp Gln Ala
           245          250          255
Ser Val Thr Arg Glu Glu Val Val Ser Glu Leu Gly Asn Gly Ile Ala
           260          265          270
Ala Phe Glu Ser Val Pro Thr Ala Ile Tyr Cys Phe Leu Arg Cys Met
           275          280          285
Glu Pro Asp Pro Glu Ile Pro Ser Ala Phe Asn Ser Leu Gln Arg Thr
           290          295          300

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385

Leu Ile Tyr Ser Ile Ser Leu Gly Gly Asp Thr Asp Thr Ile Ala Thr
 305 310 315 320
 Met Ala Gly Ala Ile Ala Gly Ala Tyr Tyr Gly Met Asp Gln Val Pro
 325 330 335
 Glu Ser Trp Gln Gln Ser Cys Glu Gly Tyr Glu Glu Thr Asp Ile Leu
 340 345 350
 Ala Gln Ser Leu His Arg Val Phe Gln Lys Ser
 355 360

<210> 263
 <211> 1239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1239)

<400> 263

atg gcc ttg gcc ctg ctg agc cgg ctg ctg ccc gga agt gag tac ctc 48
 Met Ala Leu Ala Leu Leu Ser Arg Leu Leu Pro Gly Ser Glu Tyr Leu
 1 5 10 15

acc cat gag ctg ctg ctg agc tgt gta ttc cgg ctg gag ttc ctc ccg 96
 Thr His Glu Leu Leu Leu Ser Cys Val Phe Arg Leu Glu Phe Leu Pro
 20 25 30

gaa aga aca tca ggg ggt cca gag gca gcc gac ttc tct gac cag ctg 144
 Glu Arg Thr Ser Gly Gly Pro Glu Ala Ala Asp Phe Ser Asp Gln Leu
 35 40 45

tcg tta gga agc agc agg gtc cct cgg tgt ggg caa ggg act ctg ctg 192
 Ser Leu Gly Ser Ser Arg Val Pro Arg Cys Gly Gln Gly Thr Leu Leu
 50 55 60

gct cag gcc tgc cag gac ctc ccc agc atc cgc aac tgc tac ctg act 240
 Ala Gln Ala Cys Gln Asp Leu Pro Ser Ile Arg Asn Cys Tyr Leu Thr
 65 70 75 80

cat tgc tcg cca gcc cga gcc agt ctg ctg gcc tcc cag gct ctg cac 288
 His Cys Ser Pro Ala Arg Ala Ser Leu Leu Ala Ser Gln Ala Leu His
 85 90 95

cga ggg gag cta cag cga gtc cca acc ctg cta ctg ccc atg cct acg 336

386

Arg Gly Glu	Leu Gln Arg Val	Pro Thr Leu Leu Leu Pro	Met Pro Thr	
	100	105	110	
gag ccg ctg	ctg ccc acc gac	tgg ccc ttc ctg	cca ctg att cgc ctc	384
Glu Pro Leu	Leu Pro Thr Asp	Trp Pro Phe Leu	Pro Leu Ile Arg Leu	
	115	120	125	
tac cac cgg	gct tca gac acc	ccc tcg gga ctc	tct ccc aca gac acc	432
Tyr His Arg	Ala Ser Asp Thr	Pro Ser Gly Leu	Ser Pro Thr Asp Thr	
	130	135	140	
atg ggc aca	gcc atg cgg gtc	ctg cag tgg gtg	cta gtt ttg gag agc	480
Met Gly Thr	Ala Met Arg Val	Leu Gln Trp Val	Leu Val Leu Glu Ser	
	145	150	155 160	
tgg cgc ccc	cag gct ctc tgg	gct gtg ccc cct	gct gcc cgc ctg gca	528
Trp Arg Pro	Gln Ala Leu Trp	Ala Val Pro Pro	Ala Ala Arg Leu Ala	
	165	170	175	
cgg ctc atg	tgt gtg ttc ctg	gtg gac agt gag	ctg ttc cgg gag tcc	576
Arg Leu Met	Cys Val Phe Leu	Val Asp Ser Glu	Leu Phe Arg Glu Ser	
	180	185	190	
cca gta cag	cat ctg gtg gca	gcc ctc ctc gcc	cag ctc tgt cag cct	624
Pro Val Gln	His Leu Val Ala	Ala Leu Leu Ala	Gln Leu Cys Gln Pro	
	195	200	205	
caa gtc ttg	cca aac ctc aac	ctg gac tgc cga	ctc cct ggc ctg acg	672
Gln Val Leu	Pro Asn Leu Asn	Leu Asp Cys Arg	Leu Pro Gly Leu Thr	
	210	215	220	
tct ttc cct	gac ctc tat gcc	aac ttc ctg gat	cat ttt gag gct gtc	720
Ser Phe Pro	Asp Leu Tyr Ala	Asn Phe Leu Asp	His Phe Glu Ala Val	
	225 230	235	240	
tct ttt ggg	gac cac ctc ttt	ggg gcc ctg gtc	ctc ctg ccc ctg cag	768
Ser Phe Gly	Asp His Leu Phe	Gly Ala Leu Val	Leu Leu Pro Leu Gln	
	245	250	255	
cgt cgg ttc	agt gtc acc ttg	cgc ctt gcc ctc	ttt ggg gaa cac gtg	816
Arg Arg Phe	Ser Val Thr Leu	Arg Leu Ala Leu	Phe Gly Glu His Val	
	260	265	270	
gga gcc ttg	cga gct ctg agc	ctg cct ctg acc	cag ttg cct gtg tcc	864

387

Gly	Ala	Leu	Arg	Ala	Leu	Ser	Leu	Pro	Leu	Thr	Gln	Leu	Pro	Val	Ser		
	275						280					285					
ctg	gag	tgt	tac	aca	gtg	cct	cct	gaa	gac	aac	ctg	gcc	ctc	ctt	cag		912
Leu	Glu	Cys	Tyr	Thr	Val	Pro	Pro	Glu	Asp	Asn	Leu	Ala	Leu	Leu	Gln		
	290					295					300						
ctc	tac	ttc	cgg	acc	ctg	gtt	act	ggg	gag	ctc	cgc	cca	cgt	tgg	tgc		960
Leu	Tyr	Phe	Arg	Thr	Leu	Val	Thr	Gly	Ala	Leu	Arg	Pro	Arg	Trp	Cys		
305					310				315					320			
ccc	gtg	ctc	tat	gct	gtg	gct	gtg	gct	cat	gtc	aat	agc	ttc	atc	ttc		1008
Pro	Val	Leu	Tyr	Ala	Val	Ala	Val	Ala	His	Val	Asn	Ser	Phe	Ile	Phe		
				325				330						335			
tct	cag	gac	cca	cag	agc	tca	gat	gag	gtc	aaa	gct	gcc	cgc	agg	agt		1056
Ser	Gln	Asp	Pro	Gln	Ser	Ser	Asp	Glu	Val	Lys	Ala	Ala	Arg	Arg	Ser		
			340					345					350				
atg	ctg	cag	aaa	aca	tgg	ctg	ctg	gca	gat	gag	ggg	ctc	cgg	cag	cac		1104
Met	Leu	Gln	Lys	Thr	Trp	Leu	Leu	Ala	Asp	Glu	Gly	Leu	Arg	Gln	His		
		355				360						365					
ctc	ctg	cac	tat	aag	ctt	ccc	aat	tcc	acg	ctc	cca	gag	ggc	ttt	gag		1152
Leu	Leu	His	Tyr	Lys	Leu	Pro	Asn	Ser	Thr	Leu	Pro	Glu	Gly	Phe	Glu		
	370					375					380						
ctc	tat	tct	cag	ttg	ccc	cct	ctg	cgt	cag	cac	tac	ctc	cag	aga	ctg		1200
Leu	Tyr	Ser	Gln	Leu	Pro	Pro	Leu	Arg	Gln	His	Tyr	Leu	Gln	Arg	Leu		
385					390				395					400			
act	tca	aca	gtg	ctc	caa	aat	ggg	gta	tca	gag	acc	tag					1239
Thr	Ser	Thr	Val	Leu	Gln	Asn	Gly	Val	Ser	Glu	Thr	*					
			405					410									

<210> 264

<211> 412

<212> PRT

<213> Homo sapiens

<400> 264

Met	Ala	Leu	Ala	Leu	Leu	Ser	Arg	Leu	Leu	Pro	Gly	Ser	Glu	Tyr	Leu
1				5				10					15		

388

Thr His Glu Leu Leu Leu Ser Cys Val Phe Arg Leu Glu Phe Leu Pro
 20 25 30
 Glu Arg Thr Ser Gly Gly Pro Glu Ala Ala Asp Phe Ser Asp Gln Leu
 35 40 45
 Ser Leu Gly Ser Ser Arg Val Pro Arg Cys Gly Gln Gly Thr Leu Leu
 50 55 60
 Ala Gln Ala Cys Gln Asp Leu Pro Ser Ile Arg Asn Cys Tyr Leu Thr
 65 70 75 80
 His Cys Ser Pro Ala Arg Ala Ser Leu Leu Ala Ser Gln Ala Leu His
 85 90 95
 Arg Gly Glu Leu Gln Arg Val Pro Thr Leu Leu Leu Pro Met Pro Thr
 100 105 110
 Glu Pro Leu Leu Pro Thr Asp Trp Pro Phe Leu Pro Leu Ile Arg Leu
 115 120 125
 Tyr His Arg Ala Ser Asp Thr Pro Ser Gly Leu Ser Pro Thr Asp Thr
 130 135 140
 Met Gly Thr Ala Met Arg Val Leu Gln Trp Val Leu Val Leu Glu Ser
 145 150 155 160
 Trp Arg Pro Gln Ala Leu Trp Ala Val Pro Pro Ala Ala Arg Leu Ala
 165 170 175
 Arg Leu Met Cys Val Phe Leu Val Asp Ser Glu Leu Phe Arg Glu Ser
 180 185 190
 Pro Val Gln His Leu Val Ala Ala Leu Leu Ala Gln Leu Cys Gln Pro
 195 200 205
 Gln Val Leu Pro Asn Leu Asn Leu Asp Cys Arg Leu Pro Gly Leu Thr
 210 215 220
 Ser Phe Pro Asp Leu Tyr Ala Asn Phe Leu Asp His Phe Glu Ala Val
 225 230 235 240
 Ser Phe Gly Asp His Leu Phe Gly Ala Leu Val Leu Leu Pro Leu Gln
 245 250 255
 Arg Arg Phe Ser Val Thr Leu Arg Leu Ala Leu Phe Gly Glu His Val
 260 265 270
 Gly Ala Leu Arg Ala Leu Ser Leu Pro Leu Thr Gln Leu Pro Val Ser
 275 280 285
 Leu Glu Cys Tyr Thr Val Pro Pro Glu Asp Asn Leu Ala Leu Leu Gln
 290 295 300
 Leu Tyr Phe Arg Thr Leu Val Thr Gly Ala Leu Arg Pro Arg Trp Cys
 305 310 315 320
 Pro Val Leu Tyr Ala Val Ala Val Ala His Val Asn Ser Phe Ile Phe
 325 330 335
 Ser Gln Asp Pro Gln Ser Ser Asp Glu Val Lys Ala Ala Arg Arg Ser
 340 345 350
 Met Leu Gln Lys Thr Trp Leu Leu Ala Asp Glu Gly Leu Arg Gln His
 355 360 365

389

Leu Leu His Tyr Lys Leu Pro Asn Ser Thr Leu Pro Glu Gly Phe Glu
 370 375 380
 Leu Tyr Ser Gln Leu Pro Pro Leu Arg Gln His Tyr Leu Gln Arg Leu
 385 390 395 400
 Thr Ser Thr Val Leu Gln Asn Gly Val Ser Glu Thr
 405 410

<210> 265
 <211> 576
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(576)

<400> 265
 atg gcg ggc gct gca gaa gat gcg cga gct ctt ttc cgg gct ggg gtc 48
 Met Ala Gly Ala Ala Glu Asp Ala Arg Ala Leu Phe Arg Ala Gly Val
 1 5 10 15
 tgc gcg gcc ctg gag gcc tgg ccg gcc ttg cag atc gct gtg gag aat 96
 Cys Ala Ala Leu Glu Ala Trp Pro Ala Leu Gln Ile Ala Val Glu Asn
 20 25 30
 ggc ttc ggg ggt gtg cac agc cag gag aag gcc aag tgg ctg ggg ggt 144
 Gly Phe Gly Gly Val His Ser Gln Glu Lys Ala Lys Trp Leu Gly Gly
 35 40 45
 gca gtg gag gat tac ttc atg cgc aat gct gac ttg gag cta gat gag 192
 Ala Val Glu Asp Tyr Phe Met Arg Asn Ala Asp Leu Glu Leu Asp Glu
 50 55 60
 gtg gaa gac ttc ctt gga gag ctg ttg acc aac gag ttt gat aca gtt 240
 Val Glu Asp Phe Leu Gly Glu Leu Leu Thr Asn Glu Phe Asp Thr Val
 65 70 75 80
 gtg gaa gac ggg agt ctg ccc cag gtg agc cag caa ctg cag acc atg 288
 Val Glu Asp Gly Ser Leu Pro Gln Val Ser Gln Gln Leu Gln Thr Met
 85 90 95
 ttc cac cac ttc cag agg ggt gat ggg gct gct ctg agg gag atg gcc 336
 Phe His His Phe Gln Arg Gly Asp Gly Ala Ala Leu Arg Glu Met Ala
 100 105 110

390

tcc tgc atc act cag aga aaa tgc aag gtc aca gcc act gca ctt aag 384
Ser Cys Ile Thr Gln Arg Lys Cys Lys Val Thr Ala Thr Ala Leu Lys
115 120 125

aca gct aga gag act gat gag gat gaa gat gat gtg gac agt gtg gaa 432
Thr Ala Arg Glu Thr Asp Glu Asp Glu Asp Asp Val Asp Ser Val Glu
130 135 140

gag atg gag gtc aca gct acg aat gat ggg gct gct aca gat ggg gtc 480
Glu Met Glu Val Thr Ala Thr Asn Asp Gly Ala Ala Thr Asp Gly Val
145 150 155 160

tgc ccc cag cct gaa ccc tct gat cca gac gct cag act att aag gaa 528
Cys Pro Gln Pro Glu Pro Ser Asp Pro Asp Ala Gln Thr Ile Lys Glu
165 170 175

gag gat ata gtg gaa gat ggc tgg acc att gtc cgg aga aaa aaa tga 576
Glu Asp Ile Val Glu Asp Gly Trp Thr Ile Val Arg Arg Lys Lys *
180 185 190

<210> 266

<211> 191

<212> PRT

<213> Homo sapiens

<400> 266

Met	Ala	Gly	Ala	Ala	Glu	Asp	Ala	Arg	Ala	Leu	Phe	Arg	Ala	Gly	Val
1				5					10					15	
Cys	Ala	Ala	Leu	Glu	Ala	Trp	Pro	Ala	Leu	Gln	Ile	Ala	Val	Glu	Asn
			20					25					30		
Gly	Phe	Gly	Gly	Val	His	Ser	Gln	Glu	Lys	Ala	Lys	Trp	Leu	Gly	Gly
		35					40					45			
Ala	Val	Glu	Asp	Tyr	Phe	Met	Arg	Asn	Ala	Asp	Leu	Glu	Leu	Asp	Glu
	50					55					60				
Val	Glu	Asp	Phe	Leu	Gly	Glu	Leu	Leu	Thr	Asn	Glu	Phe	Asp	Thr	Val
65					70					75					80
Val	Glu	Asp	Gly	Ser	Leu	Pro	Gln	Val	Ser	Gln	Gln	Leu	Gln	Thr	Met
				85					90					95	
Phe	His	His	Phe	Gln	Arg	Gly	Asp	Gly	Ala	Ala	Leu	Arg	Glu	Met	Ala
			100					105					110		
Ser	Cys	Ile	Thr	Gln	Arg	Lys	Cys	Lys	Val	Thr	Ala	Thr	Ala	Leu	Lys
		115					120					125			

391

Thr Ala Arg Glu Thr Asp Glu Asp Glu Asp Asp Val Asp Ser Val Glu
 130 135 140
 Glu Met Glu Val Thr Ala Thr Asn Asp Gly Ala Ala Thr Asp Gly Val
 145 150 155 160
 Cys Pro Gln Pro Glu Pro Ser Asp Pro Asp Ala Gln Thr Ile Lys Glu
 165 170 175
 Glu Asp Ile Val Glu Asp Gly Trp Thr Ile Val Arg Arg Lys Lys
 180 185 190

<210> 267
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(567)

<400> 267
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 Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu Pro
 1 5 10 15
 gcg tgc gtc gcg gcc cac ggc ttc cgt atc cat gat tat ttg tac ttt 96
 Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu Tyr Phe
 20 25 30
 caa gtg ctg agt cct ggg gac att cga tac atc ttc aca gcc aca cct 144
 Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr Ala Thr Pro
 35 40 45
 gcc aag gac ttt ggt ggt atc ttt cac aca agg tat gag cag att cac 192
 Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr Glu Gln Ile His
 50 55 60
 ctt gtc ccc gct gaa cct cca gag gcc tgc ggg gaa ctc agc aac ggt 240
 Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly Glu Leu Ser Asn Gly
 65 70 75 80
 ttc ttc atc cag gac cag att gct ctg gtg gag agg ggg ggc tgc tcc 288
 Phe Phe Ile Gln Asp Gln Ile Ala Leu Val Glu Arg Gly Gly Cys Ser
 85 90 95
 ttc ctc tcc aag act cgg gtg gtc cag gag cac ggc ggg cgg gcg gtg 336

392

Phe Leu Ser Lys Thr Arg Val Val Gln Glu His Gly Gly Arg Ala Val
 100 105 110
 atc atc tct gac aac gca gtt gac aat gac agc ttc tac gtg gag atg 384
 Ile Ile Ser Asp Asn Ala Val Asp Asn Asp Ser Phe Tyr Val Glu Met
 115 120 125
 atc cag gac agt acc cag cgc aca gct gac atc ccc gcc ctc ttc ctg 432
 Ile Gln Asp Ser Thr Gln Arg Thr Ala Asp Ile Pro Ala Leu Phe Leu
 130 135 140
 ctc ggc cga gac ggc tac atg atc cgc cgc tct ctg gaa cag cat ggg 480
 Leu Gly Arg Asp Gly Tyr Met Ile Arg Arg Ser Leu Glu Gln His Gly
 145 150 155 160
 ctg cca tgg gcc atc att tcc atc cca gtc aat gtc acc agc atc ccc 528
 Leu Pro Trp Ala Ile Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro
 165 170 175
 acc ttt gag ctg ctg caa ccg ccc tgg acc ttc tgg tag 567
 Thr Phe Glu Leu Leu Gln Pro Pro Trp Thr Phe Trp *
 180 185

<210> 268

<211> 188

<212> PRT

<213> Homo sapiens

<400> 268

Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu Pro
 1 5 10 15
 Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu Tyr Phe
 20 25 30
 Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr Ala Thr Pro
 35 40 45
 Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr Glu Gln Ile His
 50 55 60
 Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly Glu Leu Ser Asn Gly
 65 70 75 80
 Phe Phe Ile Gln Asp Gln Ile Ala Leu Val Glu Arg Gly Gly Cys Ser
 85 90 95
 Phe Leu Ser Lys Thr Arg Val Val Gln Glu His Gly Gly Arg Ala Val
 100 105 110

393

Ile Ile Ser Asp Asn Ala Val Asp Asn Asp Ser Phe Tyr Val Glu Met
 115 120 125
 Ile Gln Asp Ser Thr Gln Arg Thr Ala Asp Ile Pro Ala Leu Phe Leu
 130 135 140
 Leu Gly Arg Asp Gly Tyr Met Ile Arg Arg Ser Leu Glu Gln His Gly
 145 150 155 160
 Leu Pro Trp Ala Ile Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro
 165 170 175
 Thr Phe Glu Leu Leu Gln Pro Pro Trp Thr Phe Trp
 180 185

<210> 269

<211> 1419

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1419)

<400> 269

atg gtg ctg gcc tcg gcg ctg ctg tgt gtg att gtg tct gtt ctg acc 48
 Met Val Leu Ala Ser Ala Leu Leu Cys Val Ile Val Ser Val Leu Thr
 1 5 10 15

aac gtg ctc gtg ggt gga aac acc cca agg aag aac ccc atg cat ccc 96
 Asn Val Leu Val Gly Gly Asn Thr Pro Arg Lys Asn Pro Met His Pro
 20 25 30

agc tca agg tgg tca gag cta gac ctt ctt att ctg ttg ggg acg gcg 144
 Ser Ser Arg Trp Ser Glu Leu Asp Leu Leu Ile Leu Leu Gly Thr Ala
 35 40 45

ggc cac gtc ttg agc ctg ggc gcc agc agc ttc gtg gag gag gag cac 192
 Gly His Val Leu Ser Leu Gly Ala Ser Ser Phe Val Glu Glu Glu His
 50 55 60

cag acc tgg tac ttc ctt gtg aac acc ctg tgt cta gct ctg agc caa 240
 Gln Thr Trp Tyr Phe Leu Val Asn Thr Leu Cys Leu Ala Leu Ser Gln
 65 70 75 80

gaa acc tac aga aac tac ttt ctg gga gat gac ggt gag cct ccg tgt 288
 Glu Thr Tyr Arg Asn Tyr Phe Leu Gly Asp Asp Gly Glu Pro Pro Cys
 85 90 95

394

ggc ctc tgt gtg gaa caa ggg cat gac ggg gcc aca gca gcg tgg cag Gly Leu Cys Val Glu Gln Gly His Asp Gly Ala Thr Ala Ala Trp Gln 100 105 110	336
gac ggg cct ggc tgt gat gtc ctg gag cga gac aaa ggc cac gga agc Asp Gly Pro Gly Cys Asp Val Leu Glu Arg Asp Lys Gly His Gly Ser 115 120 125	384
ccc tct acc tcc gaa gtg ctc aga ggc cgc gag aag tgg atg gtg ctg Pro Ser Thr Ser Glu Val Leu Arg Gly Arg Glu Lys Trp Met Val Leu 130 135 140	432
gcc agt ccg tgg cta ata ctg gcc tgc tgc cgg ctg ctg cgc tcc cta Ala Ser Pro Trp Leu Ile Leu Ala Cys Cys Arg Leu Leu Arg Ser Leu 145 150 155 160	480
aac cag aca ggt gtg cag tgg gct cac cgg cct gac ctc ggc cac tgg Asn Gln Thr Gly Val Gln Trp Ala His Arg Pro Asp Leu Gly His Trp 165 170 175	528
ctc acc agc tct gac cac aaa gcc gag ctc tct gtc ctg gct gcc ctc Leu Thr Ser Ser Asp His Lys Ala Glu Leu Ser Val Leu Ala Ala Leu 180 185 190	576
tcc ctc ctc gta gtt ttt gtg ctg gtg cag agg ggg tgc tcc cct gtg Ser Leu Leu Val Val Phe Val Leu Val Gln Arg Gly Cys Ser Pro Val 195 200 205	624
tcc aag gct gcc ctg gcg ctg ggg ctg ctg ggc gtc tac tgc tac cgg Ser Lys Ala Ala Leu Ala Leu Gly Leu Leu Gly Val Tyr Cys Tyr Arg 210 215 220	672
gcg gcc atc ggg agt gtc cgg ttc ccg tgg cgg ccg gac agc aag gac Ala Ala Ile Gly Ser Val Arg Phe Pro Trp Arg Pro Asp Ser Lys Asp 225 230 235 240	720
att tcc aag ggt att att gaa gct cgt ttt gtt tat gtc ttt gtc ctt Ile Ser Lys Gly Ile Ile Glu Ala Arg Phe Val Tyr Val Phe Val Leu 245 250 255	768
ggc att ctg ttc acg ggc acc aaa gac tta ctt aaa tct caa gtc att Gly Ile Leu Phe Thr Gly Thr Lys Asp Leu Leu Lys Ser Gln Val Ile 260 265 270	816

395

gct gca gac ttc aaa ctc aag act gta ggt tta tgg gag ata tat agt Ala Ala Asp Phe Lys Leu Lys Thr Val Gly Leu Trp Glu Ile Tyr Ser 275 280 285	864
gga tta gtt ctt ctg gca gcc ttg ctc ttt aga cca cat aat ctt ccg Gly Leu Val Leu Leu Ala Ala Leu Leu Phe Arg Pro His Asn Leu Pro 290 295 300	912
gtc tta gca ttt agc ctc ttg att cag act cta atg act aaa ttc atc Val Leu Ala Phe Ser Leu Leu Ile Gln Thr Leu Met Thr Lys Phe Ile 305 310 315 320	960
tgg aag ccc ctg aga cac gat gca gct gag att act gtg atg cat tat Trp Lys Pro Leu Arg His Asp Ala Ala Glu Ile Thr Val Met His Tyr 325 330 335	1008
tgg ttt ggt caa gca ttc ttc tat ttt cag ggc aac tcc aac aac att Trp Phe Gly Gln Ala Phe Phe Tyr Phe Gln Gly Asn Ser Asn Asn Ile 340 345 350	1056
gcc acc gtg gac atc tcc gca ggc ttc gtg ggc tta gac acc tac gtg Ala Thr Val Asp Ile Ser Ala Gly Phe Val Gly Leu Asp Thr Tyr Val 355 360 365	1104
gaa atc cca gcc gtg ctc ctg aca gcg ttt ggg acg tac gca ggg cct Glu Ile Pro Ala Val Leu Leu Thr Ala Phe Gly Thr Tyr Ala Gly Pro 370 375 380	1152
gtg ctg tgg gcc agc cac tta gtg cac ttc ctg agc tca gaa aca cgc Val Leu Trp Ala Ser His Leu Val His Phe Leu Ser Ser Glu Thr Arg 385 390 395 400	1200
agt ggt tca gca ctg agt cat gct tgc ttc tgc tac gca ctg att tgt Ser Gly Ser Ala Leu Ser His Ala Cys Phe Cys Tyr Ala Leu Ile Cys 405 410 415	1248
tct att cca gtt ttc acg tac atc gtt ttg gtg aca tct ctg cgt tat Ser Ile Pro Val Phe Thr Tyr Ile Val Leu Val Thr Ser Leu Arg Tyr 420 425 430	1296
cat tta ttt ata tgg agt gta ttt tct cca aaa ctt ctc tac gag gga His Leu Phe Ile Trp Ser Val Phe Ser Pro Lys Leu Leu Tyr Glu Gly 435 440 445	1344

396

atg cac ctg ctc att aca gct gct gtc tgt gta ttc ttc acg gca atg 1392
 Met His Leu Leu Ile Thr Ala Ala Val Cys Val Phe Phe Thr Ala Met
 450 455 460

gat caa acc aga ctc aca cag tct tag 1419
 Asp Gln Thr Arg Leu Thr Gln Ser *
 465 470

<210> 270

<211> 472

<212> PRT

<213> Homo sapiens

<400> 270

Met Val Leu Ala Ser Ala Leu Leu Cys Val Ile Val Ser Val Leu Thr
 1 5 10 15
 Asn Val Leu Val Gly Gly Asn Thr Pro Arg Lys Asn Pro Met His Pro
 20 25 30
 Ser Ser Arg Trp Ser Glu Leu Asp Leu Leu Ile Leu Leu Gly Thr Ala
 35 40 45
 Gly His Val Leu Ser Leu Gly Ala Ser Ser Phe Val Glu Glu Glu His
 50 55 60
 Gln Thr Trp Tyr Phe Leu Val Asn Thr Leu Cys Leu Ala Leu Ser Gln
 65 70 75 80
 Glu Thr Tyr Arg Asn Tyr Phe Leu Gly Asp Asp Gly Glu Pro Pro Cys
 85 90 95
 Gly Leu Cys Val Glu Gln Gly His Asp Gly Ala Thr Ala Ala Trp Gln
 100 105 110
 Asp Gly Pro Gly Cys Asp Val Leu Glu Arg Asp Lys Gly His Gly Ser
 115 120 125
 Pro Ser Thr Ser Glu Val Leu Arg Gly Arg Glu Lys Trp Met Val Leu
 130 135 140
 Ala Ser Pro Trp Leu Ile Leu Ala Cys Cys Arg Leu Leu Arg Ser Leu
 145 150 155 160
 Asn Gln Thr Gly Val Gln Trp Ala His Arg Pro Asp Leu Gly His Trp
 165 170 175
 Leu Thr Ser Ser Asp His Lys Ala Glu Leu Ser Val Leu Ala Ala Leu
 180 185 190
 Ser Leu Leu Val Val Phe Val Leu Val Gln Arg Gly Cys Ser Pro Val
 195 200 205
 Ser Lys Ala Ala Leu Ala Leu Gly Leu Leu Gly Val Tyr Cys Tyr Arg
 210 215 220

397

Ala Ala Ile Gly Ser Val Arg Phe Pro Trp Arg Pro Asp Ser Lys Asp
 225 230 235 240
 Ile Ser Lys Gly Ile Ile Glu Ala Arg Phe Val Tyr Val Phe Val Leu
 245 250 255
 Gly Ile Leu Phe Thr Gly Thr Lys Asp Leu Leu Lys Ser Gln Val Ile
 260 265 270
 Ala Ala Asp Phe Lys Leu Lys Thr Val Gly Leu Trp Glu Ile Tyr Ser
 275 280 285
 Gly Leu Val Leu Leu Ala Ala Leu Leu Phe Arg Pro His Asn Leu Pro
 290 295 300
 Val Leu Ala Phe Ser Leu Leu Ile Gln Thr Leu Met Thr Lys Phe Ile
 305 310 315 320
 Trp Lys Pro Leu Arg His Asp Ala Ala Glu Ile Thr Val Met His Tyr
 325 330 335
 Trp Phe Gly Gln Ala Phe Phe Tyr Phe Gln Gly Asn Ser Asn Asn Ile
 340 345 350
 Ala Thr Val Asp Ile Ser Ala Gly Phe Val Gly Leu Asp Thr Tyr Val
 355 360 365
 Glu Ile Pro Ala Val Leu Leu Thr Ala Phe Gly Thr Tyr Ala Gly Pro
 370 375 380
 Val Leu Trp Ala Ser His Leu Val His Phe Leu Ser Ser Glu Thr Arg
 385 390 395 400
 Ser Gly Ser Ala Leu Ser His Ala Cys Phe Cys Tyr Ala Leu Ile Cys
 405 410 415
 Ser Ile Pro Val Phe Thr Tyr Ile Val Leu Val Thr Ser Leu Arg Tyr
 420 425 430
 His Leu Phe Ile Trp Ser Val Phe Ser Pro Lys Leu Leu Tyr Glu Gly
 435 440 445
 Met His Leu Leu Ile Thr Ala Ala Val Cys Val Phe Phe Thr Ala Met
 450 455 460
 Asp Gln Thr Arg Leu Thr Gln Ser
 465 470

<210> 271

<211> 1089

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1089)

<221> misc_feature

<222> (1)...(1089)

398

<223> n = A,T,C or G

<400> 271

atg	gac	agc	ccc	gag	gtg	acc	ttc	act	ctc	gcc	tat	ctg	gtg	ttc	gcc	48
Met	Asp	Ser	Pro	Glu	Val	Thr	Phe	Thr	Leu	Ala	Tyr	Leu	Val	Phe	Ala	
1				5					10					15		

gtg	tgc	ttc	gtg	ttc	acg	ccc	aac	gag	ttc	cac	gcg	gcg	ggg	ctc	acg	96
Val	Cys	Phe	Val	Phe	Thr	Pro	Asn	Glu	Phe	His	Ala	Ala	Gly	Leu	Thr	
			20					25					30			

gtg	cag	aac	ctg	ctg	tcg	ggc	tgg	ctg	ggc	agc	gag	gac	gcc	gcc	ttc	144
Val	Gln	Asn	Leu	Leu	Ser	Gly	Trp	Leu	Gly	Ser	Glu	Asp	Ala	Ala	Phe	
		35					40					45				

gtg	ccc	ttc	cac	ttg	cgc	cgc	acg	gcc	gcc	acg	ctg	ttg	tgc	cac	tcg	192
Val	Pro	Phe	His	Leu	Arg	Arg	Thr	Ala	Ala	Thr	Leu	Leu	Cys	His	Ser	
	50					55					60					

ctg	ctg	ccg	ctc	ggc	tac	tat	gtg	ggc	atg	tgc	ctt	gcg	gct	tca	gaa	240
Leu	Leu	Pro	Leu	Gly	Tyr	Tyr	Val	Gly	Met	Cys	Leu	Ala	Ala	Ser	Glu	
65					70				75					80		

aag	cgg	ctc	cac	gcc	ctc	agc	cag	gcc	cct	gag	gcc	tgg	cgg	ctc	ttc	288
Lys	Arg	Leu	His	Ala	Leu	Ser	Gln	Ala	Pro	Glu	Ala	Trp	Arg	Leu	Phe	
			85					90						95		

ctg	ctg	ctg	gcc	gtg	acc	ctc	ccc	tcc	atc	gcc	tgc	atc	ctg	atc	tac	336
Leu	Leu	Leu	Ala	Val	Thr	Leu	Pro	Ser	Ile	Ala	Cys	Ile	Leu	Ile	Tyr	
			100					105					110			

tac	tgg	tcc	cgt	gac	cgg	tgg	gcc	tgc	cac	cca	ctg	gcg	cgc	acc	ctg	384
Tyr	Trp	Ser	Arg	Asp	Arg	Trp	Ala	Cys	His	Pro	Leu	Ala	Arg	Thr	Leu	
		115					120					125				

gcc	ctc	tac	gcc	ctc	cca	cag	tct	ggc	tgg	cag	gct	gtt	gcc	tcc	tct	432
Ala	Leu	Tyr	Ala	Leu	Pro	Gln	Ser	Gly	Trp	Gln	Ala	Val	Ala	Ser	Ser	
	130					135				140						

gtc	aac	act	gag	ttc	cgg	cgg	att	gac	aag	ttt	gcc	acc	ggt	gca	cca	480
Val	Asn	Thr	Glu	Phe	Arg	Arg	Ile	Asp	Lys	Phe	Ala	Thr	Gly	Ala	Pro	
145					150					155				160		

ggt	gcc	cgt	gtg	att	gtg	aca	gac	acg	tgg	gtg	atg	aag	gta	acc	acc	528
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

399

Gly	Ala	Arg	Val	Ile	Val	Thr	Asp	Thr	Trp	Val	Met	Lys	Val	Thr	Thr		
				165					170					175			
tac	cga	gtg	cac	gtg	gcc	cag	cag	cag	gac	gtg	cac	ctg	act	gtg	acg	576	
Tyr	Arg	Val	His	Val	Ala	Gln	Gln	Gln	Asp	Val	His	Leu	Thr	Val	Thr		
			180					185					190				
gag	tct	cgg	cag	cat	gag	ctc	tcg	cca	gac	tcg	aac	ttg	ccc	gtg	cag	624	
Glu	Ser	Arg	Gln	His	Glu	Leu	Ser	Pro	Asp	Ser	Asn	Leu	Pro	Val	Gln		
		195						200				205					
ctc	ctc	acc	atc	cgt	gtg	gcc	agc	acc	aac	cct	gct	gtg	cag	gcc	ttt	672	
Leu	Leu	Thr	Ile	Arg	Val	Ala	Ser	Thr	Asn	Pro	Ala	Val	Gln	Ala	Phe		
		210				215					220						
gac	atc	tgg	ctg	aac	tcc	act	gag	tac	ggg	gag	ctc	tgc	gag	aag	ctc	720	
Asp	Ile	Trp	Leu	Asn	Ser	Thr	Glu	Tyr	Gly	Glu	Leu	Cys	Glu	Lys	Leu		
225					230					235					240		
cgg	gca	ccc	atc	cgc	agg	gca	gcc	cat	gtg	gtc	atc	cac	cag	agc	ctg	768	
Arg	Ala	Pro	Ile	Arg	Arg	Ala	Ala	His	Val	Val	Ile	His	Gln	Ser	Leu		
				245					250					255			
ggc	gac	ctg	ttc	ctg	gag	acn	ttt	gcc	tcc	ctg	gta	gag	gtc	aac	ccg	816	
Gly	Asp	Leu	Phe	Leu	Glu	Xaa	Phe	Ala	Ser	Leu	Val	Glu	Val	Asn	Pro		
		260						265						270			
gcc	tac	tca	gtg	ccc	agc	agc	cag	gag	ctg	gag	gcc	tgc	ata	ggc	tgc	864	
Ala	Tyr	Ser	Val	Pro	Ser	Ser	Gln	Glu	Leu	Glu	Ala	Cys	Ile	Gly	Cys		
		275					280					285					
atg	cag	aca	cgt	gcc	agc	gtg	aag	ctg	gtg	aag	acc	tgc	cag	gag	gca	912	
Met	Gln	Thr	Arg	Ala	Ser	Val	Lys	Leu	Val	Lys	Thr	Cys	Gln	Glu	Ala		
		290					295				300						
gcc	aca	ggc	gag	tgc	cag	cag	tgt	tac	tgc	cgc	ccc	atg	tgg	tgc	ctc	960	
Ala	Thr	Gly	Glu	Cys	Gln	Gln	Cys	Tyr	Cys	Arg	Pro	Met	Trp	Cys	Leu		
305					310					315					320		
acc	tgc	atg	ggc	aag	tgg	ttc	gcc	agc	cgc	cag	gac	ccc	ctg	cgc	cct	1008	
Thr	Cys	Met	Gly	Lys	Trp	Phe	Ala	Ser	Arg	Gln	Asp	Pro	Leu	Arg	Pro		
				325					330					335			
gac	acc	tgg	ctg	gcc	agc	cgc	gtg	ccc	tgc	ccc	acc	tgc	cgc	gca	cgc	1056	

400

Asp Thr Trp Leu Ala Ser Arg Val Pro Cys Pro Thr Cys Arg Ala Arg
 340 345 350

ttc tgc atc ctg gat gtg tgc acc gtg cgc tga 1089
 Phe Cys Ile Leu Asp Val Cys Thr Val Arg *
 355 360

<210> 272
 <211> 362
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(362)
 <223> Xaa = Any Amino Acid

<400> 272
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 1 5 10 15
 Val Cys Phe Val Phe Thr Pro Asn Glu Phe His Ala Ala Gly Leu Thr
 20 25 30
 Val Gln Asn Leu Leu Ser Gly Trp Leu Gly Ser Glu Asp Ala Ala Phe
 35 40 45
 Val Pro Phe His Leu Arg Arg Thr Ala Ala Thr Leu Leu Cys His Ser
 50 55 60
 Leu Leu Pro Leu Gly Tyr Val Gly Met Cys Leu Ala Ala Ser Glu
 65 70 75 80
 Lys Arg Leu His Ala Leu Ser Gln Ala Pro Glu Ala Trp Arg Leu Phe
 85 90 95
 Leu Leu Leu Ala Val Thr Leu Pro Ser Ile Ala Cys Ile Leu Ile Tyr
 100 105 110
 Tyr Trp Ser Arg Asp Arg Trp Ala Cys His Pro Leu Ala Arg Thr Leu
 115 120 125
 Ala Leu Tyr Ala Leu Pro Gln Ser Gly Trp Gln Ala Val Ala Ser Ser
 130 135 140
 Val Asn Thr Glu Phe Arg Arg Ile Asp Lys Phe Ala Thr Gly Ala Pro
 145 150 155 160
 Gly Ala Arg Val Ile Val Thr Asp Thr Trp Val Met Lys Val Thr Thr
 165 170 175
 Tyr Arg Val His Val Ala Gln Gln Gln Asp Val His Leu Thr Val Thr
 180 185 190
 Glu Ser Arg Gln His Glu Leu Ser Pro Asp Ser Asn Leu Pro Val Gln

401

195					200					205					
Leu	Leu	Thr	Ile	Arg	Val	Ala	Ser	Thr	Asn	Pro	Ala	Val	Gln	Ala	Phe
210					215					220					
Asp	Ile	Trp	Leu	Asn	Ser	Thr	Glu	Tyr	Gly	Glu	Leu	Cys	Glu	Lys	Leu
225					230					235					240
Arg	Ala	Pro	Ile	Arg	Arg	Ala	Ala	His	Val	Val	Ile	His	Gln	Ser	Leu
245					250					255					
Gly	Asp	Leu	Phe	Leu	Glu	Xaa	Phe	Ala	Ser	Leu	Val	Glu	Val	Asn	Pro
260					265					270					
Ala	Tyr	Ser	Val	Pro	Ser	Ser	Gln	Glu	Leu	Glu	Ala	Cys	Ile	Gly	Cys
275					280					285					
Met	Gln	Thr	Arg	Ala	Ser	Val	Lys	Leu	Val	Lys	Thr	Cys	Gln	Glu	Ala
290					295					300					
Ala	Thr	Gly	Glu	Cys	Gln	Gln	Cys	Tyr	Cys	Arg	Pro	Met	Trp	Cys	Leu
305					310					315					320
Thr	Cys	Met	Gly	Lys	Trp	Phe	Ala	Ser	Arg	Gln	Asp	Pro	Leu	Arg	Pro
325					330					335					
Asp	Thr	Trp	Leu	Ala	Ser	Arg	Val	Pro	Cys	Pro	Thr	Cys	Arg	Ala	Arg
340					345					350					
Phe	Cys	Ile	Leu	Asp	Val	Cys	Thr	Val	Arg						
355					360										

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<210> 273
<211> 723
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(723)

<400> 273																
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Met	Ser	Pro	Leu	Leu	Phe	Gly	Ala	Gly	Leu	Val	Val	Leu	Asn	Leu	Val	
1			5			10			15							
acg	tct	gcc	agg	agc	cag	aag	aca	gaa	cct	cta	agt	ggc	tct	ggg	gac	96
Thr	Ser	Ala	Arg	Ser	Gln	Lys	Thr	Glu	Pro	Leu	Ser	Gly	Ser	Gly	Asp	
			20			25						30				
cag	cca	ctc	ttc	cgt	gga	gct	gat	cga	tat	gac	ttt	gcc	atc	atg	ata	144
Gln	Pro	Leu	Phe	Arg	Gly	Ala	Asp	Arg	Tyr	Asp	Phe	Ala	Ile	Met	Ile	
			35			40						45				

402

cct cca gga ggc acg gaa tgc ttt tgg caa ttt gcc cac cag act gga Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe Ala His Gln Thr Gly 50 55 60	192
tac ttc tat ttc agt tac gag gtt cag cgg aca gtg ggg atg tca cat Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr Val Gly Met Ser His 65 70 75 80	240
gac cgg cat gtt gct gcc acg gca cat aac cca cag gga ttt ctc ata Asp Arg His Val Ala Ala Thr Ala His Asn Pro Gln Gly Phe Leu Ile 85 90 95	288
gac acc tcc cag ggt gtt cgg ggc cag att aac ttc tct acc caa gag Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn Phe Ser Thr Gln Glu 100 105 110	336
aca ggt ttt tat cag ctt tgt cta agt aat cag cat aat cac ttc ggt Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln His Asn His Phe Gly 115 120 125	384
tct gtg caa gtg tac ctc aac ttt ggg gtc ttc tat gag ggg cct gag Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe Tyr Glu Gly Pro Glu 130 135 140	432
act gat cac aaa cag aag gaa aga aaa caa ctg aat gat act ctg gat Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu Asn Asp Thr Leu Asp 145 150 155 160	480
gca att gag gac ggc aca caa aag gtg cag aac aat atc ttt cac atg Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn Asn Ile Phe His Met 165 170 175	528
tgg cga tac tac aac ttt gcc cgg atg agg aaa atg gct gac ttt ttc Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys Met Ala Asp Phe Phe 180 185 190	576
ctt atc caa tca aac tat aac tac gtg aac tgg tgg tcg aca gcc cag Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp Trp Ser Thr Ala Gln 195 200 205	624
agc ctt gtt att att ctt tct ggg atc ctg caa ctg tat ttc ttg aag Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln Leu Tyr Phe Leu Lys 210 215 220	672

403

cgt ctc ttc aat gtt cca aca act aca gat aca aag aag cca aga tgc 720
 Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr Lys Lys Pro Arg Cys
 225 230 235 240

taa 723
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<210> 274
 <211> 240
 <212> PRT
 <213> Homo sapiens

<400> 274

Met Ser Pro Leu Leu Phe Gly Ala Gly Leu Val Val Leu Asn Leu Val
 1 5 10 15
 Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu Ser Gly Ser Gly Asp
 20 25 30
 Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp Phe Ala Ile Met Ile
 35 40 45
 Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe Ala His Gln Thr Gly
 50 55 60
 Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr Val Gly Met Ser His
 65 70 75 80
 Asp Arg His Val Ala Ala Thr Ala His Asn Pro Gln Gly Phe Leu Ile
 85 90 95
 Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn Phe Ser Thr Gln Glu
 100 105 110
 Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln His Asn His Phe Gly
 115 120 125
 Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe Tyr Glu Gly Pro Glu
 130 135 140
 Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu Asn Asp Thr Leu Asp
 145 150 155 160
 Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn Asn Ile Phe His Met
 165 170 175
 Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys Met Ala Asp Phe Phe
 180 185 190
 Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp Trp Ser Thr Ala Gln
 195 200 205
 Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln Leu Tyr Phe Leu Lys
 210 215 220
 Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr Lys Lys Pro Arg Cys

404

225	230	235	240
<p><210> 275 <211> 993 <212> DNA <213> Homo sapiens</p> <p><220> <221> CDS <222> (1)...(993)</p> <p><221> misc_feature <222> (1)...(993) <223> n = A,T,C or G</p>			
<p><400> 275</p>			
atg gct gag cac gca ggg ccc cga ctc ccc ctg gtg ctg aag acg ctg			48
Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu			
1 5 10 15			
<p>gca tgc aca cac agc agt gcg tat gag aac cag agg gtg acc acc acc</p> <p>Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr</p> <p>20 25 30</p>			
<p>gcc ttc ctg gcc gag ctg ctg aac agc aac gtg gcc aac gac ctc atg</p> <p>Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met</p> <p>35 40 45</p>			
<p>ctc ttg gac tcg ctg ctg gag agc ctg gcg gct cgc cag aag gac aca</p> <p>Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr</p> <p>50 55 60</p>			
<p>tgc gcc anc gtg cgg agg ctg gtg ctc cgc ggc ctg gcc aac ctg gcc</p> <p>Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala</p> <p>65 70 75 80</p>			
<p>tcc ggc tgc cct gac aag gtg cga acc cac ggc ccc cag ctc ctc aca</p> <p>Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr</p> <p>85 90 95</p>			
<p>gcc atg att ggc ggg ctg gac gac ggg gac aac cct cac agc cca gtg</p> <p>Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val</p> <p>100 105 110</p>			

405

gcc ctg gag gcc atg ctg ggc ctt gcg agg ctg gtg cac ctg gtg gag Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu 115 120 125	384
tcc tgg gac ctg cgc tca ggg ctg ctg cac gtg gcc atc cgc atc cgg Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg 130 135 140	432
cct ttc ttc gac agt gag aag atg gag ttc cgg acg gca tct atc cgc Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg 145 150 155 160	480
ctc ttt ggg cac ctt aac aag gtc tgc cac gga gac tgt gag gac gtc Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val 165 170 175	528
ttc ctg gac cag gtg gtg ggc ggg ctg gcg ccc ctg ctg ctg cac ctg Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu 180 185 190	576
cag gac cct cag gcc acc gtg gcc agc gcc tgc agg ttt gcc ctg cgc Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg 195 200 205	624
atg tgt ggc ccc aat ctg gca tgt gag gag ctc tca gct gct ttc cag Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln 210 215 220	672
aaa cac ctg cag gag ggc cga gcc ctg cac ttc ggg gag ttc ctc aac Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn 225 230 235 240	720
acc acc tgc aag cac ctg atg cac cat ttc cca gac ctg ctg ggc cgt Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg 245 250 255	768
ctc ctg acc acc tgc ctg ttc tac ttc aag agc agc tgg gag aac gtc Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val 260 265 270	816
cga gct gct gca ccc ctg ttc acc ggg ttc ctg gtg ctg cac tcg gag Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu 275 280 285	864

406

ccc agg cag cag ccg cag gtg gac ctg gac cag ctc att gcg gcg ctc 912
 Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Ala Leu
 290 295 300

cag atc ctg ctg aag gac ccg gcc ccc gag gtg cgg acg agg gct gct 960
 Gln Ile Leu Leu Lys Asp Pro Ala Pro Glu Val Arg Thr Arg Ala Ala
 305 310 315 320

gag gcc ctg ggc cgc ctg gtg aag ctc gcc taa 993
 Glu Ala Leu Gly Arg Leu Val Lys Leu Ala *

<210> 276

<211> 330

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 276

Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu
 1 5 10 15
 Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr
 20 25 30
 Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met
 35 40 45
 Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr
 50 55 60
 Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala
 65 70 75 80
 Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr
 85 90 95
 Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val
 100 105 110
 Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu
 115 120 125
 Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg
 130 135 140
 Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg
 145 150 155 160

407

Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val
 165 170 175
 Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu
 180 185 190
 Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg
 195 200 205
 Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln
 210 215 220
 Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn
 225 230 235 240
 Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg
 245 250 255
 Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val
 260 265 270
 Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu
 275 280 285
 Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Ala Leu
 290 295 300
 Gln Ile Leu Leu Lys Asp Pro Ala Pro Glu Val Arg Thr Arg Ala Ala
 305 310 315 320
 Glu Ala Leu Gly Arg Leu Val Lys Leu Ala
 325 330

<210> 277

<211> 642

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(642)

<400> 277

atg gat caa caa ctg cgt ggg aag ccg gaa tta ttg gtc ttc ttc agc	48
Met Asp Gln Gln Leu Arg Gly Lys Pro Glu Leu Leu Val Phe Phe Ser	
1 5 10 15	
act gtg gcc tcg gcc aca gct ggc atg ctc tgc ctg atc gcc atc ctg	96
Thr Val Ala Ser Ala Thr Ala Gly Met Leu Cys Leu Ile Ala Ile Leu	
20 25 30	
ctg tat gtc ctc gtc cag tac ctc gtg aac ccc ggg gtg ctc cgc acg	144
Leu Tyr Val Leu Val Gln Tyr Leu Val Asn Pro Gly Val Leu Arg Thr	
35 40 45	

408

gac ccc aga gat gtc aag aat atg aac acg tgg ctg ctg ttc ctc ccc Asp Pro Arg Asp Val Lys Asn Met Asn Thr Trp Leu Leu Phe Leu Pro 50 55 60	192
ctg ttc ccg gtg cag gtg cag acc ctg ata gtc gtg atc atc ggg atg Leu Phe Pro Val Gln Val Gln Thr Leu Ile Val Val Ile Ile Gly Met 65 70 75 80	240
ctc gtg ctc ctg ctg gac ttt ctt ggc ttg gtg cac ctg ggc cag ctg Leu Val Leu Leu Leu Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu 85 90 95	288
ctc atc ttc cac atc tac ctg aag gcc aag aag atg acc acc ttt gag Leu Ile Phe His Ile Tyr Leu Lys Ala Lys Lys Met Thr Thr Phe Glu 100 105 110	336
tat ctc att aat aac cgc aaa gaa gag agt tca aaa cat caa gca gtg Tyr Leu Ile Asn Asn Arg Lys Glu Glu Ser Ser Lys His Gln Ala Val 115 120 125	384
agg aaa gat cca tac gtg caa atg gac aaa gga gtt ctc cag caa gga Arg Lys Asp Pro Tyr Val Gln Met Asp Lys Gly Val Leu Gln Gln Gly 130 135 140	432
gct ggc gcc ctg ggc tca tct gca cag gga gtc aaa gcc aag agc tcc Ala Gly Ala Leu Gly Ser Ser Ala Gln Gly Val Lys Ala Lys Ser Ser 145 150 155 160	480
ctg ctg att cac aag cac tta tgt cac ttc tgc act tca gta aac cag Leu Leu Ile His Lys His Leu Cys His Phe Cys Thr Ser Val Asn Gln 165 170 175	528
gac ggg gat tcg aag gca cag gaa gca gat gat gcc ccg agt aca tct Asp Gly Asp Ser Lys Ala Gln Glu Ala Asp Asp Ala Pro Ser Thr Ser 180 185 190	576
aca ctt ggg ctg caa caa gaa aca aca gag ccc atg aaa act gac agt Thr Leu Gly Leu Gln Gln Glu Thr Thr Glu Pro Met Lys Thr Asp Ser 195 200 205	624
gct gaa agt gaa gac tga Ala Glu Ser Glu Asp *	642
210	

409

<210> 278
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 278
 Met Asp Gln Gln Leu Arg Gly Lys Pro Glu Leu Leu Val Phe Phe Ser
 1 5 10 15
 Thr Val Ala Ser Ala Thr Ala Gly Met Leu Cys Leu Ile Ala Ile Leu
 20 25 30
 Leu Tyr Val Leu Val Gln Tyr Leu Val Asn Pro Gly Val Leu Arg Thr
 35 40 45
 Asp Pro Arg Asp Val Lys Asn Met Asn Thr Trp Leu Leu Phe Leu Pro
 50 55 60
 Leu Phe Pro Val Gln Val Gln Thr Leu Ile Val Val Ile Ile Gly Met
 65 70 75 80
 Leu Val Leu Leu Leu Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu
 85 90 95
 Leu Ile Phe His Ile Tyr Leu Lys Ala Lys Lys Met Thr Thr Phe Glu
 100 105 110
 Tyr Leu Ile Asn Asn Arg Lys Glu Glu Ser Ser Lys His Gln Ala Val
 115 120 125
 Arg Lys Asp Pro Tyr Val Gln Met Asp Lys Gly Val Leu Gln Gln Gly
 130 135 140
 Ala Gly Ala Leu Gly Ser Ser Ala Gln Gly Val Lys Ala Lys Ser Ser
 145 150 155 160
 Leu Leu Ile His Lys His Leu Cys His Phe Cys Thr Ser Val Asn Gln
 165 170 175
 Asp Gly Asp Ser Lys Ala Gln Glu Ala Asp Asp Ala Pro Ser Thr Ser
 180 185 190
 Thr Leu Gly Leu Gln Gln Glu Thr Thr Glu Pro Met Lys Thr Asp Ser
 195 200 205
 Ala Glu Ser Glu Asp
 210

<210> 279
 <211> 1194
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

410

<222> (1)...(1194)

<400> 279

atg agc tgg ctt ttt ccc ctg acc aag agc gcc tcc tcc tcc gcg gct	48
Met Ser Trp Leu Phe Pro Leu Thr Lys Ser Ala Ser Ser Ser Ala Ala	
1 5 10 15	
ggg tcc ccc ggt ggc ctc acc agc ctc cag cag cag aag cag cgc ctg	96
Gly Ser Pro Gly Gly Leu Thr Ser Leu Gln Gln Gln Lys Gln Arg Leu	
20 25 30	
atc gag tcc ctc cgg aac tca cac tcc agt ata gcc gaa ata cag aaa	144
Ile Glu Ser Leu Arg Asn Ser His Ser Ser Ile Ala Glu Ile Gln Lys	
35 40 45	
gat gtg gaa tac aga ttg cca ttc acc ata aac aac ctg aca att aac	192
Asp Val Glu Tyr Arg Leu Pro Phe Thr Ile Asn Asn Leu Thr Ile Asn	
50 55 60	
att aat ata ttg ctt cct cca cag ttt cct cag gaa aaa cca gtg atc	240
Ile Asn Ile Leu Leu Pro Pro Gln Phe Pro Gln Glu Lys Pro Val Ile	
65 70 75 80	
agt gtt tat cca cca ata cga cat cac tta atg gat aaa caa gga gtg	288
Ser Val Tyr Pro Pro Ile Arg His His Leu Met Asp Lys Gln Gly Val	
85 90 95	
tat gtt acc tct cca tta gta aac aat ttt aca atg cac tca gat ctt	336
Tyr Val Thr Ser Pro Leu Val Asn Asn Phe Thr Met His Ser Asp Leu	
100 105 110	
gga aaa att att cag agt ctg ttg gat gag ttt tgg aag aat cct cca	384
Gly Lys Ile Ile Gln Ser Leu Leu Asp Glu Phe Trp Lys Asn Pro Pro	
115 120 125	
gtt tta gct cct act tca aca gca ttt cct tat cta tac agt aac cca	432
Val Leu Ala Pro Thr Ser Thr Ala Phe Pro Tyr Leu Tyr Ser Asn Pro	
130 135 140	
agt ggg atg tct cct tat gct tct cag ggt ttt cca ttt ctt cct cca	480
Ser Gly Met Ser Pro Tyr Ala Ser Gln Gly Phe Pro Phe Leu Pro Pro	
145 150 155 160	
tat cct cca caa gaa gca aac agg agt atc act tct tta tct gtt gct	528

411

Tyr	Pro	Pro	Gln	Glu	Ala	Asn	Arg	Ser	Ile	Thr	Ser	Leu	Ser	Val	Ala		
				165					170					175			
gac	act	gtt	tct	tct	tca	aca	aca	agt	cat	acc	aca	gcc	aag	cct	gcc		576
Asp	Thr	Val	Ser	Ser	Ser	Thr	Thr	Ser	His	Thr	Thr	Ala	Lys	Pro	Ala		
			180					185					190				
gct	cct	tca	ttt	ggt	gtc	ctt	tca	aat	ctg	cca	tta	ccc	att	ccc	aca		624
Ala	Pro	Ser	Phe	Gly	Val	Leu	Ser	Asn	Leu	Pro	Leu	Pro	Ile	Pro	Thr		
			195					200					205				
gtg	gat	gct	tca	ata	ccg	aca	agc	caa	aat	ggt	ttt	ggg	tac	aag	atg		672
Val	Asp	Ala	Ser	Ile	Pro	Thr	Ser	Gln	Asn	Gly	Phe	Gly	Tyr	Lys	Met		
	210						215					220					
cca	gat	gtc	cct	gat	gca	ttt	cca	gaa	ctc	tca	gaa	cta	agt	gtg	tca		720
Pro	Asp	Val	Pro	Asp	Ala	Phe	Pro	Glu	Leu	Ser	Glu	Leu	Ser	Val	Ser		
	225					230				235					240		
caa	ctc	aca	gat	atg	aat	gaa	caa	gag	gag	gta	tta	cta	gaa	cag	ttt		768
Gln	Leu	Thr	Asp	Met	Asn	Glu	Gln	Glu	Glu	Val	Leu	Leu	Glu	Gln	Phe		
				245					250					255			
ctg	act	ttg	cct	caa	cta	aaa	caa	att	att	acc	gac	aaa	gat	gac	tta		816
Leu	Thr	Leu	Pro	Gln	Leu	Lys	Gln	Ile	Ile	Thr	Asp	Lys	Asp	Asp	Leu		
			260					265						270			
gta	aaa	agt	att	gag	gaa	cta	gca	aga	aaa	aat	ctc	ctt	ttg	gag	ccc		864
Val	Lys	Ser	Ile	Glu	Glu	Leu	Ala	Arg	Lys	Asn	Leu	Leu	Leu	Glu	Pro		
		275					280						285				
agc	ttg	gaa	gcc	aaa	aga	caa	act	gtt	tta	gat	aag	tat	gaa	tta	ctt		912
Ser	Leu	Glu	Ala	Lys	Arg	Gln	Thr	Val	Leu	Asp	Lys	Tyr	Glu	Leu	Leu		
	290					295					300						
aca	cag	atg	aag	tcc	act	ttc	gaa	aag	aag	atg	caa	agg	cag	cat	gaa		960
Thr	Gln	Met	Lys	Ser	Thr	Phe	Glu	Lys	Lys	Met	Gln	Arg	Gln	His	Glu		
	305					310				315					320		
ctt	agt	gag	agc	tgt	agt	gca	agt	gcc	ctt	cag	gca	aga	ttg	aaa	gta		1008
Leu	Ser	Glu	Ser	Cys	Ser	Ala	Ser	Ala	Leu	Gln	Ala	Arg	Leu	Lys	Val		
				325					330					335			
gct	gca	cat	gaa	gct	gag	gaa	gaa	tct	gat	aat	att	gca	gaa	gac	ttc		1056

412

Ala Ala His Glu Ala Glu Glu Glu Ser Asp Asn Ile Ala Glu Asp Phe
 340 345 350

ttg gag gga aag atg gaa ata gat gat ttt ctc agt agc ttc atg gaa 1104
 Leu Glu Gly Lys Met Glu Ile Asp Asp Phe Leu Ser Ser Phe Met Glu
 355 360 365

aag aga aca att tgc cac tgt aga aga gcc aag gaa gag aaa ctt cag 1152
 Lys Arg Thr Ile Cys His Cys Arg Arg Ala Lys Glu Glu Lys Leu Gln
 370 375 380

cag gcg ata gca atg cac agc caa ttt cat gct cca cta tag 1194
 Gln Ala Ile Ala Met His Ser Gln Phe His Ala Pro Leu *
 385 390 395

<210> 280

<211> 397

<212> PRT

<213> Homo sapiens

<400> 280

Met Ser Trp Leu Phe Pro Leu Thr Lys Ser Ala Ser Ser Ser Ala Ala
 1 5 10 15

Gly Ser Pro Gly Gly Leu Thr Ser Leu Gln Gln Gln Lys Gln Arg Leu
 20 25 30

Ile Glu Ser Leu Arg Asn Ser His Ser Ser Ile Ala Glu Ile Gln Lys
 35 40 45

Asp Val Glu Tyr Arg Leu Pro Phe Thr Ile Asn Asn Leu Thr Ile Asn
 50 55 60

Ile Asn Ile Leu Leu Pro Pro Gln Phe Pro Gln Glu Lys Pro Val Ile
 65 70 75 80

Ser Val Tyr Pro Pro Ile Arg His His Leu Met Asp Lys Gln Gly Val
 85 90 95

Tyr Val Thr Ser Pro Leu Val Asn Asn Phe Thr Met His Ser Asp Leu
 100 105 110

Gly Lys Ile Ile Gln Ser Leu Leu Asp Glu Phe Trp Lys Asn Pro Pro
 115 120 125

Val Leu Ala Pro Thr Ser Thr Ala Phe Pro Tyr Leu Tyr Ser Asn Pro
 130 135 140

Ser Gly Met Ser Pro Tyr Ala Ser Gln Gly Phe Pro Phe Leu Pro Pro
 145 150 155 160

Tyr Pro Pro Gln Glu Ala Asn Arg Ser Ile Thr Ser Leu Ser Val Ala
 165 170 175

413

Asp Thr Val Ser Ser Ser Thr Thr Ser His Thr Thr Ala Lys Pro Ala
 180 185 190
 Ala Pro Ser Phe Gly Val Leu Ser Asn Leu Pro Leu Pro Ile Pro Thr
 195 200 205
 Val Asp Ala Ser Ile Pro Thr Ser Gln Asn Gly Phe Gly Tyr Lys Met
 210 215 220
 Pro Asp Val Pro Asp Ala Phe Pro Glu Leu Ser Glu Leu Ser Val Ser
 225 230 235 240
 Gln Leu Thr Asp Met Asn Glu Gln Glu Glu Val Leu Leu Glu Gln Phe
 245 250 255
 Leu Thr Leu Pro Gln Leu Lys Gln Ile Ile Thr Asp Lys Asp Asp Leu
 260 265 270
 Val Lys Ser Ile Glu Glu Leu Ala Arg Lys Asn Leu Leu Leu Glu Pro
 275 280 285
 Ser Leu Glu Ala Lys Arg Gln Thr Val Leu Asp Lys Tyr Glu Leu Leu
 290 295 300
 Thr Gln Met Lys Ser Thr Phe Glu Lys Lys Met Gln Arg Gln His Glu
 305 310 315 320
 Leu Ser Glu Ser Cys Ser Ala Ser Ala Leu Gln Ala Arg Leu Lys Val
 325 330 335
 Ala Ala His Glu Ala Glu Glu Glu Ser Asp Asn Ile Ala Glu Asp Phe
 340 345 350
 Leu Glu Gly Lys Met Glu Ile Asp Asp Phe Leu Ser Ser Phe Met Glu
 355 360 365
 Lys Arg Thr Ile Cys His Cys Arg Arg Ala Lys Glu Glu Lys Leu Gln
 370 375 380
 Gln Ala Ile Ala Met His Ser Gln Phe His Ala Pro Leu
 385 390 395

<210> 281

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(579)

<400> 281

atg gcg gcg caa att cca att gtg gcc acc act tcc act ccc gga ata
 Met Ala Ala Gln Ile Pro Ile Val Ala Thr Thr Ser Thr Pro Gly Ile
 1 5 10 15

48

gtc cgg aac agc aag aag agg ccg gcc agc cct tcc cac aat ggc agc

96

414

[illegible]

415

*

<210> 282
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 282
 Met Ala Ala Gln Ile Pro Ile Val Ala Thr Thr Ser Thr Pro Gly Ile
 1 5 10 15
 Val Arg Asn Ser Lys Lys Arg Pro Ala Ser Pro Ser His Asn Gly Ser
 20 25 30
 Ser Gly Gly Gly Tyr Gly Ala Ser Lys Lys Lys Lys Ala Ser Ala Ser
 35 40 45
 Ser Phe Ala Gln Gly Ile Ser Met Glu Ala Met Ser Glu Asn Lys Met
 50 55 60
 Val Pro Ser Glu Phe Ser Thr Gly Pro Val Glu Lys Ala Ala Lys Pro
 65 70 75 80
 Leu Pro Phe Lys Asp Pro Asn Phe Val His Ser Gly His Gly Gly Ala
 85 90 95
 Val Ala Gly Lys Lys Asn Arg Thr Trp Lys Asn Leu Lys Gln Ile Leu
 100 105 110
 Ala Ser Glu Arg Ala Leu Pro Trp Gln Leu Asn Asp Pro Asn Tyr Phe
 115 120 125
 Ser Ile Asp Ala Pro Pro Ser Phe Lys Pro Ala Lys Lys Tyr Ser Asp
 130 135 140
 Val Ser Gly Leu Leu Ala Asn Tyr Thr Asp Pro Gln Ser Lys Leu Arg
 145 150 155 160
 Phe Ser Thr Ile Glu Glu Phe Ser Tyr Ile Arg Arg Leu Pro Ser Asp
 165 170 175
 Val Val Thr Gly Tyr Leu Ala Leu Arg Lys Ala Thr Ser Ile Val Pro
 180 185 190

<210> 283
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(948)

416

<400> 283

atg gcc tca gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt	48
Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe	
1 5 10 15	
gcc ctg tta caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga	96
Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly	
20 25 30	
aaa ggt aaa ggt cga aat act gga aag tct caa act tta gga agc aag	144
Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys	
35 40 45	
tca act aca aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa	192
Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu	
50 55 60	
cag caa cag agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa	240
Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys	
65 70 75 80	
att ccc cag aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt	288
Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu	
85 90 95	
cca ttg tca aac cca gta cag aag gat tca cga gaa gaa aat tgg caa	336
Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln	
100 105 110	
gag tgg aga caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca	384
Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala	
115 120 125	
gat ctt gag aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac	432
Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His	
130 135 140	
aaa aag gag tat gaa gat gct gaa aat act tca act cag tcc aaa gtt	480
Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val	
145 150 155 160	
atg aat aaa aaa gat aaa aga aag aat cat cag gga aaa gac aga cct	528
Met Asn Lys Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro	
165 170 175	

417

ctc aca gta tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa	576
Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys	
180 185 190	
aag act gag gaa gtg gtt ctg aaa gat gga aga att gaa aga cta aag	624
Lys Thr Glu Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys	
195 200 205	
tta gag ctt gaa agg aaa gat gct gaa atc cag aag ctg aaa aat gta	672
Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val	
210 215 220	
atc act caa tgg gag gca aag tat aag gaa gta aag gca aga aat gca	720
Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala	
225 230 235 240	
caa tta ttg aaa atg ctt cag gaa ggt gaa atg aaa gat aag gca gaa	768
Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu	
245 250 255	
ata ctt ctg caa gtt gat gaa tca caa agt atc aag aat gag ctc act	816
Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr	
260 265 270	
att cag gtg act tca ctt cat gct gca tta gaa caa gaa aga tct aaa	864
Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys	
275 280 285	
gtg aaa gta tta caa gca gag tta gcc aaa tac cag ggt ggc aga aaa	912
Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys	
290 295 300	
ggg aaa aga aac tct gaa tcc gac cag tgt agg tga	948
Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg *	
305 310 315	

<210> 284

<211> 315

<212> PRT

<213> Homo sapiens

<400> 284

418

Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
 1 5 10 15
 Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly
 20 25 30
 Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys
 35 40 45
 Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu
 50 55 60
 Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys
 65 70 75 80
 Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu
 85 90 95
 Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln
 100 105 110
 Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala
 115 120 125
 Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His
 130 135 140
 Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val
 145 150 155 160
 Met Asn Lys Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro
 165 170 175
 Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys
 180 185 190
 Lys Thr Glu Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys
 195 200 205
 Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val
 210 215 220
 Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala
 225 230 235 240
 Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu
 245 250 255
 Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr
 260 265 270
 Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys
 275 280 285
 Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys
 290 295 300
 Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg
 305 310 315

<210> 285

<211> 1308

<212> DNA

419

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1308)

<400> 285

atg ggc acc tct gtc acc ggc ttg tat cca gag ctg ttc act ctc ctc	48
Met Gly Thr Ser Val Thr Gly Leu Tyr Pro Glu Leu Phe Thr Leu Leu	
1 5 10 15	
ctg aag ctg gtt agc tgc aca ctg ggc cag aag atg ccc act tgt ccc	96
Leu Lys Leu Val Ser Cys Thr Leu Gly Gln Lys Met Pro Thr Cys Pro	
20 25 30	
tgg agc cat agg cgg cat gtg atg cag cag gga gaa cag cag cag atc	144
Trp Ser His Arg Arg His Val Met Gln Gln Gly Glu Gln Gln Gln Ile	
35 40 45	
cca gac ccc tgc agg ctt tca act gct act tta aaa tgt ttg caa gcc	192
Pro Asp Pro Cys Arg Leu Ser Thr Ala Thr Leu Lys Cys Leu Gln Ala	
50 55 60	
caa gcc atg aga gaa ggc ctt gca aag gaa tct gat gag ggg gac aac	240
Gln Ala Met Arg Glu Gly Leu Ala Lys Glu Ser Asp Glu Gly Asp Asn	
65 70 75 80	
tta tgg act cta ctc agc agt cct agt acc cac cac ata ggc gta tgt	288
Leu Trp Thr Leu Leu Ser Ser Pro Ser Thr His His Ile Gly Val Cys	
85 90 95	
tca ctg gcc agg agc atg gca gtg tgg caa cac gga gtc ata ctg gac	336
Ser Leu Ala Arg Ser Met Ala Val Trp Gln His Gly Val Ile Leu Asp	
100 105 110	
atc atg gaa cag ctg ctc tca tct ctt acc tcc tcc tcg gag aac tac	384
Ile Met Glu Gln Leu Leu Ser Ser Leu Thr Ser Ser Ser Glu Asn Tyr	
115 120 125	
cgg ata acc ggc gca gct ttc ttc tct gag ctc atg aag gaa cca atc	432
Arg Ile Thr Gly Ala Ala Phe Phe Ser Glu Leu Met Lys Glu Pro Ile	
130 135 140	
ctt tgg aag cat ggg aat ctg cga aat gtg ctg atc ttg atg gat caa	480

422

Pro Asp Pro Cys Arg Leu Ser Thr Ala Thr Leu Lys Cys Leu Gln Ala
 50 55 60
 Gln Ala Met Arg Glu Gly Leu Ala Lys Glu Ser Asp Glu Gly Asp Asn
 65 70 75 80
 Leu Trp Thr Leu Leu Ser Ser Pro Ser Thr His His Ile Gly Val Cys
 85 90 95
 Ser Leu Ala Arg Ser Met Ala Val Trp Gln His Gly Val Ile Leu Asp
 100 105 110
 Ile Met Glu Gln Leu Leu Ser Ser Leu Thr Ser Ser Ser Glu Asn Tyr
 115 120 125
 Arg Ile Thr Gly Ala Ala Phe Phe Ser Glu Leu Met Lys Glu Pro Ile
 130 135 140
 Leu Trp Lys His Gly Asn Leu Arg Asn Val Leu Ile Leu Met Asp Gln
 145 150 155 160
 Ser Ala Trp Asp Ser Asn Ala Thr Leu Arg Gln Met Ala Ile Arg Gly
 165 170 175
 Leu Gly Asn Thr Ala Ser Gly Ala Pro His Lys Val Lys Lys His Lys
 180 185 190
 Gln Leu Met Leu Glu Ser Ile Ile Arg Gly Leu Tyr His Leu Ala Arg
 195 200 205
 Thr Glu Val Val Cys Glu Ser Leu Lys Ala Leu Lys Lys Ile Leu Glu
 210 215 220
 Leu Leu Thr Asp Arg Asp Val Ser Phe Tyr Phe Lys Glu Ile Val Leu
 225 230 235 240
 Gln Thr Arg Thr Phe Phe Glu Asp Glu Gln Asp Asp Val Arg Leu Thr
 245 250 255
 Ala Ile Phe Leu Phe Glu Asp Leu Ala Pro Leu Thr Gly Arg Arg Trp
 260 265 270
 Lys Ile Phe Phe Ala Glu Glu Ile Lys Lys Ser Leu Ile Ser Phe Leu
 275 280 285
 Leu His Leu Trp Asp Pro Asn Pro Lys Ile Gly Val Ala Cys Arg Asp
 290 295 300
 Val Leu Met Val Cys Ile Pro Phe Leu Gly Leu Gln Glu Leu Tyr Gly
 305 310 315 320
 Val Leu Asp Arg Leu Leu Asp Gln Asp Leu Pro Arg Ala Arg Asp Phe
 325 330 335
 Tyr Arg Gln Phe Cys Val Lys Leu Ala Lys Lys Asn Gln Glu Ile Leu
 340 345 350
 Trp Ile Leu His Thr His Ser Phe Thr Phe Phe Thr Ser Thr Trp Glu
 355 360 365
 Val Ile Arg Ser Ala Ala Val Lys Leu Thr Asp Ala Val Val Leu Asn
 370 375 380
 Leu Thr Ser Gln Tyr Val Glu Leu Leu Asp Arg Glu Gln Leu Thr Thr
 385 390 395 400

423

Arg Leu Gln Ala Leu Arg Gln Asp Pro Cys Ile Ser Val Gln Arg Ala
 405 410 415
 Ala Glu Ala Ala Leu Gln Thr Leu Leu Arg Arg Cys Lys Glu Thr Ser
 420 425 430
 Ile Pro Leu
 435

<210> 287
 <211> 822
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(822)

<400> 287

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tgg tcg tcg gcc tct gca ccc ccg ccg cgg ggg ttc agc gcg atc tcc 96
 Trp Ser Ser Ala Ser Ala Pro Pro Pro Arg Gly Phe Ser Ala Ile Ser
 20 25 30

tgc acc gtc gag ggg gca ccc gcc agc ttt ggc aag agc ttc gcg cag 144
 Cys Thr Val Glu Gly Ala Pro Ala Ser Phe Gly Lys Ser Phe Ala Gln
 35 40 45

aaa tct ggc tac ttc ctg tgc ctt agt tct ctg ggc agc cta gag aac 192
 Lys Ser Gly Tyr Phe Leu Cys Leu Ser Ser Leu Gly Ser Leu Glu Asn
 50 55 60

ccg cag gag aac gtg gtg gcc gat atc cag atc gtg gtg gac aag agc 240
 Pro Gln Glu Asn Val Val Ala Asp Ile Gln Ile Val Val Asp Lys Ser
 65 70 75 80

ccc ctg ccg ctg ggc ttc tcc ccc gtc tgc gac ccc atg gat tcc aag 288
 Pro Leu Pro Leu Gly Phe Ser Pro Val Cys Asp Pro Met Asp Ser Lys
 85 90 95

gcc tct gtg tcc aag aag aaa cgc atg tgt gtg aag ctg ttg ccc ctg 336
 Ala Ser Val Ser Lys Lys Lys Arg Met Cys Val Lys Leu Leu Pro Leu
 100 105 110

424

gga gcc acg gac acg gct gtg ttt gat gtc cgg ctg agt ggg aag acc Gly Ala Thr Asp Thr Ala Val Phe Asp Val Arg Leu Ser Gly Lys Thr 115 120 125	384
aag aca gtg cct gga tac ctt cga ata ggg gac atg ggc ggc ttt gcc Lys Thr Val Pro Gly Tyr Leu Arg Ile Gly Asp Met Gly Gly Phe Ala 130 135 140	432
atc tgg tgc aag aag gcc aag gcc ccg agg cca gtg ccc aag ccc cga Ile Trp Cys Lys Lys Ala Lys Ala Pro Arg Pro Val Pro Lys Pro Arg 145 150 155 160	480
ggc ctc agc cgg gac atg cag ggc ctc tct ctg gat gca gcc agc cag Gly Leu Ser Arg Asp Met Gln Gly Leu Ser Leu Asp Ala Ala Ser Gln 165 170 175	528
cca agt aag ggc ggc ctc ctg gag cgg aca gcg tca agg ctg ggc tct Pro Ser Lys Gly Gly Leu Leu Glu Arg Thr Ala Ser Arg Leu Gly Ser 180 185 190	576
cgg gca tcc act ctg cgg agg aat gac tcc atc tac gag gcc tcc agc Arg Ala Ser Thr Leu Arg Arg Asn Asp Ser Ile Tyr Glu Ala Ser Ser 195 200 205	624
ctc tat ggc atc tca gcc atg gat ggg gtt ccc ttc aca ctc cac cca Leu Tyr Gly Ile Ser Ala Met Asp Gly Val Pro Phe Thr Leu His Pro 210 215 220	672
cga ttt gag ggc aag agc tgc agc ccc ctg gcc ttc tct gct ttt ggg Arg Phe Glu Gly Lys Ser Cys Ser Pro Leu Ala Phe Ser Ala Phe Gly 225 230 235 240	720
gac ctg acc atc aag tct ctg gcg gac att gag gag gag tat aac tac Asp Leu Thr Ile Lys Ser Leu Ala Asp Ile Glu Glu Glu Tyr Asn Tyr 245 250 255	768
ggc ttc gtg gtg gag aag acc gcg gct gcc cgc ctg ccc ccc agc gtc Gly Phe Val Val Glu Lys Thr Ala Ala Ala Arg Leu Pro Pro Ser Val 260 265 270	816
tca tag Ser *	822

425

<210> 288
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 288

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Met Asp Pro Val Pro Gly Thr Asp Ser Ala Pro Leu Ala Gly Leu Ala
 1          5          10          15
Trp Ser Ser Ala Ser Ala Pro Pro Pro Arg Gly Phe Ser Ala Ile Ser
      20          25          30
Cys Thr Val Glu Gly Ala Pro Ala Ser Phe Gly Lys Ser Phe Ala Gln
      35          40          45
Lys Ser Gly Tyr Phe Leu Cys Leu Ser Ser Leu Gly Ser Leu Glu Asn
 50          55          60
Pro Gln Glu Asn Val Val Ala Asp Ile Gln Ile Val Val Asp Lys Ser
65          70          75          80
Pro Leu Pro Leu Gly Phe Ser Pro Val Cys Asp Pro Met Asp Ser Lys
      85          90          95
Ala Ser Val Ser Lys Lys Lys Arg Met Cys Val Lys Leu Leu Pro Leu
      100          105          110
Gly Ala Thr Asp Thr Ala Val Phe Asp Val Arg Leu Ser Gly Lys Thr
      115          120          125
Lys Thr Val Pro Gly Tyr Leu Arg Ile Gly Asp Met Gly Gly Phe Ala
      130          135          140
Ile Trp Cys Lys Lys Ala Lys Ala Pro Arg Pro Val Pro Lys Pro Arg
      145          150          155          160
Gly Leu Ser Arg Asp Met Gln Gly Leu Ser Leu Asp Ala Ala Ser Gln
      165          170          175
Pro Ser Lys Gly Gly Leu Leu Glu Arg Thr Ala Ser Arg Leu Gly Ser
      180          185          190
Arg Ala Ser Thr Leu Arg Arg Asn Asp Ser Ile Tyr Glu Ala Ser Ser
      195          200          205
Leu Tyr Gly Ile Ser Ala Met Asp Gly Val Pro Phe Thr Leu His Pro
      210          215          220
Arg Phe Glu Gly Lys Ser Cys Ser Pro Leu Ala Phe Ser Ala Phe Gly
      225          230          235          240
Asp Leu Thr Ile Lys Ser Leu Ala Asp Ile Glu Glu Glu Tyr Asn Tyr
      245          250          255
Gly Phe Val Val Glu Lys Thr Ala Ala Ala Arg Leu Pro Pro Ser Val
      260          265          270
Ser

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426

<210> 289
 <211> 744
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(744)

<400> 289
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 Met Pro Gly Arg Ser Ser Ser Asn Ser Gly Ser Thr Gly Phe Ile Ser
 1 5 10 15
 ttc agt ggt gta gag tct gct ctc tcc tcc ttg aaa aac ttc caa gcc 96
 Phe Ser Gly Val Glu Ser Ala Leu Ser Ser Leu Lys Asn Phe Gln Ala
 20 25 30
 tgt atc aac tct ggt atg gac aca gct tct agt gtt gct ttg gat ctt 144
 Cys Ile Asn Ser Gly Met Asp Thr Ala Ser Ser Val Ala Leu Asp Leu
 35 40 45
 gtg gaa agt cag act gaa gtg agt agt gaa tat agt atg gac aag gca 192
 Val Glu Ser Gln Thr Glu Val Ser Ser Glu Tyr Ser Met Asp Lys Ala
 50 55 60
 atg gtt gaa ttt gct aca ttg gat cgg caa cta aac cat tat gta aag 240
 Met Val Glu Phe Ala Thr Leu Asp Arg Gln Leu Asn His Tyr Val Lys
 65 70 75 80
 gct gtt caa tct aca ata aat cat gtg aaa gaa gaa cgt cca gaa aaa 288
 Ala Val Gln Ser Thr Ile Asn His Val Lys Glu Glu Arg Pro Glu Lys
 85 90 95
 ata cca gat tta aaa tta ttg gta gag aag aaa ttt ttg gct tta cag 336
 Ile Pro Asp Leu Lys Leu Leu Val Glu Lys Lys Phe Leu Ala Leu Gln
 100 105 110
 agc aag aat tct gat gca gac ttt caa aat aat gaa aaa ttt gta cag 384
 Ser Lys Asn Ser Asp Ala Asp Phe Gln Asn Asn Glu Lys Phe Val Gln
 115 120 125
 ttt aaa caa cag ctg aaa gaa cta aag aag caa tgt ggt ctt caa gct 432

427

Phe Lys Gln Gln Leu Lys Glu Leu Lys Lys Gln Cys Gly Leu Gln Ala
 130 135 140
 gac aga gaa gct gac gga aca gaa gga gtg gat gaa gat ata att gtg 480
 Asp Arg Glu Ala Asp Gly Thr Glu Gly Val Asp Glu Asp Ile Ile Val
 145 150 155 160
 acc caa agt cag acc aac ttc acc tgc ccc att aca aag gag gaa atg 528
 Thr Gln Ser Gln Thr Asn Phe Thr Cys Pro Ile Thr Lys Glu Glu Met
 165 170 175
 aag aag cca gtg aaa aat aaa gtg tgt ggc cac acc tat gaa gag gac 576
 Lys Lys Pro Val Lys Asn Lys Val Cys Gly His Thr Tyr Glu Glu Asp
 180 185 190
 gcc att gtt cgc atg att gag tcc agg caa aag cgg aag aaa aag gcc 624
 Ala Ile Val Arg Met Ile Glu Ser Arg Gln Lys Arg Lys Lys Lys Ala
 195 200 205
 tat tgc cct caa att ggc tgt agc cac acg gat ata aga aag tca gat 672
 Tyr Cys Pro Gln Ile Gly Cys Ser His Thr Asp Ile Arg Lys Ser Asp
 210 215 220
 ctt atc cag gat gaa gca ctt aga agg gca att gag aac cat aac aag 720
 Leu Ile Gln Asp Glu Ala Leu Arg Arg Ala Ile Glu Asn His Asn Lys
 225 230 235 240
 aaa aga cat cgt cat tcc gag tag 744
 Lys Arg His Arg His Ser Glu *
 245

<210> 290

<211> 247

<212> PRT

<213> Homo sapiens

<400> 290

Met Pro Gly Arg Ser Ser Ser Asn Ser Gly Ser Thr Gly Phe Ile Ser
 1 5 10 15
 Phe Ser Gly Val Glu Ser Ala Leu Ser Ser Leu Lys Asn Phe Gln Ala
 20 25 30
 Cys Ile Asn Ser Gly Met Asp Thr Ala Ser Ser Val Ala Leu Asp Leu
 35 40 45

428

Val Glu Ser Gln Thr Glu Val Ser Ser Glu Tyr Ser Met Asp Lys Ala
 50 55 60
 Met Val Glu Phe Ala Thr Leu Asp Arg Gln Leu Asn His Tyr Val Lys
 65 70 75 80
 Ala Val Gln Ser Thr Ile Asn His Val Lys Glu Glu Arg Pro Glu Lys
 85 90 95
 Ile Pro Asp Leu Lys Leu Leu Val Glu Lys Lys Phe Leu Ala Leu Gln
 100 105 110
 Ser Lys Asn Ser Asp Ala Asp Phe Gln Asn Asn Glu Lys Phe Val Gln
 115 120 125
 Phe Lys Gln Gln Leu Lys Glu Leu Lys Lys Gln Cys Gly Leu Gln Ala
 130 135 140
 Asp Arg Glu Ala Asp Gly Thr Glu Gly Val Asp Glu Asp Ile Ile Val
 145 150 155 160
 Thr Gln Ser Gln Thr Asn Phe Thr Cys Pro Ile Thr Lys Glu Glu Met
 165 170 175
 Lys Lys Pro Val Lys Asn Lys Val Cys Gly His Thr Tyr Glu Glu Asp
 180 185 190
 Ala Ile Val Arg Met Ile Glu Ser Arg Gln Lys Arg Lys Lys Lys Ala
 195 200 205
 Tyr Cys Pro Gln Ile Gly Cys Ser His Thr Asp Ile Arg Lys Ser Asp
 210 215 220
 Leu Ile Gln Asp Glu Ala Leu Arg Arg Ala Ile Glu Asn His Asn Lys
 225 230 235 240
 Lys Arg His Arg His Ser Glu
 245

<210> 291

<211> 957

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(957)

<221> misc_feature

<222> (1)...(957)

<223> n = A,T,C or G

<400> 291

atg gct gag cac gca ggg ccc cga ctc ccc ctg gtg ctg aag acg ctg
 Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu
 1 5 10 15

48

429

gca tgc aca cac agc agt gcg tat gag aac cag agg gtg acc acc acc	96
Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr	
20 25 30	
gcc ttc ctg gcc gag ctg ctg aac agc aac gtg gcc aac gac ctc atg	144
Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met	
35 40 45	
ctc ttg gac tcg ctg ctg gag agc ctg gcg gct cgc cag aag gac aca	192
Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr	
50 55 60	
tgc gcc anc gtg cgg agg ctg gtg ctc cgc ggc ctg gcc aac ctg gcc	240
Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala	
65 70 75 80	
tcc ggc tgc cct gac aag gtg cga acc cac ggc ccc cag ctc ctc aca	288
Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr	
85 90 95	
gcc atg att ggc ggg ctg gac gac ggg gac aac cct cac agc cca gtg	336
Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val	
100 105 110	
gcc ctg gag gcc atg ctg ggc ctt gcg agg ctg gtg cac ctg gtg gag	384
Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu	
115 120 125	
tcc tgg gac ctg cgc tca ggg ctg ctg cac gtg gcc atc cgc atc cgg	432
Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg	
130 135 140	
cct ttc ttc gac agt gag aag atg gag ttc cgg acg gca tct atc cgc	480
Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg	
145 150 155 160	
ctc ttt ggg cac ctt aac aag gtc tgc cac gga gac tgt gag gac gtc	528
Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val	
165 170 175	
ttc ctg gac cag gtg gtg ggc ggg ctg gcg ccc ctg ctg ctg cac ctg	576
Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu	
180 185 190	

430

cag gac cct cag gcc acc gtg gcc agc gcc tgc agg ttt gcc ctg cgc	624
Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg	
195 200 205	
atg tgt ggc ccc aat ctg gca tgt gag gag ctc tca gct gct ttc cag	672
Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln	
210 215 220	
aaa cac ctg cag gag ggc cga gcc ctg cac ttc ggg gag ttc ctc aac	720
Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn	
225 230 235 240	
acc acc tgc aag cac ctg atg cac cat ttc cca gac ctg ctg ggc cgt	768
Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg	
245 250 255	
ctc ctg acc acc tgc ctg ttc tac ttc aag agc agc tgg gag aac gtc	816
Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val	
260 265 270	
cga gct gct gca ccc ctg ttc acc ggg ttc ctg gtg ctg cac tcg gag	864
Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu	
275 280 285	
ccc agg cag cag ccg cag gtg gac ctg gac cag ctc att gcg ggt gag	912
Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Gly Glu	
290 295 300	
cac ccc tcc acg ggg ccc ctc cgc tgg gcc ctg ctg acc ctg tag	957
His Pro Ser Thr Gly Pro Leu Arg Trp Ala Leu Leu Thr Leu *	
305 310 315	

<210> 292

<211> 318

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

431

<400> 292

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Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met
      35           40           45
Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr
 50           55           60
Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala
65           70           75           80
Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr
          85           90           95
Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val
          100          105          110
Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu
          115          120          125
Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg
          130          135          140
Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg
145          150          155          160
Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val
          165          170          175
Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu
          180          185          190
Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg
          195          200          205
Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln
210          215          220
Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn
225          230          235          240
Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg
          245          250          255
Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val
          260          265          270
Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu
          275          280          285
Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Gly Glu
          290          295          300
His Pro Ser Thr Gly Pro Leu Arg Trp Ala Leu Leu Thr Leu
305          310          315

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<210> 293

<211> 1107

432

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1107)

<400> 293

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Met Gln Pro Gly Ser Ser Arg Cys Glu Glu Glu Thr Pro Ser Leu Leu	
1 5 10 15	
tggttggttgatcctgtgtttctagccgttgcaaaactctactatcagg	96
Trp Gly Leu Asp Pro Val Phe Leu Ala Phe Ala Lys Leu Tyr Ile Arg	
20 25 30	
gat atc ctg gac atg aag gag tcc cgc cag gtg cca ggt gta ttt ttg	144
Asp Ile Leu Asp Met Lys Glu Ser Arg Gln Val Pro Gly Val Phe Leu	
35 40 45	
tac aat gga cat cca ata aaa cag gta gat gtc ttg gga act gtc att	192
Tyr Asn Gly His Pro Ile Lys Gln Val Asp Val Leu Gly Thr Val Ile	
50 55 60	
gga gtg aga gaa aga gat gct ttc tac agt tat gga gtg gat gac agc	240
Gly Val Arg Glu Arg Asp Ala Phe Tyr Ser Tyr Gly Val Asp Asp Ser	
65 70 75 80	
act gga gtt ata aac tgc atc tgc tgg aaa aag ttg aat act gag tct	288
Thr Gly Val Ile Asn Cys Ile Cys Trp Lys Lys Leu Asn Thr Glu Ser	
85 90 95	
gta tca gct gct cca agt gca gca aga gag ctc agc tta acc tca caa	336
Val Ser Ala Ala Pro Ser Ala Ala Arg Glu Leu Ser Leu Thr Ser Gln	
100 105 110	
ctt aag aag cta caa gag acc att gag cag aaa aca aag ata gag atc	384
Leu Lys Lys Leu Gln Glu Thr Ile Glu Gln Lys Thr Lys Ile Glu Ile	
115 120 125	
ggg gac acg atc cga gtc aga ggc agt atc cgc aca tac aga gaa gag	432
Gly Asp Thr Ile Arg Val Arg Gly Ser Ile Arg Thr Tyr Arg Glu Glu	
130 135 140	

433

cga gag att cat gcc acc gct tac tat aaa gtg gac gac cca gtg tgg	480
Arg Glu Ile His Ala Thr Ala Tyr Tyr Lys Val Asp Asp Pro Val Trp	
145 150 155 160	
aac att caa att gca agg atg ctt gag ctg ccc act atc tac agg aaa	528
Asn Ile Gln Ile Ala Arg Met Leu Glu Leu Pro Thr Ile Tyr Arg Lys	
165 170 175	
gtt tat gac cag cct ttt cac agc tca gcc cta gag aaa gaa gag gca	576
Val Tyr Asp Gln Pro Phe His Ser Ser Ala Leu Glu Lys Glu Glu Ala	
180 185 190	
cta agc aat cca ggc gcc ctg gac ctc ccc agt ctc acg agt ttg ctg	624
Leu Ser Asn Pro Gly Ala Leu Asp Leu Pro Ser Leu Thr Ser Leu Leu	
195 200 205	
agt gaa aaa gcc aaa gaa ttc ctc atg gag aac aga gtg cag agc ttt	672
Ser Glu Lys Ala Lys Glu Phe Leu Met Glu Asn Arg Val Gln Ser Phe	
210 215 220	
tac cag cag gag ctg gaa atg gtg gag tct ttg ctg tcc ctt gcc aat	720
Tyr Gln Gln Glu Leu Glu Met Val Glu Ser Leu Leu Ser Leu Ala Asn	
225 230 235 240	
cag cct gtg att cac agt gcc tgc tcc gac caa gtg aat ttt aag aag	768
Gln Pro Val Ile His Ser Ala Cys Ser Asp Gln Val Asn Phe Lys Lys	
245 250 255	
gac acc act tcc aag gca att cat agt ata ttt aag aat gct ata caa	816
Asp Thr Thr Ser Lys Ala Ile His Ser Ile Phe Lys Asn Ala Ile Gln	
260 265 270	
ctg ctg cag gaa aaa gga ctt gtt ttc cag aaa gat gat ggt ttt gat	864
Leu Leu Gln Glu Lys Gly Leu Val Phe Gln Lys Asp Asp Gly Phe Asp	
275 280 285	
aac cta tac tat gta acc aga gaa gac aaa gac ctg cac aga aag atc	912
Asn Leu Tyr Tyr Val Thr Arg Glu Asp Lys Asp Leu His Arg Lys Ile	
290 295 300	
cac cgg atc att cag cag gac tgc cag aaa cca aat cac atg gag aag	960
His Arg Ile Ile Gln Gln Asp Cys Gln Lys Pro Asn His Met Glu Lys	
305 310 315 320	

434

ggc tgt cac ttc ctg cac atc ttg gcc tgt gct cgc ctg agc atc cgc 1008
 Gly Cys His Phe Leu His Ile Leu Ala Cys Ala Arg Leu Ser Ile Arg
 325 330 335

ccg ggc ctg agc gag gct gtg ctg cag caa gtt ctg gag ctc ctg gag 1056
 Pro Gly Leu Ser Glu Ala Val Leu Gln Gln Val Leu Glu Leu Leu Glu
 340 345 350

gac cag agt gac att gtc agc aca atg gag cac tac tac aca gcg ttc 1104
 Asp Gln Ser Asp Ile Val Ser Thr Met Glu His Tyr Tyr Thr Ala Phe
 355 360 365

tga 1107
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<210> 294
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 294

Met Gln Pro Gly Ser Ser Arg Cys Glu Glu Glu Thr Pro Ser Leu Leu
 1 5 10 15
 Trp Gly Leu Asp Pro Val Phe Leu Ala Phe Ala Lys Leu Tyr Ile Arg
 20 25 30
 Asp Ile Leu Asp Met Lys Glu Ser Arg Gln Val Pro Gly Val Phe Leu
 35 40 45
 Tyr Asn Gly His Pro Ile Lys Gln Val Asp Val Leu Gly Thr Val Ile
 50 55 60
 Gly Val Arg Glu Arg Asp Ala Phe Tyr Ser Tyr Gly Val Asp Asp Ser
 65 70 75 80
 Thr Gly Val Ile Asn Cys Ile Cys Trp Lys Lys Leu Asn Thr Glu Ser
 85 90 95
 Val Ser Ala Ala Pro Ser Ala Ala Arg Glu Leu Ser Leu Thr Ser Gln
 100 105 110
 Leu Lys Lys Leu Gln Glu Thr Ile Glu Gln Lys Thr Lys Ile Glu Ile
 115 120 125
 Gly Asp Thr Ile Arg Val Arg Gly Ser Ile Arg Thr Tyr Arg Glu Glu
 130 135 140
 Arg Glu Ile His Ala Thr Ala Tyr Tyr Lys Val Asp Asp Pro Val Trp
 145 150 155 160
 Asn Ile Gln Ile Ala Arg Met Leu Glu Leu Pro Thr Ile Tyr Arg Lys

436

cat cgc cgg agc cat cag cat atg tct cct ctt gct gcc caa gaa atg 144
 His Arg Arg Ser His Gln His Met Ser Pro Leu Ala Ala Gln Glu Met
 35 40 45

tca gtg cgt atg tcc aac ctg gag aat gac aga gat gaa agg gac gac 192
 Ser Val Arg Met Ser Asn Leu Glu Asn Asp Arg Asp Glu Arg Asp Asp
 50 55 60

gac agc cac gaa gac aga ggc atc atc agc aac act cgg ttt ata gct 240
 Asp Ser His Glu Asp Arg Gly Ile Ile Ser Asn Thr Arg Phe Ile Ala
 65 70 75 80

gcg gtc atc gaa cga cat gca cac agt cca gaa aga agg cgc cgc tac 288
 Ala Val Ile Glu Arg His Ala His Ser Pro Glu Arg Arg Arg Arg Tyr
 85 90 95

tgg ggt cga tca gga aca gaa agt gat cat ggt tac agc acc atg agc 336
 Trp Gly Arg Ser Gly Thr Glu Ser Asp His Gly Tyr Ser Thr Met Ser
 100 105 110

cca cag gag gac agt gaa aat cct cca tgc aac aat gac ccc ttg tca 384
 Pro Gln Glu Asp Ser Glu Asn Pro Pro Cys Asn Asn Asp Pro Leu Ser
 115 120 125

gcc ggg gtc gat gtg gga aac cat gat gag gac tta gac ctg gat acc 432
 Ala Gly Val Asp Val Gly Asn His Asp Glu Asp Leu Asp Leu Asp Thr
 130 135 140

ccc cct cag act gct gcc cta cta agt cac aag ttc cac cac tac cgg 480
 Pro Pro Gln Thr Ala Ala Leu Leu Ser His Lys Phe His His Tyr Arg
 145 150 155 160

tca cac cac cct aca ctt cat cat agc cac cac tta cag gcg gcc gtc 528
 Ser His His Pro Thr Leu His His Ser His His Leu Gln Ala Ala Val
 165 170 175

acg gta cac act gtc gat gca gaa tgc taa 558
 Thr Val His Thr Val Asp Ala Glu Cys *
 180 185

<210> 296

<211> 185

<212> PRT

437

<213> Homo sapiens

<400> 296

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Met Ile Lys Ser Ala Pro Val Gly Pro Val Ala Gly Gly Ile Met Gly
 1           5           10           15
Cys Ile Met Val Leu Val Leu Ala Val Tyr Ala Tyr Arg His Gln Ile
      20           25           30
His Arg Arg Ser His Gln His Met Ser Pro Leu Ala Ala Gln Glu Met
      35           40           45
Ser Val Arg Met Ser Asn Leu Glu Asn Asp Arg Asp Glu Arg Asp Asp
      50           55           60
Asp Ser His Glu Asp Arg Gly Ile Ile Ser Asn Thr Arg Phe Ile Ala
      65           70           75           80
Ala Val Ile Glu Arg His Ala His Ser Pro Glu Arg Arg Arg Arg Tyr
      85           90           95
Trp Gly Arg Ser Gly Thr Glu Ser Asp His Gly Tyr Ser Thr Met Ser
      100          105          110
Pro Gln Glu Asp Ser Glu Asn Pro Pro Cys Asn Asn Asp Pro Leu Ser
      115          120          125
Ala Gly Val Asp Val Gly Asn His Asp Glu Asp Leu Asp Leu Asp Thr
      130          135          140
Pro Pro Gln Thr Ala Ala Leu Leu Ser His Lys Phe His His Tyr Arg
      145          150          155          160
Ser His His Pro Thr Leu His His Ser His His Leu Gln Ala Ala Val
      165          170          175
Thr Val His Thr Val Asp Ala Glu Cys
      180          185

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<210> 297

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(501)

<400> 297

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atg gat gat att gtg gtt gta gct cag ggc tcc cag gcc tca cgg aac      48
Met Asp Asp Ile Val Val Val Ala Gln Gly Ser Gln Ala Ser Arg Asn
 1           5           10           15

gtc agc aac gat ccc gat gtc atc aag ttg caa gag att cca acc ttc      96
Val Ser Asn Asp Pro Asp Val Ile Lys Leu Gln Glu Ile Pro Thr Phe

```

438

20	25	30	
cag ccc ctt ttg aaa ggg cta ttg agt ggc cag act tcc cca aca aat			144
Gln Pro Leu Leu Lys Gly Leu Leu Ser Gly Gln Thr Ser Pro Thr Asn			
35	40	45	
gcc aaa ttg gag aaa ctg gac tct cag cag gtg ttg cag ctc tgc ctc			192
Ala Lys Leu Glu Lys Leu Asp Ser Gln Gln Val Leu Gln Leu Cys Leu			
50	55	60	
cga tat caa gat cac ctg cat cag tgt gca gag gcc gtt gct ttt gac			240
Arg Tyr Gln Asp His Leu His Gln Cys Ala Glu Ala Val Ala Phe Asp			
65	70	75	80
cag aat gct ttg gtt aaa cga atc aaa gag atg gat ctg tct gta gaa			288
Gln Asn Ala Leu Val Lys Arg Ile Lys Glu Met Asp Leu Ser Val Glu			
85	90	95	
act ctg ttc agc ttc atg cag gag cgc cag aaa aga tac gcc aag tat			336
Thr Leu Phe Ser Phe Met Gln Glu Arg Gln Lys Arg Tyr Ala Lys Tyr			
100	105	110	
gcc gag cag atc cag aaa gtg aac gag atg tcc gcc atc ctc cgc cgc			384
Ala Glu Gln Ile Gln Lys Val Asn Glu Met Ser Ala Ile Leu Arg Arg			
115	120	125	
ata cag atg ggc atc gac cag act gtg ccc ctg ctg gac agg ctc aac			432
Ile Gln Met Gly Ile Asp Gln Thr Val Pro Leu Leu Asp Arg Leu Asn			
130	135	140	
agc atg ctg ccc gag ggc gag cgg ctg gag ccc ttc agc atg aag ccc			480
Ser Met Leu Pro Glu Gly Glu Arg Leu Glu Pro Phe Ser Met Lys Pro			
145	150	155	160
gac cgc gag ctc agg ctg tag			501
Asp Arg Glu Leu Arg Leu *			
165			

<210> 298

<211> 166

<212> PRT

<213> Homo sapiens

439

<400> 298

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Met Asp Asp Ile Val Val Val Ala Gln Gly Ser Gln Ala Ser Arg Asn
 1           5           10           15
Val Ser Asn Asp Pro Asp Val Ile Lys Leu Gln Glu Ile Pro Thr Phe
          20           25           30
Gln Pro Leu Leu Lys Gly Leu Leu Ser Gly Gln Thr Ser Pro Thr Asn
          35           40           45
Ala Lys Leu Glu Lys Leu Asp Ser Gln Gln Val Leu Gln Leu Cys Leu
          50           55           60
Arg Tyr Gln Asp His Leu His Gln Cys Ala Glu Ala Val Ala Phe Asp
65           70           75           80
Gln Asn Ala Leu Val Lys Arg Ile Lys Glu Met Asp Leu Ser Val Glu
          85           90           95
Thr Leu Phe Ser Phe Met Gln Glu Arg Gln Lys Arg Tyr Ala Lys Tyr
          100          105          110
Ala Glu Gln Ile Gln Lys Val Asn Glu Met Ser Ala Ile Leu Arg Arg
          115          120          125
Ile Gln Met Gly Ile Asp Gln Thr Val Pro Leu Leu Asp Arg Leu Asn
          130          135          140
Ser Met Leu Pro Glu Gly Glu Arg Leu Glu Pro Phe Ser Met Lys Pro
145          150          155          160
Asp Arg Glu Leu Arg Leu
          165

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<210> 299

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(828)

<221> misc_feature

<222> (1)...(828)

<223> n = A,T,C or G

<400> 299

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atg agt gaa gag cct gac gct cta tcg gta gtt aac cag tta cgg gat      48
Met Ser Glu Glu Pro Asp Ala Leu Ser Val Val Asn Gln Leu Arg Asp
 1           5           10           15

cta gca gca gat ccg tta aac aga aga gcc atc gtc cag gat cag gga      96
Leu Ala Ala Asp Pro Leu Asn Arg Arg Ala Ile Val Gln Asp Gln Gly

```

440

20	25	30	
tgt ctg cct ggc ctt att tta ttt atg gac cat ccc aac cct cca gtc			144
Cys Leu Pro Gly Leu Ile Leu Phe Met Asp His Pro Asn Pro Pro Val			
35	40	45	
gtc cac tcc gct ttg ctt gct ctt cga tac ttg gca gaa tgc cgt gca			192
Val His Ser Ala Leu Leu Ala Leu Arg Tyr Leu Ala Glu Cys Arg Ala			
50	55	60	
aac aga gaa aag atg aaa gga gaa ctg ggt atg atg ttg agc tta caa			240
Asn Arg Glu Lys Met Lys Gly Glu Leu Gly Met Met Leu Ser Leu Gln			
65	70	75	80
aat gtt ata cag aaa act aca act cca gga gaa aca aaa ctt ctg gcc			288
Asn Val Ile Gln Lys Thr Thr Thr Pro Gly Glu Thr Lys Leu Leu Ala			
85	90	95	
tct gaa atc tat gac att ctt cag tcc tcc aat atg gca gat ggt gat			336
Ser Glu Ile Tyr Asp Ile Leu Gln Ser Ser Asn Met Ala Asp Gly Asp			
100	105	110	
agt ttt aat gag atg aat tca cgt cga agg aaa gct can ttt ttt ctg			384
Ser Phe Asn Glu Met Asn Ser Arg Arg Arg Lys Ala Xaa Phe Phe Leu			
115	120	125	
gga act aca aac aaa cgt gcc aaa aca gtg gtt ttg cat ata gat ggc			432
Gly Thr Thr Asn Lys Arg Ala Lys Thr Val Val Leu His Ile Asp Gly			
130	135	140	
ctt gat gat acg tct cgg aga aat cta tgt gaa gag gct ttg tta aaa			480
Leu Asp Asp Thr Ser Arg Arg Asn Leu Cys Glu Glu Ala Leu Leu Lys			
145	150	155	160
att aaa ggt gtt att agc ttt act ttt caa atg gct gtt caa agg tgt			528
Ile Lys Gly Val Ile Ser Phe Thr Phe Gln Met Ala Val Gln Arg Cys			
165	170	175	
gtg gtg cga atc cgt tca gat ttg aaa gct gag gct ttg gca tca gca			576
Val Val Arg Ile Arg Ser Asp Leu Lys Ala Glu Ala Leu Ala Ser Ala			
180	185	190	
ata gca tca acc aag gtt atg aaa gct cag caa gtt gtg aaa agt gaa			624
Ile Ala Ser Thr Lys Val Met Lys Ala Gln Gln Val Val Lys Ser Glu			

441

195	200	205	
agt gga gaa gag atg ttg gtc cca ttc caa gat act cct gtg gaa gtt			672
Ser Gly Glu Glu Met Leu Val Pro Phe Gln Asp Thr Pro Val Glu Val			
210	215	220	
gaa cag aac aca gag cta cct gac tac ctg cct gag gat gag agt ccc			720
Glu Gln Asn Thr Glu Leu Pro Asp Tyr Leu Pro Glu Asp Glu Ser Pro			
225	230	235	240
aca aag gaa cag gac aaa gcg gtg tcc cgg gtc ggc tca cac cca gaa			768
Thr Lys Glu Gln Asp Lys Ala Val Ser Arg Val Gly Ser His Pro Glu			
	245	250	255
ggc gga gct agc tgg ctt agc aca gct gca aac ttt tta tcc aga tca			816
Gly Gly Ala Ser Trp Leu Ser Thr Ala Ala Asn Phe Leu Ser Arg Ser			
	260	265	270
ttt tat tgg tga			828
Phe Tyr Trp *			
275			

<210> 300

<211> 275

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(275)

<223> Xaa = Any Amino Acid

<400> 300

Met Ser Glu Glu Pro Asp Ala Leu Ser Val Val Asn Gln Leu Arg Asp			
1	5	10	15
Leu Ala Ala Asp Pro Leu Asn Arg Arg Ala Ile Val Gln Asp Gln Gly			
	20	25	30
Cys Leu Pro Gly Leu Ile Leu Phe Met Asp His Pro Asn Pro Pro Val			
	35	40	45
Val His Ser Ala Leu Leu Ala Leu Arg Tyr Leu Ala Glu Cys Arg Ala			
	50	55	60
Asn Arg Glu Lys Met Lys Gly Glu Leu Gly Met Met Leu Ser Leu Gln			
65	70	75	80

442

Asn Val Ile Gln Lys Thr Thr Thr Pro Gly Glu Thr Lys Leu Leu Ala
 85 90 95
 Ser Glu Ile Tyr Asp Ile Leu Gln Ser Ser Asn Met Ala Asp Gly Asp
 100 105 110
 Ser Phe Asn Glu Met Asn Ser Arg Arg Arg Lys Ala Xaa Phe Phe Leu
 115 120 125
 Gly Thr Thr Asn Lys Arg Ala Lys Thr Val Val Leu His Ile Asp Gly
 130 135 140
 Leu Asp Asp Thr Ser Arg Arg Asn Leu Cys Glu Glu Ala Leu Leu Lys
 145 150 155 160
 Ile Lys Gly Val Ile Ser Phe Thr Phe Gln Met Ala Val Gln Arg Cys
 165 170 175
 Val Val Arg Ile Arg Ser Asp Leu Lys Ala Glu Ala Leu Ala Ser Ala
 180 185 190
 Ile Ala Ser Thr Lys Val Met Lys Ala Gln Gln Val Val Lys Ser Glu
 195 200 205
 Ser Gly Glu Glu Met Leu Val Pro Phe Gln Asp Thr Pro Val Glu Val
 210 215 220
 Glu Gln Asn Thr Glu Leu Pro Asp Tyr Leu Pro Glu Asp Glu Ser Pro
 225 230 235 240
 Thr Lys Glu Gln Asp Lys Ala Val Ser Arg Val Gly Ser His Pro Glu
 245 250 255
 Gly Gly Ala Ser Trp Leu Ser Thr Ala Ala Asn Phe Leu Ser Arg Ser
 260 265 270
 Phe Tyr Trp
 275

<210> 301

<211> 1101

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1101)

<221> misc_feature

<222> (1)...(1101)

<223> n = A,T,C or G

<400> 301

atg gcc tca gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt
 Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
 1 5 10 15

48

443

gcc ctg tta caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga	96
Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly	
20 25 30	
aaa ggt aaa ggt cga aat act gga aag tct caa act tta gga agc aag	144
Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys	
35 40 45	
tca act aca aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa	192
Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu	
50 55 60	
cag caa cag agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa	240
Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys	
65 70 75 80	
att ccc cag aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt	288
Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu	
85 90 95	
cca ttg tca aac cca gta cag aag gat tca cga gaa gaa aat tgg caa	336
Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln	
100 105 110	
gag tgg aga caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca	384
Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala	
115 120 125	
gat ctt gag aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac	432
Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His	
130 135 140	
aaa aag gag tat gaa gat gct gaa aat act tca act cag tcc aaa gtt	480
Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val	
145 150 155 160	
atg aat ann aaa gat aaa aga aag aat cat cag gga aaa gac aga cct	528
Met Asn Xaa Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro	
165 170 175	
ctc aca gta tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa	576
Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys	
180 185 190	

444

aag act gag gaa ttg agt tct tct cag act tta tca cat gat gga gga Lys Thr Glu Glu Leu Ser Ser Ser Gln Thr Leu Ser His Asp Gly Gly 195 200 205	624
ttc ttc aat aga ctg gaa gat gat gtt cat aaa att ctt att aga gaa Phe Phe Asn Arg Leu Glu Asp Asp Val His Lys Ile Leu Ile Arg Glu 210 215 220	672
aaa cga aga gaa cag ctt aca gaa tat aat gga aca gat aat tgt aca Lys Arg Arg Glu Gln Leu Thr Glu Tyr Asn Gly Thr Asp Asn Cys Thr 225 230 235 240	720
gct cat gaa cac aac cag gaa gtg gtt ctg aaa gat gga aga att gaa Ala His Glu His Asn Gln Glu Val Val Leu Lys Asp Gly Arg Ile Glu 245 250 255	768
aga cta aag tta gag ctt gaa agg aaa gat gct gaa atc cag aag ctg Arg Leu Lys Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu 260 265 270	816
aaa aat gta atc act caa tgg gag gca aag tat aag gaa gta aag gca Lys Asn Val Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala 275 280 285	864
aga aat gca caa tta ttg aaa atg ctt cag gaa ggt gaa atg aaa gat Arg Asn Ala Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp 290 295 300	912
aag gca gaa ata ctt ctg caa gtt gat gaa tca caa agt atc aag aat Lys Ala Glu Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn 305 310 315 320	960
gag ctc act att cag gtg act tca ctt cat gct gca tta gaa caa gaa Glu Leu Thr Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu 325 330 335	1008
aga tct aaa gtg aaa gta tta caa gca gag tta gcc aaa tac cag ggt Arg Ser Lys Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly 340 345 350	1056
ggc aga aaa ggg aaa aga aac tct gaa tcc gac cag tgt agg tga Gly Arg Lys Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg * 355 360 365	1101

445

<210> 302
 <211> 366
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(366)
 <223> Xaa = Any Amino Acid

<400> 302
 Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
 1 5 10 15
 Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly
 20 25 30
 Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys
 35 40 45
 Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu
 50 55 60
 Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys
 65 70 75 80
 Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu
 85 90 95
 Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln
 100 105 110
 Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala
 115 120 125
 Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His
 130 135 140
 Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val
 145 150 155 160
 Met Asn Xaa Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro
 165 170 175
 Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys
 180 185 190
 Lys Thr Glu Glu Leu Ser Ser Ser Gln Thr Leu Ser His Asp Gly Gly
 195 200 205
 Phe Phe Asn Arg Leu Glu Asp Asp Val His Lys Ile Leu Ile Arg Glu
 210 215 220
 Lys Arg Arg Glu Gln Leu Thr Glu Tyr Asn Gly Thr Asp Asn Cys Thr
 225 230 235 240
 Ala His Glu His Asn Gln Glu Val Val Leu Lys Asp Gly Arg Ile Glu

446

245 250 255
 Arg Leu Lys Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu
 260 265 270
 Lys Asn Val Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala
 275 280 285
 Arg Asn Ala Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp
 290 295 300
 Lys Ala Glu Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn
 305 310 315 320
 Glu Leu Thr Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu
 325 330 335
 Arg Ser Lys Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly
 340 345 350
 Gly Arg Lys Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg
 355 360 365

<210> 303

<211> 807

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(807)

<400> 303

atg cta agg aag ctg tgg caa gaa aat aaa gca acc aac aca gac cat 48
 Met Leu Arg Lys Leu Trp Gln Glu Asn Lys Ala Thr Asn Thr Asp His
 1 5 10 15

tta acc acg gta ctc tac ctc cag ctt gct att tgt tca agt ttg cag 96
 Leu Thr Thr Val Leu Tyr Leu Gln Leu Ala Ile Cys Ser Ser Leu Gln
 20 25 30

aac ttg gag aaa aca att ttc tgc ctg cag aaa ctg att tct ttg cat 144
 Asn Leu Glu Lys Thr Ile Phe Cys Leu Gln Lys Leu Ile Ser Leu His
 35 40 45

cct ttt aat cct tgg aac tgg ggc aaa ttg gca gag gct tac ctg aat 192
 Pro Phe Asn Pro Trp Asn Trp Gly Lys Leu Ala Glu Ala Tyr Leu Asn
 50 55 60

ctg ggg cca gct ctt tca gca gca ctt gcg tca tct cag aaa cag cac 240
 Leu Gly Pro Ala Leu Ser Ala Ala Leu Ala Ser Ser Gln Lys Gln His

447

65	70	75	80	
agt ttc acc tca agt gac aaa act atc aaa tcc ttc ttt cca cac tca				288
Ser Phe Thr Ser Ser Asp Lys Thr Ile Lys Ser Phe Phe Pro His Ser				
	85	90	95	
gga aaa gac tgt ctt ttg tgt ttt cct gaa acc ttg cct gag agc tct				336
Gly Lys Asp Cys Leu Leu Cys Phe Pro Glu Thr Leu Pro Glu Ser Ser				
	100	105	110	
tta ttt tct gtg gaa gcg aat agc agt aat agc cag aaa aat gag aaa				384
Leu Phe Ser Val Glu Ala Asn Ser Ser Asn Ser Gln Lys Asn Glu Lys				
	115	120	125	
gct ctg aca aat atc caa aac tgt atg gca gaa aag aga gaa aca gtg				432
Ala Leu Thr Asn Ile Gln Asn Cys Met Ala Glu Lys Arg Glu Thr Val				
	130	135	140	
ttg ata gag act cag ctg aaa gca tgt gcc tct ttt ata cga acc agg				480
Leu Ile Glu Thr Gln Leu Lys Ala Cys Ala Ser Phe Ile Arg Thr Arg				
	145	150	155	160
ctt ctg ctt cag ttt acc caa cct cag caa aca tcg ttt gct ttg gag				528
Leu Leu Leu Gln Phe Thr Gln Pro Gln Gln Thr Ser Phe Ala Leu Glu				
	165	170	175	
agg aac tta agg act cag cag gaa att gaa gat aaa atg aaa ggg ttc				576
Arg Asn Leu Arg Thr Gln Gln Glu Ile Glu Asp Lys Met Lys Gly Phe				
	180	185	190	
agc ttc aaa gaa gac act ttg ctg ttg ata gct gag gtt atg gga gaa				624
Ser Phe Lys Glu Asp Thr Leu Leu Leu Ile Ala Glu Val Met Gly Glu				
	195	200	205	
gat atc cca gaa aaa ata aaa gat gaa gtt cac cca gag gtg aag tgt				672
Asp Ile Pro Glu Lys Ile Lys Asp Glu Val His Pro Glu Val Lys Cys				
	210	215	220	
gtt ggc tcc gta gcc ctg act gcc ttg gtg act gta tcc tca gaa gaa				720
Val Gly Ser Val Ala Leu Thr Ala Leu Val Thr Val Ser Ser Glu Glu				
	225	230	235	240
ttt gaa gac aag tgg ttc aga aag atc aaa gac cat ttc tgt cca ttt				768
Phe Glu Asp Lys Trp Phe Arg Lys Ile Lys Asp His Phe Cys Pro Phe				

448

245

250

255

gaa aat cag ttc cat aca gag ata caa atc ttg gct tag
 Glu Asn Gln Phe His Thr Glu Ile Gln Ile Leu Ala *
 260 265

807

<210> 304

<211> 268

<212> PRT

<213> Homo sapiens

<400> 304

Met Leu Arg Lys Leu Trp Gln Glu Asn Lys Ala Thr Asn Thr Asp His
 1 5 10 15
 Leu Thr Thr Val Leu Tyr Leu Gln Leu Ala Ile Cys Ser Ser Leu Gln
 20 25 30
 Asn Leu Glu Lys Thr Ile Phe Cys Leu Gln Lys Leu Ile Ser Leu His
 35 40 45
 Pro Phe Asn Pro Trp Asn Trp Gly Lys Leu Ala Glu Ala Tyr Leu Asn
 50 55 60
 Leu Gly Pro Ala Leu Ser Ala Ala Leu Ala Ser Ser Gln Lys Gln His
 65 70 75 80
 Ser Phe Thr Ser Ser Asp Lys Thr Ile Lys Ser Phe Phe Pro His Ser
 85 90 95
 Gly Lys Asp Cys Leu Leu Cys Phe Pro Glu Thr Leu Pro Glu Ser Ser
 100 105 110
 Leu Phe Ser Val Glu Ala Asn Ser Ser Asn Ser Gln Lys Asn Glu Lys
 115 120 125
 Ala Leu Thr Asn Ile Gln Asn Cys Met Ala Glu Lys Arg Glu Thr Val
 130 135 140
 Leu Ile Glu Thr Gln Leu Lys Ala Cys Ala Ser Phe Ile Arg Thr Arg
 145 150 155 160
 Leu Leu Leu Gln Phe Thr Gln Pro Gln Gln Thr Ser Phe Ala Leu Glu
 165 170 175
 Arg Asn Leu Arg Thr Gln Gln Glu Ile Glu Asp Lys Met Lys Gly Phe
 180 185 190
 Ser Phe Lys Glu Asp Thr Leu Leu Leu Ile Ala Glu Val Met Gly Glu
 195 200 205
 Asp Ile Pro Glu Lys Ile Lys Asp Glu Val His Pro Glu Val Lys Cys
 210 215 220
 Val Gly Ser Val Ala Leu Thr Ala Leu Val Thr Val Ser Ser Glu Glu
 225 230 235 240
 Phe Glu Asp Lys Trp Phe Arg Lys Ile Lys Asp His Phe Cys Pro Phe

449

	245	250	255
Glu Asn Gln Phe His Thr Glu Ile Gln Ile Leu Ala			
260	265		
 <210> 305			
<211> 810			
<212> DNA			
<213> Homo sapiens			
 <220>			
<221> CDS			
<222> (1)...(810)			
 <400> 305			
atg gcc ata ttt ctg cag cat gcc gca gga ctc tta cat gca atg tgt			48
Met Ala Ile Phe Leu Gln His Ala Ala Gly Leu Leu His Ala Met Cys			
1	5	10	15
 aca ctg tgc ttt gct gtc act gga agg tca tac agc ata ttt gac aat			
Thr Leu Cys Phe Ala Val Thr Gly Arg Ser Tyr Ser Ile Phe Asp Asn			96
20	25	30	
 aat cgc cag gat ccc aca ggg ctg aca gct gct ctt cag gca acc gac			
Asn Arg Gln Asp Pro Thr Gly Leu Thr Ala Ala Leu Gln Ala Thr Asp			144
35	40	45	
 ctg gct gga gtt ctt cat atg ctc tac tgt gtc ctc ttc cat ggc acc			
Leu Ala Gly Val Leu His Met Leu Tyr Cys Val Leu Phe His Gly Thr			192
50	55	60	
 atc ttg gac ccc agc act gcc agt ccc aag gag aat tac act caa aat			
Ile Leu Asp Pro Ser Thr Ala Ser Pro Lys Glu Asn Tyr Thr Gln Asn			240
65	70	75	80
 acc atc caa gtg gcc att cag agt tta cgt ttc ttc aac agc ttt gca			
Thr Ile Gln Val Ala Ile Gln Ser Leu Arg Phe Phe Asn Ser Phe Ala			288
85	90	95	
 gct ctt cat ctg cct gct ttt cag tct att gta ggg gca gag ggc ttg			
Ala Leu His Leu Pro Ala Phe Gln Ser Ile Val Gly Ala Glu Gly Leu			336
100	105	110	
 tcc ctt gca ttc cgg cac atg gcc agc tcc ctg ctg ggc cac tgc agc			
Ser Leu Ala Phe Arg His Met Ala Ser Ser Leu Leu Gly His Cys Ser			384

450

115	120	125	
caa gtc tcc tgt gaa agc ctc ctt cat gag gtc atc gtc tgt gtg ggc			432
Gln Val Ser Cys Glu Ser Leu Leu His Glu Val Ile Val Cys Val Gly			
130	135	140	
tac ttc act gtc aac cac cca gat aac cag gtg atc gtg cag tcc ggc			480
Tyr Phe Thr Val Asn His Pro Asp Asn Gln Val Ile Val Gln Ser Gly			
145	150	155	160
cgc cac ccc aca gtg ctg cag aag ctc tgc cag ttg ccc ttc cag tat			528
Arg His Pro Thr Val Leu Gln Lys Leu Cys Gln Leu Pro Phe Gln Tyr			
	165	170	175
ttc agt gac cca cgg ctg atc aaa gta ctg ttc cct tca ctt atc gct			576
Phe Ser Asp Pro Arg Leu Ile Lys Val Leu Phe Pro Ser Leu Ile Ala			
	180	185	190
gct tgt tac aac aac cat cag aac aag atc att ctg gag caa gag atg			624
Ala Cys Tyr Asn Asn His Gln Asn Lys Ile Ile Leu Glu Gln Glu Met			
	195	200	205
agc tgt gtt tta ctg gcc act ttc att cag gat ttg gca cag act cca			672
Ser Cys Val Leu Leu Ala Thr Phe Ile Gln Asp Leu Ala Gln Thr Pro			
	210	215	220
ggt caa gcg gaa aac cag cct tac caa ccc aaa ggg aaa tgc ctt ggt			720
Gly Gln Ala Glu Asn Gln Pro Tyr Gln Pro Lys Gly Lys Cys Leu Gly			
	225	230	235
tcc caa gac tat ctt gag ctg gct aac aga ttt cct cag cag gcc tgg			768
Ser Gln Asp Tyr Leu Glu Leu Ala Asn Arg Phe Pro Gln Gln Ala Trp			
	245	250	255
gaa gaa gct cga cag ttt ttc ttg aaa aaa gag aaa aaa taa			810
Glu Glu Ala Arg Gln Phe Phe Leu Lys Lys Glu Lys Lys *			
	260	265	

<210> 306

<211> 269

<212> PRT

<213> Homo sapiens

451

<400> 306

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Met Ala Ile Phe Leu Gln His Ala Ala Gly Leu Leu His Ala Met Cys
 1           5           10           15
Thr Leu Cys Phe Ala Val Thr Gly Arg Ser Tyr Ser Ile Phe Asp Asn
          20           25           30
Asn Arg Gln Asp Pro Thr Gly Leu Thr Ala Ala Leu Gln Ala Thr Asp
          35           40           45
Leu Ala Gly Val Leu His Met Leu Tyr Cys Val Leu Phe His Gly Thr
          50           55           60
Ile Leu Asp Pro Ser Thr Ala Ser Pro Lys Glu Asn Tyr Thr Gln Asn
65           70           75           80
Thr Ile Gln Val Ala Ile Gln Ser Leu Arg Phe Phe Asn Ser Phe Ala
          85           90           95
Ala Leu His Leu Pro Ala Phe Gln Ser Ile Val Gly Ala Glu Gly Leu
          100          105          110
Ser Leu Ala Phe Arg His Met Ala Ser Ser Leu Leu Gly His Cys Ser
          115          120          125
Gln Val Ser Cys Glu Ser Leu Leu His Glu Val Ile Val Cys Val Gly
          130          135          140
Tyr Phe Thr Val Asn His Pro Asp Asn Gln Val Ile Val Gln Ser Gly
145          150          155          160
Arg His Pro Thr Val Leu Gln Lys Leu Cys Gln Leu Pro Phe Gln Tyr
          165          170          175
Phe Ser Asp Pro Arg Leu Ile Lys Val Leu Phe Pro Ser Leu Ile Ala
          180          185          190
Ala Cys Tyr Asn Asn His Gln Asn Lys Ile Ile Leu Glu Gln Glu Met
          195          200          205
Ser Cys Val Leu Leu Ala Thr Phe Ile Gln Asp Leu Ala Gln Thr Pro
          210          215          220
Gly Gln Ala Glu Asn Gln Pro Tyr Gln Pro Lys Gly Lys Cys Leu Gly
225          230          235          240
Ser Gln Asp Tyr Leu Glu Leu Ala Asn Arg Phe Pro Gln Gln Ala Trp
          245          250          255
Glu Glu Ala Arg Gln Phe Phe Leu Lys Lys Glu Lys Lys
          260          265

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<210> 307

<211> 831

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(831)

452

<400> 307

atg cag aac aag gtg act cag cta gtc ctg tct gcc ttg cag tcc ctg	48
Met Gln Asn Lys Val Thr Gln Leu Val Leu Ser Ala Leu Gln Ser Leu	
1 5 10 15	
act gac acc ttg ctt ttt ccc ttt tat tct ggg ccg agt ggt acc ctg	96
Thr Asp Thr Leu Leu Phe Pro Phe Tyr Ser Gly Pro Ser Gly Thr Leu	
20 25 30	
aaa aca gcc ctg ctg gac tac atc aaa cgc tgc cgt cct gga gac agt	144
Lys Thr Ala Leu Leu Asp Tyr Ile Lys Arg Cys Arg Pro Gly Asp Ser	
35 40 45	
gaa aag cac aat atg att gcc ctg tgc ttc agc atg tgc cgg gag att	192
Glu Lys His Asn Met Ile Ala Leu Cys Phe Ser Met Cys Arg Glu Ile	
50 55 60	
ggc gag aac cac gag gca gct gcc cgc atc caa ctg aaa ttg att gag	240
Gly Glu Asn His Glu Ala Ala Ala Arg Ile Gln Leu Lys Leu Ile Glu	
65 70 75 80	
tct cag ccc tgg gag gac agc ctc aag gat ggg cac cag ctg aaa caa	288
Ser Gln Pro Trp Glu Asp Ser Leu Lys Asp Gly His Gln Leu Lys Gln	
85 90 95	
ctg ctg ctg aag gcc ctg act ctg atg ttg gat gca gca gag agt tat	336
Leu Leu Leu Lys Ala Leu Thr Leu Met Leu Asp Ala Ala Glu Ser Tyr	
100 105 110	
gcc aag gac tcc tgt gtg cga cag gcc cag cac tgt cag cgg ctc acc	384
Ala Lys Asp Ser Cys Val Arg Gln Ala Gln His Cys Gln Arg Leu Thr	
115 120 125	
aag ttg ata act ctg cag att cac ttt ctg aac act ggc cag aac aca	432
Lys Leu Ile Thr Leu Gln Ile His Phe Leu Asn Thr Gly Gln Asn Thr	
130 135 140	
atg ctc atc aac ttg ggc cgc cac aag ctg atg gac tgt att ctg gcc	480
Met Leu Ile Asn Leu Gly Arg His Lys Leu Met Asp Cys Ile Leu Ala	
145 150 155 160	
cta cct cgg ttc tac cag gct tct att gtg gct gag gcc tac gat ttt	528
Leu Pro Arg Phe Tyr Gln Ala Ser Ile Val Ala Glu Ala Tyr Asp Phe	

453

165	170	175	
ggt cca gat tgg gct gaa att tta tac cag caa gtg att ctt aaa gga			576
Val Pro Asp Trp Ala Glu Ile Leu Tyr Gln Gln Val Ile Leu Lys Gly			
180	185	190	
gac ttt aat tac ttg gaa gaa ttt aag cag caa agg tta tta aag tcc			624
Asp Phe Asn Tyr Leu Glu Glu Phe Lys Gln Gln Arg Leu Leu Lys Ser			
195	200	205	
agt ata ttt gaa gag att tcc aaa aaa tat aaa caa cat cag cct act			672
Ser Ile Phe Glu Glu Ile Ser Lys Lys Tyr Lys Gln His Gln Pro Thr			
210	215	220	
gac atg gtc atg gaa aac ctg aag aaa tta ctc aca tat tgt gaa gat			720
Asp Met Val Met Glu Asn Leu Lys Lys Leu Leu Thr Tyr Cys Glu Asp			
225	230	235	240
ggt tac ctg tat tac aag ttg gca tac gaa cac aag ttt tat gaa att			768
Val Tyr Leu Tyr Tyr Lys Leu Ala Tyr Glu His Lys Phe Tyr Glu Ile			
245	250	255	
gta aat gtg ctt ctg aag gac cct cag aca ggt tgc tgt cta aag gac			816
Val Asn Val Leu Leu Lys Asp Pro Gln Thr Gly Cys Cys Leu Lys Asp			
260	265	270	
atg cta gca ggt tag			831
Met Leu Ala Gly *			
275			

<210> 308

<211> 276

<212> PRT

<213> Homo sapiens

<400> 308

Met	Gln	Asn	Lys	Val	Thr	Gln	Leu	Val	Leu	Ser	Ala	Leu	Gln	Ser	Leu
1				5					10					15	
Thr	Asp	Thr	Leu	Leu	Phe	Pro	Phe	Tyr	Ser	Gly	Pro	Ser	Gly	Thr	Leu
			20					25					30		
Lys	Thr	Ala	Leu	Leu	Asp	Tyr	Ile	Lys	Arg	Cys	Arg	Pro	Gly	Asp	Ser
		35					40					45			
Glu	Lys	His	Asn	Met	Ile	Ala	Leu	Cys	Phe	Ser	Met	Cys	Arg	Glu	Ile

454

50 55 60
 Gly Glu Asn His Glu Ala Ala Ala Arg Ile Gln Leu Lys Leu Ile Glu
 65 70 75 80
 Ser Gln Pro Trp Glu Asp Ser Leu Lys Asp Gly His Gln Leu Lys Gln
 85 90 95
 Leu Leu Leu Lys Ala Leu Thr Leu Met Leu Asp Ala Ala Glu Ser Tyr
 100 105 110
 Ala Lys Asp Ser Cys Val Arg Gln Ala Gln His Cys Gln Arg Leu Thr
 115 120 125
 Lys Leu Ile Thr Leu Gln Ile His Phe Leu Asn Thr Gly Gln Asn Thr
 130 135 140
 Met Leu Ile Asn Leu Gly Arg His Lys Leu Met Asp Cys Ile Leu Ala
 145 150 155 160
 Leu Pro Arg Phe Tyr Gln Ala Ser Ile Val Ala Glu Ala Tyr Asp Phe
 165 170 175
 Val Pro Asp Trp Ala Glu Ile Leu Tyr Gln Gln Val Ile Leu Lys Gly
 180 185 190
 Asp Phe Asn Tyr Leu Glu Glu Phe Lys Gln Gln Arg Leu Leu Lys Ser
 195 200 205
 Ser Ile Phe Glu Glu Ile Ser Lys Lys Tyr Lys Gln His Gln Pro Thr
 210 215 220
 Asp Met Val Met Glu Asn Leu Lys Lys Leu Leu Thr Tyr Cys Glu Asp
 225 230 235 240
 Val Tyr Leu Tyr Tyr Lys Leu Ala Tyr Glu His Lys Phe Tyr Glu Ile
 245 250 255
 Val Asn Val Leu Leu Lys Asp Pro Gln Thr Gly Cys Cys Leu Lys Asp
 260 265 270
 Met Leu Ala Gly
 275

<210> 309

<211> 369

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(369)

<400> 309

atg agg aca att gat gac aga ata gta cat gaa tta aac act acg gtt
 Met Arg Thr Ile Asp Asp Arg Ile Val His Glu Leu Asn Thr Thr Val
 1 5 10 15

48

455

cca aca gct tcc ttt gca ggg aaa att gat gcc agc caa acc tgt aaa 96
 Pro Thr Ala Ser Phe Ala Gly Lys Ile Asp Ala Ser Gln Thr Cys Lys
 20 25 30

caa ctt tat gag tct ttg atg gca gct cat gcc agt aga gac aga gtc 144
 Gln Leu Tyr Glu Ser Leu Met Ala Ala His Ala Ser Arg Asp Arg Val
 35 40 45

ata aaa aac tgt ata gcc cag act tca gca gta gta aaa aac ctc cga 192
 Ile Lys Asn Cys Ile Ala Gln Thr Ser Ala Val Val Lys Asn Leu Arg
 50 55 60

gaa gag aga gaa aag aat ttg gac gat tta acg tta tta aaa caa ctt 240
 Glu Glu Arg Glu Lys Asn Leu Asp Asp Leu Thr Leu Leu Lys Gln Leu
 65 70 75 80

aga aaa gag cag aca aag ttg aaa tgg atg cag tca gaa ctg aat gtt 288
 Arg Lys Glu Gln Thr Lys Leu Lys Trp Met Gln Ser Glu Leu Asn Val
 85 90 95

gaa gaa gtg gta aat gac agg agc tgg aag gtg ttt aat gaa cgc tgc 336
 Glu Glu Val Val Asn Asp Arg Ser Trp Lys Val Phe Asn Glu Arg Cys
 100 105 110

cga att cac ttc aag cct cca aag aat gaa taa 369
 Arg Ile His Phe Lys Pro Pro Lys Asn Glu *
 115 120

<210> 310

<211> 122

<212> PRT

<213> Homo sapiens

<400> 310

Met Arg Thr Ile Asp Asp Arg Ile Val His Glu Leu Asn Thr Thr Val
 1 5 10 15
 Pro Thr Ala Ser Phe Ala Gly Lys Ile Asp Ala Ser Gln Thr Cys Lys
 20 25 30
 Gln Leu Tyr Glu Ser Leu Met Ala Ala His Ala Ser Arg Asp Arg Val
 35 40 45
 Ile Lys Asn Cys Ile Ala Gln Thr Ser Ala Val Val Lys Asn Leu Arg
 50 55 60
 Glu Glu Arg Glu Lys Asn Leu Asp Asp Leu Thr Leu Leu Lys Gln Leu

456

65 70 75 80
 Arg Lys Glu Gln Thr Lys Leu Lys Trp Met Gln Ser Glu Leu Asn Val
 85 90 95
 Glu Glu Val Val Asn Asp Arg Ser Trp Lys Val Phe Asn Glu Arg Cys
 100 105 110
 Arg Ile His Phe Lys Pro Pro Lys Asn Glu
 115 120

<210> 311
 <211> 549
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(549)

<400> 311
 atg gtc ccc gcc gcc ggc gcg ctg ctg tgg gtc ctg ctg ctg aat ctg 48
 Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn Leu
 1 5 10 15
 ggt ccc cgg gcg gcg ggg gcc caa ggc ctg acc cag act ccg acc gaa 96
 Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu
 20 25 30
 atg cag cgg gtc agt tta cgc ttt ggg ggc ccc atg acc cgc agc tac 144
 Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr Arg Ser Tyr
 35 40 45
 cgg agc acc gcc cgg act ggt ctt ccc cgg aag aca agg ata atc cta 192
 Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr Arg Ile Ile Leu
 50 55 60
 gag gac gag aat gat gcc atg gcc gac gcc gac cgc ctg gct gga cca 240
 Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp Arg Leu Ala Gly Pro
 65 70 75 80
 gcg gct gcc gag ctc ttg gcc gcc acg gtg tcc acc ggc ttt agc cgg 288
 Ala Ala Ala Glu Leu Leu Ala Ala Thr Val Ser Thr Gly Phe Ser Arg
 85 90 95
 tcg tcc gcc att aac gag gag gat ggg tct tca gaa gag ggg gtt gtg 336
 Ser Ser Ala Ile Asn Glu Glu Asp Gly Ser Ser Glu Glu Gly Val Val

457

100	105	110	
att aat gct gat gcc ctg ggg ccc gtg gca ctg cca ctg caa gtc ggg			384
Ile Asn Ala Asp Ala Leu Gly Pro Val Ala Leu Pro Leu Gln Val Gly			
115	120	125	
cac cat gag ccg gag ccg gtc tgg gaa gct gca cgg cct ttc cgg gcg			432
His His Glu Pro Glu Pro Val Trp Glu Ala Ala Arg Pro Phe Arg Ala			
130	135	140	
cct tcg agt tgg ggc gct gag cca gct ccg cac gga gca caa gcc ttg			480
Pro Ser Ser Trp Gly Ala Glu Pro Ala Pro His Gly Ala Gln Ala Leu			
145	150	155	160
cac cta tca aca atg tcc ctg caa ccg act tcg gga aga gtg ccc cct			528
His Leu Ser Thr Met Ser Leu Gln Pro Thr Ser Gly Arg Val Pro Pro			
165	170	175	
gga cac aag tct ctg tac tga			549
Gly His Lys Ser Leu Tyr *			
180			

<210> 312

<211> 182

<212> PRT

<213> Homo sapiens

<400> 312

Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn Leu			
1	5	10	15
Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu			
20	25	30	
Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr Arg Ser Tyr			
35	40	45	
Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr Arg Ile Ile Leu			
50	55	60	
Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp Arg Leu Ala Gly Pro			
65	70	75	80
Ala Ala Ala Glu Leu Leu Ala Ala Thr Val Ser Thr Gly Phe Ser Arg			
85	90	95	
Ser Ser Ala Ile Asn Glu Glu Asp Gly Ser Ser Glu Glu Gly Val Val			
100	105	110	
Ile Asn Ala Asp Ala Leu Gly Pro Val Ala Leu Pro Leu Gln Val Gly			

458

115 120 125
 His His Glu Pro Glu Pro Val Trp Glu Ala Ala Arg Pro Phe Arg Ala
 130 135 140
 Pro Ser Ser Trp Gly Ala Glu Pro Ala Pro His Gly Ala Gln Ala Leu
 145 150 155 160
 His Leu Ser Thr Met Ser Leu Gln Pro Thr Ser Gly Arg Val Pro Pro
 165 170 175
 Gly His Lys Ser Leu Tyr
 180

<210> 313

<211> 225

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(225)

<221> misc_feature

<222> (1)...(225)

<223> n = A,T,C or G

<400> 313

atg cac cca gct aag act ggc ttg acc gnn agc ctg gcc ttt ggt ggg 48
 Met His Pro Ala Lys Thr Gly Leu Thr Xaa Ser Leu Ala Phe Gly Gly
 1 5 10 15
 ggg ctt cct ggg gcc tgg gga aag ctg gcc acc ttc aac agc tgg tac 96
 Gly Leu Pro Gly Ala Trp Gly Lys Leu Ala Thr Phe Asn Ser Trp Tyr
 20 25 30
 ctc ttc aac agt gtg gcc ttt caa aat gca gat gcc acc agg aga aca 144
 Leu Phe Asn Ser Val Ala Phe Gln Asn Ala Asp Ala Thr Arg Arg Thr
 35 40 45
 tgc cca cag ctc acc acc tat gga tgc cat ggc tct ggg cag ctt tca 192
 Cys Pro Gln Leu Thr Thr Tyr Gly Cys His Gly Ser Gly Gln Leu Ser
 50 55 60
 aag cag gtt cct gtg gtc tcc tca gct gtt tga 225
 Lys Gln Val Pro Val Ser Ser Ala Val *
 65 70

459

<210> 314
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(74)
 <223> Xaa = Any Amino Acid

<400> 314
 Met His Pro Ala Lys Thr Gly Leu Thr Xaa Ser Leu Ala Phe Gly Gly
 1 5 10 15
 Gly Leu Pro Gly Ala Trp Gly Lys Leu Ala Thr Phe Asn Ser Trp Tyr
 20 25 30
 Leu Phe Asn Ser Val Ala Phe Gln Asn Ala Asp Ala Thr Arg Arg Thr
 35 40 45
 Cys Pro Gln Leu Thr Thr Tyr Gly Cys His Gly Ser Gly Gln Leu Ser
 50 55 60
 Lys Gln Val Pro Val Val Ser Ser Ala Val
 65 70

<210> 315
 <211> 1086
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1086)

<400> 315
 atg gcc agc ctg ggg ctg ctg ctc ctg ctc tta ctg aca gca ctg cca 48
 Met Ala Ser Leu Gly Leu Leu Leu Leu Leu Leu Thr Ala Leu Pro
 1 5 10 15
 ccg ctg tgg tcc tcc tca ctg cct ggg ctg gac act gct gaa agt aaa 96
 Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
 20 25 30
 gcc acc att gca gac ctg atc ctg tct gcg ctg gag aga gcc acc gtc 144
 Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
 35 40 45

460

ttc cta gaa cag agg ctg cct gaa atc aac ctg gat ggc atg gtg ggg Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly 50 55 60	192
gtc cga gtg ctg gaa gag cag cta aaa agt gtc cgg gag aag tgg gcc Val Arg Val Leu Glu Glu Gln Leu Lys Ser Val Arg Glu Lys Trp Ala 65 70 75 80	240
cag gag ccc ctg ctg cag ccg ctg agc ctg cgc gtg ggg atg ctg ggg Gln Glu Pro Leu Leu Gln Pro Leu Ser Leu Arg Val Gly Met Leu Gly 85 90 95	288
gag aag ctg gag gct gcc atc cag aga tcc ctc cac tac ctc aag ctg Glu Lys Leu Glu Ala Ala Ile Gln Arg Ser Leu His Tyr Leu Lys Leu 100 105 110	336
agt gat ccc aag tac cta aga gag ttc cag ctg acc ctc cag ccc ggg Ser Asp Pro Lys Tyr Leu Arg Glu Phe Gln Leu Thr Leu Gln Pro Gly 115 120 125	384
ttt tgg aag ctc cca cat gcc tgg atc cac act gat gcc tcc ttg gtg Phe Trp Lys Leu Pro His Ala Trp Ile His Thr Asp Ala Ser Leu Val 130 135 140	432
tac ccc acg ttc ggg ccc cag gac tca ttc tca gag gag aga agt gac Tyr Pro Thr Phe Gly Pro Gln Asp Ser Phe Ser Glu Glu Arg Ser Asp 145 150 155 160	480
gtg tgc ctg gtg cag ctg ctg gga acc ggg acg gac agc agc gag ccc Val Cys Leu Val Gln Leu Leu Gly Thr Gly Thr Asp Ser Ser Glu Pro 165 170 175	528
tgc ggc ctc tca gac ctc tgc agg agc ctc atg acc aag ccc ggc tgc Cys Gly Leu Ser Asp Leu Cys Arg Ser Leu Met Thr Lys Pro Gly Cys 180 185 190	576
tca ggc tac tgc ctg tcc cac caa ctg ctc ttc ttc ctc tgg gcc aga Ser Gly Tyr Cys Leu Ser His Gln Leu Leu Phe Phe Leu Trp Ala Arg 195 200 205	624
atg agg gga tgc aca cag gga cca ctc caa cag agc cag gac tat atc Met Arg Gly Cys Thr Gln Gly Pro Leu Gln Gln Ser Gln Asp Tyr Ile 210 215 220	672

461

aac ctc ttc tgc gcc aac atg atg gac ttg aac cgc aga gct gag gcc Asn Leu Phe Cys Ala Asn Met Met Asp Leu Asn Arg Arg Ala Glu Ala 225 230 235 240	720
atc gga tac gcc tac cct acc cgg gac atc ttc atg gaa aac atc atg Ile Gly Tyr Ala Tyr Pro Thr Arg Asp Ile Phe Met Glu Asn Ile Met 245 250 255	768
ttc tgt gga atg ggc ggc ttc tcc gac ttc tac aag ctc cgg tgg ctg Phe Cys Gly Met Gly Gly Phe Ser Asp Phe Tyr Lys Leu Arg Trp Leu 260 265 270	816
gag gcc att ctc agc tgg cag aaa cag cag gaa gga tgc ttc ggg gag Glu Ala Ile Leu Ser Trp Gln Lys Gln Gln Glu Gly Cys Phe Gly Glu 275 280 285	864
cct gat gct gaa gat gaa gaa tca tct aaa gct att caa tat cag cag Pro Asp Ala Glu Asp Glu Glu Ser Ser Lys Ala Ile Gln Tyr Gln Gln 290 295 300	912
cat ttt tcg agg aga gtg aag agg cga gaa aaa caa ttt cca gat ggc His Phe Ser Arg Arg Val Lys Arg Arg Glu Lys Gln Phe Pro Asp Gly 305 310 315 320	960
tgc tcc tcc cac aac aca gcc aca gca gtg gca gcc ctg ggt ggc ttc Cys Ser Ser His Asn Thr Ala Thr Ala Val Ala Ala Leu Gly Gly Phe 325 330 335	1008
cta tac atc ctg gca gaa tac ccc cca gca aac aga gag cca cac cca Leu Tyr Ile Leu Ala Glu Tyr Pro Pro Ala Asn Arg Glu Pro His Pro 340 345 350	1056
tcc aca ccg cca cca cca agc agc cgc tga Ser Thr Pro Pro Pro Ser Ser Arg *	1086
355 360	

<210> 316

<211> 361

<212> PRT

<213> Homo sapiens

<400> 316

462

Met Ala Ser Leu Gly Leu Leu Leu Leu Leu Leu Thr Ala Leu Pro
 1 5 10 15
 Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
 20 25 30
 Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
 35 40 45
 Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly
 50 55 60
 Val Arg Val Leu Glu Glu Gln Leu Lys Ser Val Arg Glu Lys Trp Ala
 65 70 75 80
 Gln Glu Pro Leu Leu Gln Pro Leu Ser Leu Arg Val Gly Met Leu Gly
 85 90 95
 Glu Lys Leu Glu Ala Ala Ile Gln Arg Ser Leu His Tyr Leu Lys Leu
 100 105 110
 Ser Asp Pro Lys Tyr Leu Arg Glu Phe Gln Leu Thr Leu Gln Pro Gly
 115 120 125
 Phe Trp Lys Leu Pro His Ala Trp Ile His Thr Asp Ala Ser Leu Val
 130 135 140
 Tyr Pro Thr Phe Gly Pro Gln Asp Ser Phe Ser Glu Glu Arg Ser Asp
 145 150 155 160
 Val Cys Leu Val Gln Leu Leu Gly Thr Gly Thr Asp Ser Ser Glu Pro
 165 170 175
 Cys Gly Leu Ser Asp Leu Cys Arg Ser Leu Met Thr Lys Pro Gly Cys
 180 185 190
 Ser Gly Tyr Cys Leu Ser His Gln Leu Leu Phe Phe Leu Trp Ala Arg
 195 200 205
 Met Arg Gly Cys Thr Gln Gly Pro Leu Gln Gln Ser Gln Asp Tyr Ile
 210 215 220
 Asn Leu Phe Cys Ala Asn Met Met Asp Leu Asn Arg Arg Ala Glu Ala
 225 230 235 240
 Ile Gly Tyr Ala Tyr Pro Thr Arg Asp Ile Phe Met Glu Asn Ile Met
 245 250 255
 Phe Cys Gly Met Gly Gly Phe Ser Asp Phe Tyr Lys Leu Arg Trp Leu
 260 265 270
 Glu Ala Ile Leu Ser Trp Gln Lys Gln Gln Glu Gly Cys Phe Gly Glu
 275 280 285
 Pro Asp Ala Glu Asp Glu Glu Ser Ser Lys Ala Ile Gln Tyr Gln Gln
 290 295 300
 His Phe Ser Arg Arg Val Lys Arg Arg Glu Lys Gln Phe Pro Asp Gly
 305 310 315 320
 Cys Ser Ser His Asn Thr Ala Thr Ala Val Ala Ala Leu Gly Gly Phe
 325 330 335
 Leu Tyr Ile Leu Ala Glu Tyr Pro Pro Ala Asn Arg Glu Pro His Pro
 340 345 350

463

Ser Thr Pro Pro Pro Ser Ser Arg
 355 360

<210> 317
 <211> 1440
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1440)

<221> misc_feature
 <222> (1)...(1440)
 <223> n = A,T,C or G

<400> 317

atg gcg gtc ctc gga gta cag ctg gtg gtg acc ctg ctc act gcc acc 48
 Met Ala Val Leu Gly Val Gln Leu Val Val Thr Leu Leu Thr Ala Thr
 1 5 10 15

ctc atg cac agg ctg gcg cca cac tgc tcc ttc gcg cgc tgg ctg ctc 96
 Leu Met His Arg Leu Ala Pro His Cys Ser Phe Ala Arg Trp Leu Leu
 20 25 30

tgt aac ggc agt ttg ttc cga tac aag cac ccg tct gag gag gag ctt 144
 Cys Asn Gly Ser Leu Phe Arg Tyr Lys His Pro Ser Glu Glu Glu Leu
 35 40 45

cgg gcc ctg gcg ggg aag ccg agg ccc aga ggc agg aaa gag cgg tgg 192
 Arg Ala Leu Ala Gly Lys Pro Arg Pro Arg Gly Arg Lys Glu Arg Trp
 50 55 60

gcc aat ggc ctt agt gag gag aag cca ctg tct gtg ccc cga gat gcc 240
 Ala Asn Gly Leu Ser Glu Glu Lys Pro Leu Ser Val Pro Arg Asp Ala
 65 70 75 80

ccg ttc cag ctg gag acc tgc ccc ctc acg acc gtg gat gcc ctg gtc 288
 Pro Phe Gln Leu Glu Thr Cys Pro Leu Thr Thr Val Asp Ala Leu Val
 85 90 95

ctg cgc ttc ttc ctg gag tac cag tgg ttt gtg gac ttt gct gtg tac 336
 Leu Arg Phe Phe Leu Glu Tyr Gln Trp Phe Val Asp Phe Ala Val Tyr
 100 105 110

464

tcg ggc ggc gtg tac ctc ttc aca gag gcc tac tac tac atg ctg gga Ser Gly Gly Val Tyr Leu Phe Thr Glu Ala Tyr Tyr Tyr Met Leu Gly 115 120 125	384
cca gcc aag gag act aac att gct gtg ttc tgg tgc ctg ctc acg gtg Pro Ala Lys Glu Thr Asn Ile Ala Val Phe Trp Cys Leu Leu Thr Val 130 135 140	432
acc ttc tcc atc aag atg ttc ctg aca gtg aca cgg ctg tac ttc agc Thr Phe Ser Ile Lys Met Phe Leu Thr Val Thr Arg Leu Tyr Phe Ser 145 150 155 160	480
gcc gag gag ggg ggt gag cgc tct gtc tgc ctc acc ttt gcc ttc ctc Ala Glu Glu Gly Gly Glu Arg Ser Val Cys Leu Thr Phe Ala Phe Leu 165 170 175	528
ttc ctg ctg ctg gcc atg ctg gtg caa gtg gtg cgg gag gag acc ctc Phe Leu Leu Leu Ala Met Leu Val Gln Val Val Arg Glu Glu Thr Leu 180 185 190	576
gag ctg ggc ctg gag cct ggt ctg gcc agc atg acc cag aac tta gag Glu Leu Gly Leu Glu Pro Gly Leu Ala Ser Met Thr Gln Asn Leu Glu 195 200 205	624
cca ctt ctg aag aag cag ggc tgg gac tgg gcg ctt cct gtg gcc aag Pro Leu Leu Lys Lys Gln Gly Trp Asp Trp Ala Leu Pro Val Ala Lys 210 215 220	672
ctg gct atc cgc gtg gga ctg gca gtg gtg ggc tct gtg ctg ggt gcc Leu Ala Ile Arg Val Gly Leu Ala Val Val Gly Ser Val Leu Gly Ala 225 230 235 240	720
ttc ctc acc ttc cca ggc ctg cgg ctg gcc cag acc cac cgg gac gca Phe Leu Thr Phe Pro Gly Leu Arg Leu Ala Gln Thr His Arg Asp Ala 245 250 255	768
ctg acc atg tcg gag gac aga ccc atg ctg cag ttc ctc ctg cac acc Leu Thr Met Ser Glu Asp Arg Pro Met Leu Gln Phe Leu Leu His Thr 260 265 270	816
agc ttc ctg tct ccc ctg ttc atc ctg tgg ctc tgg aca aag ccc att Ser Phe Leu Ser Pro Leu Phe Ile Leu Trp Leu Trp Thr Lys Pro Ile 275 280 285	864

465

gca cgg gac ttc ctg cac cag ccg ccg ttt ggg gag acg cgt ttc tcc Ala Arg Asp Phe Leu His Gln Pro Pro Phe Gly Glu Thr Arg Phe Ser 290 295 300	912
ctg ctg tcc gat tct gcc ttc gac tct ggg cgc ctc tgg ttg ctg gtg Leu Leu Ser Asp Ser Ala Phe Asp Ser Gly Arg Leu Trp Leu Leu Val 305 310 315 320	960
gtg ctg tgc ctg ctg cgg ctg gcg gtg acc cgg ccc cac ctg cag gcc Val Leu Cys Leu Leu Arg Leu Ala Val Thr Arg Pro His Leu Gln Ala 325 330 335	1008
tac ctg tgc ctg gcc aag gcc cgg gtg gag cag ctg cga agg gag gct Tyr Leu Cys Leu Ala Lys Ala Arg Val Glu Gln Leu Arg Arg Glu Ala 340 345 350	1056
ggc cgc atc gaa gcc cgt gaa atc cag cag agg gtg gtc cga gtc tac Gly Arg Ile Glu Ala Arg Glu Ile Gln Gln Arg Val Val Arg Val Tyr 355 360 365	1104
tgc tat gtg acc gtg gtg agc ttg cag tac ctg acg ccg ctc atc ctc Cys Tyr Val Thr Val Val Ser Leu Gln Tyr Leu Thr Pro Leu Ile Leu 370 375 380	1152
acc ctc aac tgc aca ctt ctg ctc aag acg ctg gga ggc tat tcc tgg Thr Leu Asn Cys Thr Leu Leu Lys Thr Leu Gly Gly Tyr Ser Trp 385 390 395 400	1200
ggc ctg ggc cca gct cct cta cta tcc ccc gac cca tcc tca gcc agc Gly Leu Gly Pro Ala Pro Leu Leu Ser Pro Asp Pro Ser Ser Ala Ser 405 410 415	1248
gct gcc ccc atc ggc tct ggg gag gac gaa gtc nag cag act gca gcg Ala Ala Pro Ile Gly Ser Gly Glu Asp Glu Val Xaa Gln Thr Ala Ala 420 425 430	1296
cgg att gcc ggg gcc ctg ggt ggc ctg ctt act ccc ctc ttc ctc cgt Arg Ile Ala Gly Ala Leu Gly Gly Leu Leu Thr Pro Leu Phe Leu Arg 435 440 445	1344
ggc gtc ctg gcc tac ctc atc tgg tgg acg gct gcc tgc cag ctg ctc Gly Val Leu Ala Tyr Leu Ile Trp Trp Thr Ala Ala Cys Gln Leu Leu 450 455 460	1392

466

gcc agc ctt ttc ggc ctc tac ttc cac cag cac ttg gca ggc tcc tag 1440
 Ala Ser Leu Phe Gly Leu Tyr Phe His Gln His Leu Ala Gly Ser *
 465 470 475

<210> 318
 <211> 479
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(479)
 <223> Xaa = Any Amino Acid

<400> 318
 Met Ala Val Leu Gly Val Gln Leu Val Val Thr Leu Leu Thr Ala Thr
 1 5 10 15
 Leu Met His Arg Leu Ala Pro His Cys Ser Phe Ala Arg Trp Leu Leu
 20 25 30
 Cys Asn Gly Ser Leu Phe Arg Tyr Lys His Pro Ser Glu Glu Glu Leu
 35 40 45
 Arg Ala Leu Ala Gly Lys Pro Arg Pro Arg Gly Arg Lys Glu Arg Trp
 50 55 60
 Ala Asn Gly Leu Ser Glu Glu Lys Pro Leu Ser Val Pro Arg Asp Ala
 65 70 75 80
 Pro Phe Gln Leu Glu Thr Cys Pro Leu Thr Thr Val Asp Ala Leu Val
 85 90 95
 Leu Arg Phe Phe Leu Glu Tyr Gln Trp Phe Val Asp Phe Ala Val Tyr
 100 105 110
 Ser Gly Gly Val Tyr Leu Phe Thr Glu Ala Tyr Tyr Tyr Met Leu Gly
 115 120 125
 Pro Ala Lys Glu Thr Asn Ile Ala Val Phe Trp Cys Leu Leu Thr Val
 130 135 140
 Thr Phe Ser Ile Lys Met Phe Leu Thr Val Thr Arg Leu Tyr Phe Ser
 145 150 155 160
 Ala Glu Glu Gly Gly Glu Arg Ser Val Cys Leu Thr Phe Ala Phe Leu
 165 170 175
 Phe Leu Leu Leu Ala Met Leu Val Gln Val Val Arg Glu Glu Thr Leu
 180 185 190
 Glu Leu Gly Leu Glu Pro Gly Leu Ala Ser Met Thr Gln Asn Leu Glu
 195 200 205
 Pro Leu Leu Lys Lys Gln Gly Trp Asp Trp Ala Leu Pro Val Ala Lys

467

210	215	220
Leu Ala Ile Arg Val Gly	Leu Ala Val Val Gly	Ser Val Leu Gly Ala
225	230	235
Phe Leu Thr Phe Pro Gly	Leu Arg Leu Ala Gln	Thr His Arg Asp Ala
245	250	255
Leu Thr Met Ser Glu Asp	Arg Pro Met Leu Gln	Phe Leu Leu His Thr
260	265	270
Ser Phe Leu Ser Pro Leu	Phe Ile Leu Trp Leu	Trp Thr Lys Pro Ile
275	280	285
Ala Arg Asp Phe Leu His	Gln Pro Pro Phe Gly	Glu Thr Arg Phe Ser
290	295	300
Leu Leu Ser Asp Ser Ala	Phe Asp Ser Gly Arg	Leu Trp Leu Leu Val
305	310	315
Val Leu Cys Leu Leu Arg	Leu Ala Val Thr Arg	Pro His Leu Gln Ala
325	330	335
Tyr Leu Cys Leu Ala Lys	Ala Arg Val Glu Gln	Leu Arg Arg Glu Ala
340	345	350
Gly Arg Ile Glu Ala Arg	Glu Ile Gln Gln Arg	Val Val Arg Val Tyr
355	360	365
Cys Tyr Val Thr Val Val	Ser Leu Gln Tyr Leu	Thr Pro Leu Ile Leu
370	375	380
Thr Leu Asn Cys Thr Leu	Leu Leu Lys Thr Leu	Gly Gly Tyr Ser Trp
385	390	395
Gly Leu Gly Pro Ala Pro	Leu Leu Ser Pro Asp	Pro Ser Ser Ala Ser
405	410	415
Ala Ala Pro Ile Gly Ser	Gly Glu Asp Glu Val	Xaa Gln Thr Ala Ala
420	425	430
Arg Ile Ala Gly Ala Leu	Gly Gly Leu Leu Thr	Pro Leu Phe Leu Arg
435	440	445
Gly Val Leu Ala Tyr Leu	Ile Trp Trp Thr Ala	Ala Cys Gln Leu Leu
450	455	460
Ala Ser Leu Phe Gly Leu	Tyr Phe His Gln His	Leu Ala Gly Ser
465	470	475

<210> 319
 <211> 333
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(333)

<400> 319

468

atg gct gct tca tca tca tcc tcc tca gct ggt ggg gtc agt gga agt 48
 Met Ala Ala Ser Ser Ser Ser Ser Ser Ala Gly Gly Val Ser Gly Ser
 1 5 10 15

tct gtc act gga tct ggt ttc agt gtc tca gac ctt gcc cca cca cgg 96
 Ser Val Thr Gly Ser Gly Phe Ser Val Ser Asp Leu Ala Pro Pro Arg
 20 25 30

aaa gcc ctt ttc acc tac ccc aaa gga gct gga gag atg tta gaa gat 144
 Lys Ala Leu Phe Thr Tyr Pro Lys Gly Ala Gly Glu Met Leu Glu Asp
 35 40 45

ggc tct gag aga ttc ctc tgc gaa tct gtt ttt agc tat caa gtg gca 192
 Gly Ser Glu Arg Phe Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala
 50 55 60

tcc acg ctt aaa cag gtg aaa cat gat cag caa gtt gct cgg atg gaa 240
 Ser Thr Leu Lys Gln Val Lys His Asp Gln Gln Val Ala Arg Met Glu
 65 70 75 80

aaa cta gct ggt ttg gta gaa gag ctg gag gct gac gag tgg cgg ttt 288
 Lys Leu Ala Gly Leu Val Glu Glu Leu Glu Ala Asp Glu Trp Arg Phe
 85 90 95

aag ccc atc gag cag ctg ctg gga ttc acc ccc tct tca ggt tga 333
 Lys Pro Ile Glu Gln Leu Leu Gly Phe Thr Pro Ser Ser Gly *
 100 105 110

<210> 320

<211> 110

<212> PRT

<213> Homo sapiens

<400> 320

Met Ala Ala Ser Ser Ser Ser Ser Ser Ala Gly Gly Val Ser Gly Ser
 1 5 10 15

Ser Val Thr Gly Ser Gly Phe Ser Val Ser Asp Leu Ala Pro Pro Arg
 20 25 30

Lys Ala Leu Phe Thr Tyr Pro Lys Gly Ala Gly Glu Met Leu Glu Asp
 35 40 45

Gly Ser Glu Arg Phe Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala
 50 55 60

Ser Thr Leu Lys Gln Val Lys His Asp Gln Gln Val Ala Arg Met Glu

469

65		70		75		80									
Lys	Leu	Ala	Gly	Leu	Val	Glu	Glu	Leu	Glu	Ala	Asp	Glu	Trp	Arg	Phe
			85					90						95	
Lys	Pro	Ile	Glu	Gln	Leu	Leu	Gly	Phe	Thr	Pro	Ser	Ser	Gly		
			100					105					110		

<210> 321
 <211> 1383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1383)

<221> misc_feature
 <222> (1)...(1383)
 <223> n = A,T,C or G

<400> 321

atg	ctt	tgt	ctg	gca	gct	ctt	cat	ggc	atg	gng	gcc	ttg	gta	ggc	tct	48
Met	Leu	Cys	Leu	Ala	Ala	Leu	His	Gly	Met	Xaa	Ala	Leu	Val	Gly	Ser	
1			5					10				15				

gaa	ggg	gat	gta	atg	cag	ctg	aaa	tca	gaa	gcc	atc	cag	acc	tct	cat	96
Glu	Gly	Asp	Val	Met	Gln	Leu	Lys	Ser	Glu	Ala	Ile	Gln	Thr	Ser	His	
			20					25				30				

ttt	caa	ggc	aga	ctt	aat	gaa	gtc	att	aga	acc	tta	act	cag	gtc	att	144
Phe	Gln	Gly	Arg	Leu	Asn	Glu	Val	Ile	Arg	Thr	Leu	Thr	Gln	Val	Ile	
			35				40					45				

agt	gtc	tct	ggg	gtg	att	ggg	ctc	cag	tca	aat	gca	gtc	tgg	ctt	ctt	192
Ser	Val	Ser	Gly	Val	Ile	Gly	Leu	Gln	Ser	Asn	Ala	Val	Trp	Leu	Leu	
			50			55				60						

gga	cat	ctt	cat	cta	tct	act	cta	tcc	tca	agt	caa	agt	aga	gcc	tct	240
Gly	His	Leu	His	Leu	Ser	Thr	Leu	Ser	Ser	Ser	Gln	Ser	Arg	Ala	Ser	
			65			70				75				80		

gtt	cct	act	gac	tat	agc	tac	ttg	cct	gaa	agc	agt	ttt	att	gga	gca	288
Val	Pro	Thr	Asp	Tyr	Ser	Tyr	Leu	Pro	Glu	Ser	Ser	Phe	Ile	Gly	Ala	
				85				90						95		

470

gct att ggc ttc ttc att aca gga gga aaa aaa ggt cct gaa tct gtg Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val 100 105 110	336
cct cct tcc ctt ctt aaa gta gtg atg aaa ccc ata gca act gtt gga Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly 115 120 125	384
gaa agc tac caa tat cct cct gtg aac tgg gct gca ctt ctc tct cca Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro 130 135 140	432
ctt atg agg cta aat ttt ggt gaa gag atc cag caa ctg tgc ctt gaa Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu 145 150 155 160	480
att atg gtg acc cag gca cag tca tcc cag aat gca gct gca cta ttg Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu 165 170 175	528
ggc ttg tgg gtg aca cca cca ctg atc cac agt ctg agt ctg aat acc Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr 180 185 190	576
aag aga tat ctc ctg ata tct gca cct ctg tgg ata aaa cac atc tct Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser 195 200 205	624
gat gaa cag atc ctg ggt ttt gtt gaa aat tta atg gtg gca gtt ttt Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe 210 215 220	672
aaa gca gct tcc cca ctt gga agt cct gag cta tgc cca agt gct tta Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu 225 230 235 240	720
cac ggt ctg agc cag gcc atg aaa ctg ccc agc cct gcc cac cac ctc His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu 245 250 255	768
tgg agt ctg ctc tct gaa gct act ggg aaa att ttt gac ctc ctg cca Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro 260 265 270	816

471

aat aag att cgg aga aag gat cta gag ctg tat atc agc ata gca aaa Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys 275 280 285	864
tgc ctc tta gaa atg aca gat gat gat gcc aat cgg atc gcc cag gtt Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val 290 295 300	912
act aag agc aac ata gaa aaa gct gcc ttt gtc aaa ctg tac tta gtc Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val 305 310 315 320	960
tct caa gga cga ttc ccc ttg gtg aac ctg acc gat atg ctg aga ttt Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Arg Phe 325 330 335	1008
gca acc gca gtg gtt gca tgg gct gac cac act gcc cct ctc ctc ctc Ala Thr Ala Val Val Ala Trp Ala Asp His Thr Ala Pro Leu Leu Leu 340 345 350	1056
ggc ctc agt gcc agt tgg ttg cca tgg cat cag gag aat ggc ccg gct Gly Leu Ser Ala Ser Trp Leu Pro Trp His Gln Glu Asn Gly Pro Ala 355 360 365	1104
ggg cca gta cca agc ttc ctt ggc agg agt cca atg cac agg gtc act Gly Pro Val Pro Ser Phe Leu Gly Arg Ser Pro Met His Arg Val Thr 370 375 380	1152
ctg cag gag gtt ctc act ctc ctt ccc aat agc atg gct ctg ctg ctg Leu Gln Glu Val Leu Thr Leu Leu Pro Asn Ser Met Ala Leu Leu Leu 385 390 395 400	1200
cag aaa gag cca tgg aag gaa cag acc cag aag ttc att gac tgg cta Gln Lys Glu Pro Trp Lys Glu Gln Thr Gln Lys Phe Ile Asp Trp Leu 405 410 415	1248
ttc agc atc atg gaa agc cct aaa gaa gcc ctc tca gca cag tcc agg Phe Ser Ile Met Glu Ser Pro Lys Glu Ala Leu Ser Ala Gln Ser Arg 420 425 430	1296
gat ctt ttg aaa gcc acc ctg ctg tcc ttg aga gtt ctc cca gag ttt Asp Leu Leu Lys Ala Thr Leu Leu Ser Leu Arg Val Leu Pro Glu Phe 435 440 445	1344

472

aag aag aaa gct gta tgg acc aga gca tat ggt tgg tga
 Lys Lys Lys Ala Val Trp Thr Arg Ala Tyr Gly Trp *
 450 455 460

1383

<210> 322
 <211> 460
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(460)
 <223> Xaa = Any Amino Acid

<400> 322
 Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser
 1 5 10 15
 Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His
 20 25 30
 Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile
 35 40 45
 Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu
 50 55 60
 Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser
 65 70 75 80
 Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala
 85 90 95
 Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val
 100 105 110
 Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly
 115 120 125
 Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro
 130 135 140
 Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu
 145 150 155 160
 Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu
 165 170 175
 Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr
 180 185 190
 Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser
 195 200 205
 Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe
 210 215 220

473

Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu
 225 230 235 240
 His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu
 245 250 255
 Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro
 260 265 270
 Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys
 275 280 285
 Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val
 290 295 300
 Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val
 305 310 315 320
 Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Arg Phe
 325 330 335
 Ala Thr Ala Val Val Ala Trp Ala Asp His Thr Ala Pro Leu Leu Leu
 340 345 350
 Gly Leu Ser Ala Ser Trp Leu Pro Trp His Gln Glu Asn Gly Pro Ala
 355 360 365
 Gly Pro Val Pro Ser Phe Leu Gly Arg Ser Pro Met His Arg Val Thr
 370 375 380
 Leu Gln Glu Val Leu Thr Leu Leu Pro Asn Ser Met Ala Leu Leu Leu
 385 390 395 400
 Gln Lys Glu Pro Trp Lys Glu Gln Thr Gln Lys Phe Ile Asp Trp Leu
 405 410 415
 Phe Ser Ile Met Glu Ser Pro Lys Glu Ala Leu Ser Ala Gln Ser Arg
 420 425 430
 Asp Leu Leu Lys Ala Thr Leu Leu Ser Leu Arg Val Leu Pro Glu Phe
 435 440 445
 Lys Lys Lys Ala Val Trp Thr Arg Ala Tyr Gly Trp
 450 455 460

<210> 323

<211> 1596

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1596)

<221> misc_feature

<222> (1)...(1596)

<223> n = A,T,C or G

474

<400> 323

atg ctt tgt ctg gca gct ctt cat ggc atg gng gcc ttg gta ggc tct	48
Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser	
1 5 10 15	
gaa ggg gat gta atg cag ctg aaa tca gaa gcc atc cag acc tct cat	96
Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His	
20 25 30	
ttt caa ggc aga ctt aat gaa gtc att aga acc tta act cag gtc att	144
Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile	
35 40 45	
agt gtc tct ggg gtg att ggt ctc cag tca aat gca gtc tgg ctt ctt	192
Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu	
50 55 60	
gga cat ctt cat cta tct act cta tcc tca agt caa agt aga gcc tct	240
Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser	
65 70 75 80	
gtt cct act gac tat agc tac ttg cct gaa agc agt ttt att gga gca	288
Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala	
85 90 95	
gct att ggc ttc ttc att aca gga gga aaa aaa ggt cct gaa tct gtg	336
Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val	
100 105 110	
cct cct tcc ctt ctt aaa gta gtg atg aaa ccc ata gca act gtt gga	384
Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly	
115 120 125	
gaa agc tac caa tat cct cct gtg aac tgg gct gca ctt ctc tct cca	432
Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro	
130 135 140	
ctt atg agg cta aat ttt ggt gaa gag atc cag caa ctg tgc ctt gaa	480
Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu	
145 150 155 160	
att atg gtg acc cag gca cag tca tcc cag aat gca gct gca cta ttg	528
Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu	
165 170 175	

475

ggc ttg tgg gtg aca cca cca ctg atc cac agt ctg agt ctg aat acc	576
Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr	
180 185 190	
aag aga tat ctc ctg ata tct gca cct ctg tgg ata aaa cac atc tct	624
Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser	
195 200 205	
gat gaa cag atc ctg ggt ttt gtt gaa aat tta atg gtg gca gtt ttt	672
Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe	
210 215 220	
aaa gca gct tcc cca ctt gga agt cct gag cta tgc cca agt gct tta	720
Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu	
225 230 235 240	
cac ggt ctg agc cag gcc atg aaa ctg ccc agc cct gcc cac cac ctc	768
His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu	
245 250 255	
tgg agt ctg ctc tct gaa gct act ggg aaa att ttt gac ctc ctg cca	816
Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro	
260 265 270	
aat aag att cgg aga aag gat cta gag ctg tat atc agc ata gca aaa	864
Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys	
275 280 285	
tgc ctc tta gaa atg aca gat gat gat gcc aat cgg atc gcc cag gtt	912
Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val	
290 295 300	
act aag agc aac ata gaa aaa gct gcc ttt gtc aaa ctg tac tta gtc	960
Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val	
305 310 315 320	
tct caa gga cga ttc ccc ttg gtg aac ctg acc gat atg ctg agc gtt	1008
Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Ser Val	
325 330 335	
gct gtg cag cac cgt gag aaa gag gtg ttg gcc tgg atg att ctg cac	1056
Ala Val Gln His Arg Glu Lys Glu Val Leu Ala Trp Met Ile Leu His	
340 345 350	

476

agc tta tac cag gca cgg att gtg agc cat gcc aat acg ggc gtt ttg	1104
Ser Leu Tyr Gln Ala Arg Ile Val Ser His Ala Asn Thr Gly Val Leu	
355 360 365	
aag aga atg gag tgg ctc ttg gaa ctg atg ggt tat att aga aat gtt	1152
Lys Arg Met Glu Trp Leu Leu Glu Leu Met Gly Tyr Ile Arg Asn Val	
370 375 380	
gct tac cag tca aca tcc ttt cac aat acg gct ctt gac gag gct ttg	1200
Ala Tyr Gln Ser Thr Ser Phe His Asn Thr Ala Leu Asp Glu Ala Leu	
385 390 395 400	
gac ttc ttc ttg ctg ata ttt gca acc gca gtg gtt gca tgg gct gac	1248
Asp Phe Phe Leu Leu Ile Phe Ala Thr Ala Val Val Ala Trp Ala Asp	
405 410 415	
cac act gcc cct ctc ctc ctc ggc ctc agt gcc agt tgg ttg cca tgg	1296
His Thr Ala Pro Leu Leu Leu Gly Leu Ser Ala Ser Trp Leu Pro Trp	
420 425 430	
cat cag gag aat ggc ccg gct ggg cca gta cca agc ttc ctt ggc agg	1344
His Gln Glu Asn Gly Pro Ala Gly Pro Val Pro Ser Phe Leu Gly Arg	
435 440 445	
agt cca atg cac agg gtc act ctg cag gag gtt ctc act ctc ctt ccc	1392
Ser Pro Met His Arg Val Thr Leu Gln Glu Val Leu Thr Leu Leu Pro	
450 455 460	
aat agc atg gct ctg ctg ctg cag aaa gag cca tgg aag gaa cag acc	1440
Asn Ser Met Ala Leu Leu Leu Gln Lys Glu Pro Trp Lys Glu Gln Thr	
465 470 475 480	
cag aag ttc att gac tgg cta ttc agc atc atg gaa agc cct aaa gaa	1488
Gln Lys Phe Ile Asp Trp Leu Phe Ser Ile Met Glu Ser Pro Lys Glu	
485 490 495	
gcc ctc tca gca cag tcc agg gat ctt ttg aaa gcc acc ctg ctg tcc	1536
Ala Leu Ser Ala Gln Ser Arg Asp Leu Leu Lys Ala Thr Leu Leu Ser	
500 505 510	
ttg aga gtt ctc cca gag ttt aag aag aaa gct gta tgg acc aga gca	1584
Leu Arg Val Leu Pro Glu Phe Lys Lys Lys Ala Val Trp Thr Arg Ala	
515 520 525	

477

tat ggt tgg tga
 Tyr Gly Trp *
 530

1596

<210> 324
 <211> 531
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(531)
 <223> Xaa = Any Amino Acid

<400> 324

Met	Leu	Cys	Leu	Ala	Ala	Leu	His	Gly	Met	Xaa	Ala	Leu	Val	Gly	Ser
1			5					10					15		
Glu	Gly	Asp	Val	Met	Gln	Leu	Lys	Ser	Glu	Ala	Ile	Gln	Thr	Ser	His
		20					25					30			
Phe	Gln	Gly	Arg	Leu	Asn	Glu	Val	Ile	Arg	Thr	Leu	Thr	Gln	Val	Ile
		35				40					45				
Ser	Val	Ser	Gly	Val	Ile	Gly	Leu	Gln	Ser	Asn	Ala	Val	Trp	Leu	Leu
	50				55				60						
Gly	His	Leu	His	Leu	Ser	Thr	Leu	Ser	Ser	Ser	Gln	Ser	Arg	Ala	Ser
65				70					75					80	
Val	Pro	Thr	Asp	Tyr	Ser	Tyr	Leu	Pro	Glu	Ser	Ser	Phe	Ile	Gly	Ala
			85					90				95			
Ala	Ile	Gly	Phe	Phe	Ile	Thr	Gly	Gly	Lys	Lys	Gly	Pro	Glu	Ser	Val
		100					105					110			
Pro	Pro	Ser	Leu	Leu	Lys	Val	Val	Met	Lys	Pro	Ile	Ala	Thr	Val	Gly
		115				120						125			
Glu	Ser	Tyr	Gln	Tyr	Pro	Pro	Val	Asn	Trp	Ala	Ala	Leu	Leu	Ser	Pro
	130				135					140					
Leu	Met	Arg	Leu	Asn	Phe	Gly	Glu	Glu	Ile	Gln	Gln	Leu	Cys	Leu	Glu
145				150					155					160	
Ile	Met	Val	Thr	Gln	Ala	Gln	Ser	Ser	Gln	Asn	Ala	Ala	Ala	Leu	Leu
			165					170						175	
Gly	Leu	Trp	Val	Thr	Pro	Pro	Leu	Ile	His	Ser	Leu	Ser	Leu	Asn	Thr
		180					185					190			
Lys	Arg	Tyr	Leu	Leu	Ile	Ser	Ala	Pro	Leu	Trp	Ile	Lys	His	Ile	Ser
		195				200						205			
Asp	Glu	Gln	Ile	Leu	Gly	Phe	Val	Glu	Asn	Leu	Met	Val	Ala	Val	Phe

478

210 215 220
 Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu
 225 230 235 240
 His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu
 245 250 255
 Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro
 260 265 270
 Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys
 275 280 285
 Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val
 290 295 300
 Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val
 305 310 315 320
 Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Ser Val
 325 330 335
 Ala Val Gln His Arg Glu Lys Glu Val Leu Ala Trp Met Ile Leu His
 340 345 350
 Ser Leu Tyr Gln Ala Arg Ile Val Ser His Ala Asn Thr Gly Val Leu
 355 360 365
 Lys Arg Met Glu Trp Leu Leu Glu Leu Met Gly Tyr Ile Arg Asn Val
 370 375 380
 Ala Tyr Gln Ser Thr Ser Phe His Asn Thr Ala Leu Asp Glu Ala Leu
 385 390 395 400
 Asp Phe Phe Leu Leu Ile Phe Ala Thr Ala Val Val Ala Trp Ala Asp
 405 410 415
 His Thr Ala Pro Leu Leu Leu Gly Leu Ser Ala Ser Trp Leu Pro Trp
 420 425 430
 His Gln Glu Asn Gly Pro Ala Gly Pro Val Pro Ser Phe Leu Gly Arg
 435 440 445
 Ser Pro Met His Arg Val Thr Leu Gln Glu Val Leu Thr Leu Leu Pro
 450 455 460
 Asn Ser Met Ala Leu Leu Leu Gln Lys Glu Pro Trp Lys Glu Gln Thr
 465 470 475 480
 Gln Lys Phe Ile Asp Trp Leu Phe Ser Ile Met Glu Ser Pro Lys Glu
 485 490 495
 Ala Leu Ser Ala Gln Ser Arg Asp Leu Leu Lys Ala Thr Leu Leu Ser
 500 505 510
 Leu Arg Val Leu Pro Glu Phe Lys Lys Lys Ala Val Trp Thr Arg Ala
 515 520 525
 Tyr Gly Trp
 530

<210> 325

<211> 666

479

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(666)

<400> 325

atg gcc ggg act ggg ctg ctg gcg ctg cgg acg ctg cca ggg ccc agc	48
Met Ala Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser	
1 5 10 15	

tgg gtg cga ggc tcg ggc cct tcc gtg ctg agc cgc ctg cag gac gcg	96
Trp Val Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala	
20 25 30	

gcc gtg gtg cgg cct ggc ttc ctg agc acg gca gag gag gag acg ctg	144
Ala Val Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu	
35 40 45	

agc cga gaa ctg gag ccc gag ctg cgc cgc cgc cgc tac gaa tac gat	192
Ser Arg Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp	
50 55 60	

cac tgg gac gcg gcc atc cac ggc ttc cga gag aca gag aag tcg cgc	240
His Trp Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg	
65 70 75 80	

tgg tca gaa gcc agc cgg gcc atc ctg cag cgc gtg cag gcg gcc gcc	288
Trp Ser Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala	
85 90 95	

ttt ggc ccc ggc cag acc ctg ctc tcc tcc gtg cac gtg ctg gac ctg	336
Phe Gly Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu	
100 105 110	

gaa gcc cgc ggc tac atc aag ccc cac gtg gac agc atc aag ttc tgc	384
Glu Ala Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys	
115 120 125	

ggg gcc acc atc gcc ggc ctg tct ctc ctg tct ccc agc gtt atg cgg	432
Gly Ala Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg	
130 135 140	

480

ctg gtg cac acc cag gag ccg ggg gag tgg ctg gaa ctc ttg ctg gag 480
 Leu Val His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu
 145 150 155 160

ccg ggc tcc ctc tac atc ctt agg ggc tca gcc cgt tat gac ttc tcc 528
 Pro Gly Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser
 165 170 175

cat gag atc ctt cgg gat gaa gag tcc ttc ttt ggg gaa cgc cgg att 576
 His Glu Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Arg Ile
 180 185 190

ccc cgg ggc cgg cgc atc tcc gtg atc tgc cgc tcc ctc cct gag ggc 624
 Pro Arg Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly
 195 200 205

atg ggg cca ggg gag tct gga cag ccg ccc cca gcc tgc tga 666
 Met Gly Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys *
 210 215 220

<210> 326

<211> 221

<212> PRT

<213> Homo sapiens

<400> 326

Met Ala Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser
 1 5 10 15
 Trp Val Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala
 20 25 30
 Ala Val Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu
 35 40 45
 Ser Arg Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp
 50 55 60
 His Trp Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg
 65 70 75 80
 Trp Ser Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala
 85 90 95
 Phe Gly Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu
 100 105 110
 Glu Ala Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys
 115 120 125
 Gly Ala Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg

481

130	135	140
Leu Val His Thr Gln Glu	Pro Gly Glu Trp	Leu Glu Leu Leu Leu Glu
145	150	155
Pro Gly Ser Leu Tyr Ile	Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser	160
165	170	175
His Glu Ile Leu Arg Asp Glu Glu	Ser Phe Phe Gly Glu Arg Arg Ile	
180	185	190
Pro Arg Gly Arg Arg Ile Ser Val	Ile Cys Arg Ser Leu Pro Glu Gly	
195	200	205
Met Gly Pro Gly Glu Ser Gly Gln	Pro Pro Pro Ala Cys	
210	215	220

<210> 327
 <211> 294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(294)

<400> 327

atg gct gaa aat agt gta tta aca tcc act act ggg agg act agc ttg	48
Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu	
1 5 10 15	
gca gac tct tcc att ttt gat tct aaa gtt act gag att tcc aag gaa	96
Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu	
20 25 30	
aac tta ctt att gga tct act tca tat gta gaa gaa gag atg cct cag	144
Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln	
35 40 45	
att gaa aca aga gtg ata ttg gtt caa gaa gct gga aaa caa gaa gaa	192
Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu	
50 55 60	
ctt ata aaa gcc tta aag gac att aaa gtg ggc ttt gta aag atg gag	240
Leu Ile Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu	
65 70 75 80	
tca gtg gaa gaa ttt gaa ggt ttg gat tct ccg gaa ttt gaa atg tat	288
Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Met Tyr	

482

85

90

95

ttg tag
Leu *

294

<210> 328
<211> 97
<212> PRT
<213> Homo sapiens

<400> 328

Met	Ala	Glu	Asn	Ser	Val	Leu	Thr	Ser	Thr	Thr	Gly	Arg	Thr	Ser	Leu
1				5					10					15	
Ala	Asp	Ser	Ser	Ile	Phe	Asp	Ser	Lys	Val	Thr	Glu	Ile	Ser	Lys	Glu
			20					25					30		
Asn	Leu	Leu	Ile	Gly	Ser	Thr	Ser	Tyr	Val	Glu	Glu	Glu	Met	Pro	Gln
		35					40					45			
Ile	Glu	Thr	Arg	Val	Ile	Leu	Val	Gln	Glu	Ala	Gly	Lys	Gln	Glu	Glu
	50					55				60					
Leu	Ile	Lys	Ala	Leu	Lys	Asp	Ile	Lys	Val	Gly	Phe	Val	Lys	Met	Glu
65					70					75				80	
Ser	Val	Glu	Glu	Phe	Glu	Gly	Leu	Asp	Ser	Pro	Glu	Phe	Glu	Met	Tyr
				85					90					95	

Leu

<210> 329
<211> 270
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(270)

<400> 329

atg	gtg	tca	gct	agc	gtg	ttt	gtg	ggc	ctg	gtg	atc	ttc	tac	atc	gcc	48
Met	Val	Ser	Ala	Ser	Val	Phe	Val	Gly	Leu	Val	Ile	Phe	Tyr	Ile	Ala	
1				5					10					15		
ttc	tgc	ctc	ctg	tgg	ccc	ctc	gtg	gtg	aag	ggc	tgc	acg	atg	atc	cgg	96
Phe	Cys	Leu	Leu	Trp	Pro	Leu	Val	Val	Lys	Gly	Cys	Thr	Met	Ile	Arg	

483

20	25	30	
tgg aag ata aac aac ctc att gcc tca gaa tcc tac tac acc tac gcc			144
Trp Lys Ile Asn Asn Leu Ile Ala Ser Glu Ser Tyr Tyr Thr Tyr Ala			
35	40	45	
tcc att tcc gga atc tcg agc atg cca tct ctg aga cat tcc agg atg			192
Ser Ile Ser Gly Ile Ser Ser Met Pro Ser Leu Arg His Ser Arg Met			
50	55	60	
ggc tcc atg ttc agc tcc agg atg aca gag gac agg gct gaa ccc aag			240
Gly Ser Met Phe Ser Ser Arg Met Thr Glu Asp Arg Ala Glu Pro Lys			
65	70	75	80
gaa gcc gtg gag aga cag ttg atg acc tga			270
Glu Ala Val Glu Arg Gln Leu Met Thr *			
85			

<210> 330

<211> 89

<212> PRT

<213> Homo sapiens

<400> 330

Met Val Ser Ala Ser Val Phe Val Gly Leu Val Ile Phe Tyr Ile Ala			
1	5	10	15
Phe Cys Leu Leu Trp Pro Leu Val Val Lys Gly Cys Thr Met Ile Arg			
20	25	30	
Trp Lys Ile Asn Asn Leu Ile Ala Ser Glu Ser Tyr Tyr Thr Tyr Ala			
35	40	45	
Ser Ile Ser Gly Ile Ser Ser Met Pro Ser Leu Arg His Ser Arg Met			
50	55	60	
Gly Ser Met Phe Ser Ser Arg Met Thr Glu Asp Arg Ala Glu Pro Lys			
65	70	75	80
Glu Ala Val Glu Arg Gln Leu Met Thr			
85			

<210> 331

<211> 255

<212> DNA

<213> Homo sapiens

<220>

484

<221> CDS

<222> (1)...(255)

<400> 331

atg	tta	ggc	ctt	ttg	cag	ttt	gac	tct	ggc	ttt	att	tgc	ctt	tgt	gct	48
Met	Leu	Gly	Leu	Leu	Gln	Phe	Asp	Ser	Gly	Phe	Ile	Cys	Leu	Cys	Ala	
1				5					10					15		

cgt	gtt	tat	cct	tcc	tgc	ctt	gaa	cct	ggg	cag	agt	ttt	att	act	gag	96
Arg	Val	Tyr	Pro	Ser	Cys	Leu	Glu	Pro	Gly	Gln	Ser	Phe	Ile	Thr	Glu	
			20					25					30			

gaa	gat	gat	gca	cgg	agt	gag	tct	agt	act	gaa	tgg	gac	tta	gat	gga	144
Glu	Asp	Asp	Ala	Arg	Ser	Glu	Ser	Ser	Thr	Glu	Trp	Asp	Leu	Asp	Gly	
			35				40					45				

ttc	agt	gag	ctg	gac	tct	gag	tca	gga	agt	tca	agt	tct	ttt	tca	gat	192
Phe	Ser	Glu	Leu	Asp	Ser	Glu	Ser	Gly	Ser	Ser	Ser	Ser	Phe	Ser	Asp	
	50					55					60					

gat	gaa	gtc	tgg	gtg	caa	gta	gca	cct	cag	cga	aat	gca	cag	gat	cag	240
Asp	Glu	Val	Trp	Val	Gln	Val	Ala	Pro	Gln	Arg	Asn	Ala	Gln	Asp	Gln	
65					70				75					80		

cag	ggg	tct	ttg	taa												255
Gln	Gly	Ser	Leu	*												

<210> 332

<211> 84

<212> PRT

<213> Homo sapiens

<400> 332

Met	Leu	Gly	Leu	Leu	Gln	Phe	Asp	Ser	Gly	Phe	Ile	Cys	Leu	Cys	Ala
1				5					10					15	

Arg	Val	Tyr	Pro	Ser	Cys	Leu	Glu	Pro	Gly	Gln	Ser	Phe	Ile	Thr	Glu
			20					25				30			

Glu	Asp	Asp	Ala	Arg	Ser	Glu	Ser	Ser	Thr	Glu	Trp	Asp	Leu	Asp	Gly
			35				40					45			

Phe	Ser	Glu	Leu	Asp	Ser	Glu	Ser	Gly	Ser	Ser	Ser	Ser	Phe	Ser	Asp
	50					55				60					

Asp	Glu	Val	Trp	Val	Gln	Val	Ala	Pro	Gln	Arg	Asn	Ala	Gln	Asp	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

485

65 70 75 80
Gln Gly Ser Leu

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<210> 333
<211> 243
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(243)

<400> 333																
atg	gag	att	ctc	tgg	ctg	atg	gtc	aag	tcc	tgg	aat	acc	gga	gta	ctt	48
Met	Glu	Ile	Leu	Trp	Leu	Met	Val	Lys	Ser	Trp	Asn	Thr	Gly	Val	Leu	
1				5					10					15		
atg	ttt	agc	agg	agc	aag	tat	gca	tct	gct	gaa	aag	tgg	tgt	ggc	ctg	96
Met	Phe	Ser	Arg	Ser	Lys	Tyr	Ala	Ser	Ala	Glu	Lys	Trp	Cys	Gly	Leu	
			20					25					30			
gcc	ttg	cgt	ttc	ctt	aac	cac	ctt	acc	tcc	ttc	aag	gaa	agc	tat	gaa	144
Ala	Leu	Arg	Phe	Leu	Asn	His	Leu	Thr	Ser	Phe	Lys	Glu	Ser	Tyr	Glu	
			35				40					45				
act	cag	atg	aat	atg	ctg	tat	agt	cag	ctt	gtg	gaa	gca	ttg	agt	aac	192
Thr	Gln	Met	Asn	Met	Leu	Tyr	Ser	Gln	Leu	Val	Glu	Ala	Leu	Ser	Asn	
		50				55				60						
aac	aag	ggc	cca	ggt	ttt	cat	gaa	cat	ggc	tac	tgg	agc	aag	tca	gat	240
Asn	Lys	Gly	Pro	Val	Phe	His	Glu	His	Gly	Tyr	Trp	Ser	Lys	Ser	Asp	
	65				70					75				80		
tag															243	
*																

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<210> 334
<211> 80
<212> PRT
<213> Homo sapiens
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486

<400> 334

Met	Glu	Ile	Leu	Trp	Leu	Met	Val	Lys	Ser	Trp	Asn	Thr	Gly	Val	Leu
1			5					10					15		
Met	Phe	Ser	Arg	Ser	Lys	Tyr	Ala	Ser	Ala	Glu	Lys	Trp	Cys	Gly	Leu
			20					25					30		
Ala	Leu	Arg	Phe	Leu	Asn	His	Leu	Thr	Ser	Phe	Lys	Glu	Ser	Tyr	Glu
			35				40					45			
Thr	Gln	Met	Asn	Met	Leu	Tyr	Ser	Gln	Leu	Val	Glu	Ala	Leu	Ser	Asn
	50					55					60				
Asn	Lys	Gly	Pro	Val	Phe	His	Glu	His	Gly	Tyr	Trp	Ser	Lys	Ser	Asp
65					70					75					80

<210> 335

<211> 237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(237)

<400> 335

atg	cct	gtg	gtc	ctg	tcg	caa	gag	gtg	gag	tcc	gtt	ctt	gtg	ggg	gct	48
Met	Pro	Val	Val	Leu	Ser	Gln	Glu	Val	Glu	Ser	Val	Leu	Val	Gly	Ala	
1			5					10					15			
gct	gtt	ctg	ggg	gcc	tgt	gcc	tca	ggg	gat	ttc	gct	tct	gta	cag	gaa	96
Ala	Val	Leu	Gly	Ala	Cys	Ala	Ser	Gly	Asp	Phe	Ala	Ser	Val	Gln	Glu	
			20					25					30			
gca	atg	gca	aaa	atg	agc	aaa	gtt	ggg	aaa	gtt	gtg	ttc	ccg	aga	cta	144
Ala	Met	Ala	Lys	Met	Ser	Lys	Val	Gly	Lys	Val	Val	Phe	Pro	Arg	Leu	
			35				40					45				
cag	gat	aaa	aaa	tac	tat	gat	aag	aaa	tac	caa	gta	ttc	ctg	aag	ctg	192
Gln	Asp	Lys	Lys	Tyr	Tyr	Asp	Lys	Lys	Tyr	Gln	Val	Phe	Leu	Lys	Leu	
	50					55				60						
gtt	gaa	cac	cag	aag	gag	tat	ttg	gcg	atc	atg	aat	gat	gac	tga		237
Val	Glu	His	Gln	Lys	Glu	Tyr	Leu	Ala	Ile	Met	Asn	Asp	Asp	*		
65					70					75						

<210> 336

487

<211> 78
 <212> PRT
 <213> Homo sapiens

<400> 336
 Met Pro Val Val Leu Ser Gln Glu Val Glu Ser Val Leu Val Gly Ala
 1 5 10 15
 Ala Val Leu Gly Ala Cys Ala Ser Gly Asp Phe Ala Ser Val Gln Glu
 20 25 30
 Ala Met Ala Lys Met Ser Lys Val Gly Lys Val Val Phe Pro Arg Leu
 35 40 45
 Gln Asp Lys Lys Tyr Tyr Asp Lys Lys Tyr Gln Val Phe Leu Lys Leu
 50 55 60
 Val Glu His Gln Lys Glu Tyr Leu Ala Ile Met Asn Asp Asp
 65 70 75

<210> 337
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(567)

<400> 337
 atg cac tct att ctg gat att att gct gga ttc cta tat acc att tta 48
 Met His Ser Ile Leu Asp Ile Ile Ala Gly Phe Leu Tyr Thr Ile Leu
 1 5 10 15
 atc tta gct gtc ttc tat cca ttt gtg gac ctg att gac aac ttc aac 96
 Ile Leu Ala Val Phe Tyr Pro Phe Val Asp Leu Ile Asp Asn Phe Asn
 20 25 30
 caa act cac aaa tat gct cca ttc atc atc atc ggg ctt cat tta gct 144
 Gln Thr His Lys Tyr Ala Pro Phe Ile Ile Ile Gly Leu His Leu Ala
 35 40 45
 ttg ggg atc ttt tct ttc act ctt gac acc tgg agc aca tcc cga gga 192
 Leu Gly Ile Phe Ser Phe Thr Leu Asp Thr Trp Ser Thr Ser Arg Gly
 50 55 60
 gac aca gcc gag ata cta gga agt ggt gct gga att gca tgt gga tct 240
 Asp Thr Ala Glu Ile Leu Gly Ser Gly Ala Gly Ile Ala Cys Gly Ser

488

65	70	75	80	
cat gtt act tat aac atg ggt cta gta tta gat cct tct cta gat aca	288			
His Val Thr Tyr Asn Met Gly Leu Val Leu Asp Pro Ser Leu Asp Thr				
85	90	95		
tta cct tta gct ggg ccc ccc att act gtg act ctg ttt gga aaa gcc	336			
Leu Pro Leu Ala Gly Pro Pro Ile Thr Val Thr Leu Phe Gly Lys Ala				
100	105	110		
ata ttg cgg atc ctc ata ggg atg gta ttt gta cta ata atc aga gat	384			
Ile Leu Arg Ile Leu Ile Gly Met Val Phe Val Leu Ile Ile Arg Asp				
115	120	125		
gta atg aaa aag atc acc att cct tta gcc tgc aaa atc ttc aat ata	432			
Val Met Lys Lys Ile Thr Ile Pro Leu Ala Cys Lys Ile Phe Asn Ile				
130	135	140		
ccg tgt gat gat att cga aaa gca aga cag cac atg gaa gtt gaa ctt	480			
Pro Cys Asp Asp Ile Arg Lys Ala Arg Gln His Met Glu Val Glu Leu				
145	150	155	160	
cct tat cgg tat att acc tat gga atg gtt ggt ttc tcc atc aca ttt	528			
Pro Tyr Arg Tyr Ile Thr Tyr Gly Met Val Gly Phe Ser Ile Thr Phe				
165	170	175		
ttt gtt cct tac ata ttt ttc ttt att ggt atc tct tga	567			
Phe Val Pro Tyr Ile Phe Phe Phe Ile Gly Ile Ser *				
180	185			

<210> 338

<211> 188

<212> PRT

<213> Homo sapiens

<400> 338

Met His Ser Ile Leu Asp Ile Ile Ala Gly Phe Leu Tyr Thr Ile Leu	
1	5
Ile Leu Ala Val Phe Tyr Pro Phe Val Asp Leu Ile Asp Asn Phe Asn	
20	25
Gln Thr His Lys Tyr Ala Pro Phe Ile Ile Ile Gly Leu His Leu Ala	
35	40
Leu Gly Ile Phe Ser Phe Thr Leu Asp Thr Trp Ser Thr Ser Arg Gly	

489

50 55 60
 Asp Thr Ala Glu Ile Leu Gly Ser Gly Ala Gly Ile Ala Cys Gly Ser
 65 70 75 80
 His Val Thr Tyr Asn Met Gly Leu Val Leu Asp Pro Ser Leu Asp Thr
 85 90 95
 Leu Pro Leu Ala Gly Pro Pro Ile Thr Val Thr Leu Phe Gly Lys Ala
 100 105 110
 Ile Leu Arg Ile Leu Ile Gly Met Val Phe Val Leu Ile Ile Arg Asp
 115 120 125
 Val Met Lys Lys Ile Thr Ile Pro Leu Ala Cys Lys Ile Phe Asn Ile
 130 135 140
 Pro Cys Asp Asp Ile Arg Lys Ala Arg Gln His Met Glu Val Glu Leu
 145 150 155 160
 Pro Tyr Arg Tyr Ile Thr Tyr Gly Met Val Gly Phe Ser Ile Thr Phe
 165 170 175
 Phe Val Pro Tyr Ile Phe Phe Phe Ile Gly Ile Ser
 180 185

<210> 339
 <211> 210
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)...(210)

<400> 339
 atg gtt tcc cat ttc atg ggg tct ctc agt gtc ctg tgt ttc ctt ctg 48
 Met Val Ser His Phe Met Gly Ser Leu Ser Val Leu Cys Phe Leu Leu
 1 5 10 15

 ctg ctt gga ttc cag ttc gtc tgc cca cag ccc tcc act caa cac agg 96
 Leu Leu Gly Phe Gln Phe Val Cys Pro Gln Pro Ser Thr Gln His Arg
 20 25 30

 aag gtc ccg cag cgg atg gcg gcg gag ggc gcc ccc gag gac gac ggc 144
 Lys Val Pro Gln Arg Met Ala Ala Glu Gly Ala Pro Glu Asp Asp Gly
 35 40 45

 ggc ggc ggc gcc ccg gga gtg tgg ggc gct ggg gcc cct gct gaa ggt 192
 Gly Gly Gly Ala Pro Gly Val Trp Gly Ala Gly Ala Pro Ala Glu Gly
 50 55 60

490

tac cta acc att ctt taa
 Tyr Leu Thr Ile Leu *
 65

210

<210> 340
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 340
 Met Val Ser His Phe Met Gly Ser Leu Ser Val Leu Cys Phe Leu Leu
 1 5 10 15
 Leu Leu Gly Phe Gln Phe Val Cys Pro Gln Pro Ser Thr Gln His Arg
 20 25 30
 Lys Val Pro Gln Arg Met Ala Ala Glu Gly Ala Pro Glu Asp Asp Gly
 35 40 45
 Gly Gly Gly Ala Pro Gly Val Trp Gly Ala Gly Ala Pro Ala Glu Gly
 50 55 60
 Tyr Leu Thr Ile Leu
 65

<210> 341
 <211> 225
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(225)

<400> 341
 atg ccg gct aag gac aca agt tca gtg ttt gcc ctg gct tgt agc cca 48
 Met Pro Ala Lys Asp Thr Ser Ser Val Phe Ala Leu Ala Cys Ser Pro
 1 5 10 15
 gcg ggg gct ccg tca tcc cct ggg gaa tgc ctc ggc ctg caa gac cgc 96
 Ala Gly Ala Pro Ser Ser Pro Gly Glu Cys Leu Gly Leu Gln Asp Arg
 20 25 30
 ata ccg cat tgg aac agg gaa acc acc tac ttc agc acc tcc ctc agc 144
 Ile Pro His Trp Asn Arg Glu Thr Thr Tyr Phe Ser Thr Ser Leu Ser
 35 40 45

491

aag gtg gca ggt ccc aac aag cct tgc acc acg agg aag tgg cag tgg 192
Lys Val Ala Gly Pro Asn Lys Pro Cys Thr Thr Arg Lys Trp Gln Trp
50 55 60

cat tcg gga tat ggc tcc ctg gcc agc ttg tga 225
His Ser Gly Tyr Gly Ser Leu Ala Ser Leu *
65 70

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<210> 342
<211> 74
<212> PRT
<213> Homo sapiens
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<400> 342

Met Pro Ala Lys Asp Thr Ser Ser Val Phe Ala Leu Ala Cys Ser Pro
1 5 10 15
Ala Gly Ala Pro Ser Ser Pro Gly Glu Cys Leu Gly Leu Gln Asp Arg
20 25 30
Ile Pro His Trp Asn Arg Glu Thr Thr Tyr Phe Ser Thr Ser Leu Ser
35 40 45
Lys Val Ala Gly Pro Asn Lys Pro Cys Thr Thr Arg Lys Trp Gln Trp
50 55 60
His Ser Gly Tyr Gly Ser Leu Ala Ser Leu
65 70

```
<210> 343
<211> 240
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(240)
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<400> 343																
atg	tgc	atc	acg	cac	ctg	gac	cac	aaa	gac	tac	atc	ttc	ctg	ctg	ctc	48
Met	Cys	Ile	Thr	His	Leu	Asp	His	Lys	Asp	Tyr	Ile	Phe	Leu	Leu	Leu	
1				5				10					15			
atc	ggc	ttc	tgc	atc	ttc	gcc	gcg	gga	act	gtg	gct	gcc	tgg	ctc	aca	96
Ile	Gly	Phe	Cys	Ile	Phe	Ala	Ala	Gly	Thr	Val	Ala	Ala	Trp	Leu	Thr	
			20					25					30			

492

ggt gtg tgt gct gtg ctc tac cag aac acc cgc cac aag tcg agt gaa 144
 Gly Val Cys Ala Val Leu Tyr Gln Asn Thr Arg His Lys Ser Ser Glu
 35 40 45

gaa gat gag gac gag gcc ggg act agg gtg gaa gtc agc cgg cgg att 192
 Glu Asp Glu Asp Glu Ala Gly Thr Arg Val Glu Val Ser Arg Arg Ile
 50 55 60

ttt caa acc cag acg agc tcg gtc cag gag ttc cct cag ctt att tag 240
 Phe Gln Thr Gln Thr Ser Ser Val Gln Glu Phe Pro Gln Leu Ile *
 65 70 75

<210> 344

<211> 79

<212> PRT

<213> Homo sapiens

<400> 344

Met Cys Ile Thr His Leu Asp His Lys Asp Tyr Ile Phe Leu Leu Leu
 1 5 10 15
 Ile Gly Phe Cys Ile Phe Ala Ala Gly Thr Val Ala Ala Trp Leu Thr
 20 25 30
 Gly Val Cys Ala Val Leu Tyr Gln Asn Thr Arg His Lys Ser Ser Glu
 35 40 45
 Glu Asp Glu Asp Glu Ala Gly Thr Arg Val Glu Val Ser Arg Arg Ile
 50 55 60
 Phe Gln Thr Gln Thr Ser Ser Val Gln Glu Phe Pro Gln Leu Ile
 65 70 75

<210> 345

<211> 285

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(285)

<400> 345

atg act gcc aag gac tgc tcc atc atg att gca ctg tct ccc tgt ctg 48
 Met Thr Ala Lys Asp Cys Ser Ile Met Ile Ala Leu Ser Pro Cys Leu
 1 5 10 15

493

cag gat gcc agc tct gat caa agg cct gtc gtc cct tca tcg agg tcc 96
 Gln Asp Ala Ser Ser Asp Gln Arg Pro Val Val Pro Ser Ser Arg Ser
 20 25 30

agg ttt gcc ttt tcc gtg tct gtg ctg gac ctt gac ctc aag ccc tac 144
 Arg Phe Ala Phe Ser Val Ser Val Leu Asp Leu Asp Leu Lys Pro Tyr
 35 40 45

gag agc att ccc cat cag tat aaa ctg gac ggc aag atc gtc aac tat 192
 Glu Ser Ile Pro His Gln Tyr Lys Leu Asp Gly Lys Ile Val Asn Tyr
 50 55 60

tat tca aag act gta cgt gcc aaa gac aac gcc gtg atg tcg act cgg 240
 Tyr Ser Lys Thr Val Arg Ala Lys Asp Asn Ala Val Met Ser Thr Arg
 65 70 75 80

ttc aag gaa agc gaa gat tgc aca tta gtt ctc cac aag gtc taa 285
 Phe Lys Glu Ser Glu Asp Cys Thr Leu Val Leu His Lys Val *
 85 90

<210> 346

<211> 94

<212> PRT

<213> Homo sapiens

<400> 346

Met Thr Ala Lys Asp Cys Ser Ile Met Ile Ala Leu Ser Pro Cys Leu
 1 5 10 15
 Gln Asp Ala Ser Ser Asp Gln Arg Pro Val Val Pro Ser Ser Arg Ser
 20 25 30
 Arg Phe Ala Phe Ser Val Ser Val Leu Asp Leu Asp Leu Lys Pro Tyr
 35 40 45
 Glu Ser Ile Pro His Gln Tyr Lys Leu Asp Gly Lys Ile Val Asn Tyr
 50 55 60
 Tyr Ser Lys Thr Val Arg Ala Lys Asp Asn Ala Val Met Ser Thr Arg
 65 70 75 80
 Phe Lys Glu Ser Glu Asp Cys Thr Leu Val Leu His Lys Val
 85 90

<210> 347

<211> 474

<212> DNA

<213> Homo sapiens

494

<220>

<221> CDS

<222> (1)...(474)

<400> 347

atg gag gcc ctg agg agg gcc cac gag gtc gcg ctc cgc ctg ctg ctg	48
Met Glu Ala Leu Arg Arg Ala His Glu Val Ala Leu Arg Leu Leu Leu	
1 5 10 15	
tgt agg ccg tgg gcc tcg cgc gcc gcc gcc cgc ccc aag ccc agc gcc	96
Cys Arg Pro Trp Ala Ser Arg Ala Ala Ala Arg Pro Lys Pro Ser Ala	
20 25 30	
tcg gag gtg ctg acg cgg cat ctg ctg cag cgg cgc ctg ccg cac tgg	144
Ser Glu Val Leu Thr Arg His Leu Leu Gln Arg Arg Leu Pro His Trp	
35 40 45	
acc tcc ttc tgc gtg ccc tac agc gcc gtc cgc aac gac cag ttc ggc	192
Thr Ser Phe Cys Val Pro Tyr Ser Ala Val Arg Asn Asp Gln Phe Gly	
50 55 60	
ctc tcg cac ttc aac tgg ccg gtg cag ggc gcc aac tac cac gtc ctg	240
Leu Ser His Phe Asn Trp Pro Val Gln Gly Ala Asn Tyr His Val Leu	
65 70 75 80	
cgc acc ggc tgc ttc ccc ttc atc aag tac cac tgc tcc aag gct ccc	288
Arg Thr Gly Cys Phe Pro Phe Ile Lys Tyr His Cys Ser Lys Ala Pro	
85 90 95	
tgg cag gac ctg gcc cgg cag aac cgc ttc ttc acg gcg ctc aag gtc	336
Trp Gln Asp Leu Ala Arg Gln Asn Arg Phe Phe Thr Ala Leu Lys Val	
100 105 110	
gtc aac ctc ggt att cca act tta tta tat gga ctt ggc tcc tgg tta	384
Val Asn Leu Gly Ile Pro Thr Leu Leu Tyr Gly Leu Gly Ser Trp Leu	
115 120 125	
ttt gcc aga gtc aca gag act gtg cat acc agt tat gga ccc ata aca	432
Phe Ala Arg Val Thr Glu Thr Val His Thr Ser Tyr Gly Pro Ile Thr	
130 135 140	
gtt tat ttt ctc aat aaa gaa gat gaa ggt gcc atg tat tga	474
Val Tyr Phe Leu Asn Lys Glu Asp Glu Gly Ala Met Tyr *	

495

145

150

155

<210> 348
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 348

```

Met Glu Ala Leu Arg Arg Ala His Glu Val Ala Leu Arg Leu Leu Leu
 1           5           10           15
Cys Arg Pro Trp Ala Ser Arg Ala Ala Arg Pro Lys Pro Ser Ala
      20           25           30
Ser Glu Val Leu Thr Arg His Leu Leu Gln Arg Arg Leu Pro His Trp
      35           40           45
Thr Ser Phe Cys Val Pro Tyr Ser Ala Val Arg Asn Asp Gln Phe Gly
      50           55           60
Leu Ser His Phe Asn Trp Pro Val Gln Gly Ala Asn Tyr His Val Leu
65           70           75           80
Arg Thr Gly Cys Phe Pro Phe Ile Lys Tyr His Cys Ser Lys Ala Pro
      85           90           95
Trp Gln Asp Leu Ala Arg Gln Asn Arg Phe Phe Thr Ala Leu Lys Val
      100          105          110
Val Asn Leu Gly Ile Pro Thr Leu Leu Tyr Gly Leu Gly Ser Trp Leu
      115          120          125
Phe Ala Arg Val Thr Glu Thr Val His Thr Ser Tyr Gly Pro Ile Thr
      130          135          140
Val Tyr Phe Leu Asn Lys Glu Asp Glu Gly Ala Met Tyr
145           150           155

```

<210> 349
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(288)

<400> 349

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atg gcg aaa gca ctg att gtc att ttt agc agt cac tta agg cct ata
Met Ala Lys Ala Leu Ile Val Ile Phe Ser Ser His Leu Arg Pro Ile
 1           5           10           15

```

48

496

gaa ctt ttt tca agt cgg aag gtc ctg ttc tta cta tct caa aaa tgg 96
 Glu Leu Phe Ser Ser Arg Lys Val Leu Phe Leu Leu Ser Gln Lys Trp
 20 25 30

gca tcg aac aat caa tct agg agc gtg gca gtg ggt aaa atg gtg gac 144
 Ala Ser Asn Asn Gln Ser Arg Ser Val Ala Val Gly Lys Met Val Asp
 35 40 45

agg cac caa agc tat ttt ctc atc tgt cct gtg gat gag tgg aac tgt 192
 Arg His Gln Ser Tyr Phe Leu Ile Cys Pro Val Asp Glu Trp Asn Cys
 50 55 60

gga aca agt gat gtg gaa tta atg ggt gca aca gct gta cag aca atc 240
 Gly Thr Ser Asp Val Glu Leu Met Gly Ala Thr Ala Val Gln Thr Ile
 65 70 75 80

aat aac aca cac agt tct gga aag aac aca tca ctt gtg ctt gtt tga 288
 Asn Asn Thr His Ser Ser Gly Lys Asn Thr Ser Leu Val Leu Val *
 85 90 95

<210> 350

<211> 95

<212> PRT

<213> Homo sapiens

<400> 350

Met Ala Lys Ala Leu Ile Val Ile Phe Ser Ser His Leu Arg Pro Ile
 1 5 10 15
 Glu Leu Phe Ser Ser Arg Lys Val Leu Phe Leu Leu Ser Gln Lys Trp
 20 25 30
 Ala Ser Asn Asn Gln Ser Arg Ser Val Ala Val Gly Lys Met Val Asp
 35 40 45
 Arg His Gln Ser Tyr Phe Leu Ile Cys Pro Val Asp Glu Trp Asn Cys
 50 55 60
 Gly Thr Ser Asp Val Glu Leu Met Gly Ala Thr Ala Val Gln Thr Ile
 65 70 75 80
 Asn Asn Thr His Ser Ser Gly Lys Asn Thr Ser Leu Val Leu Val
 85 90 95

<210> 351

<211> 165

<212> DNA

<213> Homo sapiens

497

<220>

<221> CDS

<222> (1)...(165)

<400> 351

atg tgc tcc atc ccc cgg cat ctg ctg cca ttg gtc ctg cct gtt gcg	48
Met Cys Ser Ile Pro Arg His Leu Leu Pro Leu Val Leu Pro Val Ala	
1 5 10 15	

tta ctt ctc tgt gcc ctg gag ccc ctc aag cac aga ggc ctc gaa agg	96
Leu Leu Leu Cys Ala Leu Glu Pro Leu Lys His Arg Gly Leu Glu Arg	
20 25 30	

ttg atc aga cat cct cag cac ctg gag cgg ggc ctg gca cac aag acg	144
Leu Ile Arg His Pro Gln His Leu Glu Arg Gly Leu Ala His Lys Thr	
35 40 45	

gca atg aac ggc caa ccc tag	165
Ala Met Asn Gly Gln Pro *	
50	

<210> 352

<211> 54

<212> PRT

<213> Homo sapiens

<400> 352

Met Cys Ser Ile Pro Arg His Leu Leu Pro Leu Val Leu Pro Val Ala
1 5 10 15

Leu Leu Leu Cys Ala Leu Glu Pro Leu Lys His Arg Gly Leu Glu Arg
20 25 30

Leu Ile Arg His Pro Gln His Leu Glu Arg Gly Leu Ala His Lys Thr
35 40 45

Ala Met Asn Gly Gln Pro
50

<210> 353

<211> 159

<212> DNA

<213> Homo sapiens

<220>

498

<221> CDS

<222> (1)...(159)

<400> 353

atg tgc ttg	agg gtt ttc acc	ctg gcc ctc	agt tgc ctg	ctg tgc ggg	48
Met Cys Leu	Arg Val Phe Thr	Leu Ala Leu	Ser Cys Leu	Leu Cys Gly	
1	5	10	15		

tcc ctg ggg	cag ctg cag ggg	ctc acg gac	cca tca ggg	tct cca cag	96
Ser Leu Gly	Gln Leu Gln Gly	Leu Thr Asp	Pro Ser Gly	Ser Pro Gln	
	20	25	30		

ctc ccc tgc	agt gtg tgc acc	cca caa tgt	ctg cgg ctc	ttc ttc cgg	144
Leu Pro Cys	Ser Val Cys Thr	Pro Gln Cys	Leu Arg Leu	Phe Phe Arg	
	35	40	45		

cgt gtc ggg	ctt tga	159
Arg Val Gly	Leu *	
50		

<210> 354

<211> 52

<212> PRT

<213> Homo sapiens

<400> 354

Met Cys Leu	Arg Val Phe Thr	Leu Ala Leu	Ser Cys Leu	Leu Cys Gly
1	5	10	15	

Ser Leu Gly	Gln Leu Gln Gly	Leu Thr Asp	Pro Ser Gly	Ser Pro Gln
	20	25	30	

Leu Pro Cys	Ser Val Cys Thr	Pro Gln Cys	Leu Arg Leu	Phe Phe Arg
	35	40	45	

Arg Val Gly	Leu
50	

<210> 355

<211> 210

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(210)

499

<400> 355
 atg ggt gcc atg aac cat gat acc aac tac agc ttt cag gtt caa tgt 48
 Met Gly Ala Met Asn His Asp Thr Asn Tyr Ser Phe Gln Val Gln Cys
 1 5 10 15
 ggc tta att gtg gtg gcc tac aaa gat gga tca cct gcc cac cca cat 96
 Gly Leu Ile Val Val Ala Tyr Lys Asp Gly Ser Pro Ala His Pro His
 20 25 30
 ttc atg gat gca gag ctc tgt tcc cag tac tgg acc aag tgg ctt ctt 144
 Phe Met Asp Ala Glu Leu Cys Ser Gln Tyr Trp Thr Lys Trp Leu Leu
 35 40 45
 cga cta gaa gaa tat acg gaa aag aaa aag aac cag aat att cag aaa 192
 Arg Leu Glu Glu Tyr Thr Glu Lys Lys Lys Asn Gln Asn Ile Gln Lys
 50 55 60
 cca gaa tat tca gaa tag 210
 Pro Glu Tyr Ser Glu *
 65

<210> 356
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 356
 Met Gly Ala Met Asn His Asp Thr Asn Tyr Ser Phe Gln Val Gln Cys
 1 5 10 15
 Gly Leu Ile Val Val Ala Tyr Lys Asp Gly Ser Pro Ala His Pro His
 20 25 30
 Phe Met Asp Ala Glu Leu Cys Ser Gln Tyr Trp Thr Lys Trp Leu Leu
 35 40 45
 Arg Leu Glu Glu Tyr Thr Glu Lys Lys Lys Asn Gln Asn Ile Gln Lys
 50 55 60
 Pro Glu Tyr Ser Glu
 65

<210> 357
 <211> 243
 <212> DNA
 <213> Homo sapiens

500

<220>

<221> CDS

<222> (1)...(243)

<221> misc_feature

<222> (1)...(243)

<223> n = A,T,C or G

<400> 357

atg gtc ctg ccg gtg gca gcc tat ggn ctg atc ctg atg gcc atg ctg	48
Met Val Leu Pro Val Ala Ala Tyr Xaa Leu Ile Leu Met Ala Met Leu	
1 5 10 15	

tgg cgc ggc ctg gcc cag ggc ggg agt gcc ggc tgg ggc gcg ctg ctc	96
Trp Arg Gly Leu Ala Gln Gly Gly Ser Ala Gly Trp Gly Ala Leu Leu	
20 25 30	

ttc acg ctc tct gat ggc gtg ctg gcc tgg gac acc ttc gcc cag ccc	144
Phe Thr Leu Ser Asp Gly Val Leu Ala Trp Asp Thr Phe Ala Gln Pro	
35 40 45	

ctg ccc cat gcc cgc ctg gtg atc atg acc acc tac tat gct gcc cag	192
Leu Pro His Ala Arg Leu Val Ile Met Thr Thr Tyr Tyr Ala Ala Gln	
50 55 60	

ctc ctc atc aca ctg tca gcc ctc agg agc ccg gtg ccc aag act gac	240
Leu Leu Ile Thr Leu Ser Ala Leu Arg Ser Pro Val Pro Lys Thr Asp	
65 70 75 80	

tga	243
*	

<210> 358

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(80)

<223> Xaa = Any Amino Acid

501

<400> 358

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Met Val Leu Pro Val Ala Ala Tyr Xaa Leu Ile Leu Met Ala Met Leu
 1           5           10           15
Trp Arg Gly Leu Ala Gln Gly Gly Ser Ala Gly Trp Gly Ala Leu Leu
           20           25           30
Phe Thr Leu Ser Asp Gly Val Leu Ala Trp Asp Thr Phe Ala Gln Pro
           35           40           45
Leu Pro His Ala Arg Leu Val Ile Met Thr Thr Tyr Tyr Ala Ala Gln
           50           55           60
Leu Leu Ile Thr Leu Ser Ala Leu Arg Ser Pro Val Pro Lys Thr Asp
65           70           75           80

```

<210> 359

<211> 324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(324)

<400> 359

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atg aag agc acc tgt ggt tcc ctt gtg gcc atg agt gtt gtg gtg gga      48
Met Lys Ser Thr Cys Gly Ser Leu Val Ala Met Ser Val Val Val Gly
 1           5           10           15

cca gca tca agc gca aga gat ctg ccg agt cca cgt gga tac act atg      96
Pro Ala Ser Ser Ala Arg Asp Leu Pro Ser Pro Arg Gly Tyr Thr Met
           20           25           30

acc ccg cag acc atg aag gta gat gag gag gta atg gca ttc cgt ggt      144
Thr Pro Gln Thr Met Lys Val Asp Glu Glu Val Met Ala Phe Arg Gly
           35           40           45

gcc cga tgt gat ggc atc agg gtt ctt cct agc agc gtg gaa gac act      192
Ala Arg Cys Asp Gly Ile Arg Val Leu Pro Ser Ser Val Glu Asp Thr
           50           55           60

cct gcc ctc aag agg gct aag tcc agt aaa acc caa cca aca gga gac      240
Pro Ala Leu Lys Arg Ala Lys Ser Ser Lys Thr Gln Pro Thr Gly Asp
65           70           75           80

agt tgg gca gga aga ctc att ctg agt gta gat ggc tct ggg ttt tgt      288

```

502

Ser Trp Ala Gly Arg Leu Ile Leu Ser Val Asp Gly Ser Gly Phe Cys
 85 90 95

gag agg gtg aaa tct ttg gtc gtt aaa caa ttc tag 324
 Glu Arg Val Lys Ser Leu Val Val Lys Gln Phe *
 100 105

<210> 360
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 360
 Met Lys Ser Thr Cys Gly Ser Leu Val Ala Met Ser Val Val Val Gly
 1 5 10 15
 Pro Ala Ser Ser Ala Arg Asp Leu Pro Ser Pro Arg Gly Tyr Thr Met
 20 25 30
 Thr Pro Gln Thr Met Lys Val Asp Glu Glu Val Met Ala Phe Arg Gly
 35 40 45
 Ala Arg Cys Asp Gly Ile Arg Val Leu Pro Ser Ser Val Glu Asp Thr
 50 55 60
 Pro Ala Leu Lys Arg Ala Lys Ser Ser Lys Thr Gln Pro Thr Gly Asp
 65 70 75 80
 Ser Trp Ala Gly Arg Leu Ile Leu Ser Val Asp Gly Ser Gly Phe Cys
 85 90 95
 Glu Arg Val Lys Ser Leu Val Val Lys Gln Phe
 100 105

<210> 361
 <211> 252
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(252)

<400> 361
 atg gag gaa gga ggc ggc ggc gta cgg agt ctg gtc ccg ggc ggg ccg 48
 Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro
 1 5 10 15
 gtg tta ctg gtc ctc tgc ggc ctc ctg gag gcg tcc ggc ggc cga 96

503

Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg
 20 25 30
 gcc ctt cct caa ctc agc gat gac atc cct ttc cga gtc aac tgg ccc 144
 Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro
 35 40 45
 ggc acc gag ttc tct ctg ccc aca act gga gtt tta tat aaa gaa gat 192
 Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp
 50 55 60
 aat tat gtc atc atg aca act gca cat aaa gaa aaa tat aaa aaa aaa 240
 Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Lys Lys
 65 70 75 80
 aaa aaa aac taa 252
 Lys Lys Asn *

<210> 362
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 362
 Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro
 1 5 10 15
 Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg
 20 25 30
 Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro
 35 40 45
 Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp
 50 55 60
 Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Lys Lys
 65 70 75 80
 Lys Lys Asn

<210> 363
 <211> 459
 <212> DNA
 <213> Homo sapiens

504

 $\langle 220 \rangle$

<221> CDS

<222> (1)...(459)

<400> 363

atg gat gga aca caa cag cag att ttt aaa atg tta gca gag gta cta 48
Met Asp Gly Thr Gln Gln Gln Ile Phe Lys Met Leu Ala Glu Val Leu
1 5 10 15

gga gga atc aat tgt gta aaa gcc tcg gtt ctt acg cct tat tac cac 96
Gly Gly Ile Asn Cys Val Lys Ala Ser Val Leu Thr Pro Tyr Tyr His
20 25 30

aaa gta gat ttt gag tgt atc ttg gat aaa aga aaa aaa cct ctt ccg 144
Lys Val Asp Phe Glu Cys Ile Leu Asp Lys Arg Lys Lys Pro Leu Pro
35 40 45

tat gga agc cat aat ata gca ttg gga caa cta cca gaa atg ccc tgg 192
Tyr Gly Ser His Asn Ile Ala Leu Gly Gln Leu Pro Glu Met Pro Trp
50 55 60

gaa tca aat atc gaa ata gtt gga tca agg ctg cca cca ggg gct gaa 240
Glu Ser Asn Ile Glu Ile Val Gly Ser Arg Leu Pro Pro Gly Ala Glu
65 70 75 80

agg att gct ttg gaa ttt ttg gat tca aaa gca ctt tgt aga aat atc 288
Arg Ile Ala Leu Glu Phe Leu Asp Ser Lys Ala Leu Cys Arg Asn Ile
85 90 95

cct cac atg aaa gga aaa tct gct atg aaa aaa cga cat ttg gaa att 336
Pro His Met Lys Gly Lys Ser Ala Met Lys Lys Arg His Leu Glu Ile
100 105 110

ctg ggg tat cgt gta att cag att tcc cag ttt gaa tgg aac tct atg 384
Leu Gly Tyr Arg Val Ile Gln Ile Ser Gln Phe Glu Trp Asn Ser Met
115 120 125

gca ctg tca aca aag gat gct cgg atg gac tac ctg aga gaa tgt ata 432
Ala Leu Ser Thr Lys Asp Ala Arg Met Asp Tyr Leu Arg Glu Cys Ile
130 135 140

ttt gga gaa gtc aag tca tgt ttg tag 459
Phe Gly Glu Val Lys Ser Cys Leu *
145 150

505

<210> 364
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 364
 Met Asp Gly Thr Gln Gln Gln Ile Phe Lys Met Leu Ala Glu Val Leu
 1 5 10 15
 Gly Gly Ile Asn Cys Val Lys Ala Ser Val Leu Thr Pro Tyr Tyr His
 20 25 30
 Lys Val Asp Phe Glu Cys Ile Leu Asp Lys Arg Lys Lys Pro Leu Pro
 35 40 45
 Tyr Gly Ser His Asn Ile Ala Leu Gly Gln Leu Pro Glu Met Pro Trp
 50 55 60
 Glu Ser Asn Ile Glu Ile Val Gly Ser Arg Leu Pro Pro Gly Ala Glu
 65 70 75 80
 Arg Ile Ala Leu Glu Phe Leu Asp Ser Lys Ala Leu Cys Arg Asn Ile
 85 90 95
 Pro His Met Lys Gly Lys Ser Ala Met Lys Lys Arg His Leu Glu Ile
 100 105 110
 Leu Gly Tyr Arg Val Ile Gln Ile Ser Gln Phe Glu Trp Asn Ser Met
 115 120 125
 Ala Leu Ser Thr Lys Asp Ala Arg Met Asp Tyr Leu Arg Glu Cys Ile
 130 135 140
 Phe Gly Glu Val Lys Ser Cys Leu
 145 150

<210> 365
 <211> 600
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(600)

<400> 365
 atg gtg tgg cgc cgg ctt ctg cgg aag agg tgg gtg ctc gcc ctg gtc 48
 Met Val Trp Arg Arg Leu Leu Arg Lys Arg Trp Val Leu Ala Leu Val
 1 5 10 15
 ttc ggg ctg tcg ctc gtc tac ttc ctc agc agc acc ttc aag cag gag 96

506

Phe Gly Leu Ser Leu Val Tyr Phe Leu Ser Ser Thr Phe Lys Gln Glu	
20 25 30	
gag agg gca gtg aga gat agg aat ctc ctc cag gtt cat gac cat aat	144
Glu Arg Ala Val Arg Asp Arg Asn Leu Leu Gln Val His Asp His Asn	
35 40 45	
cag ccc atc ccg tgg aaa gtg cag ttt aac ttg ggc aat agc agt cgt	192
Gln Pro Ile Pro Trp Lys Val Gln Phe Asn Leu Gly Asn Ser Ser Arg	
50 55 60	
ccg agc aat cag tgc cgc aac tcc att caa ggg aag cac ctc atc acg	240
Pro Ser Asn Gln Cys Arg Asn Ser Ile Gln Gly Lys His Leu Ile Thr	
65 70 75 80	
gat gaa ctc ggc tac gtt tgc gag agg aag gat ttg ctg gta aat ggc	288
Asp Glu Leu Gly Tyr Val Cys Glu Arg Lys Asp Leu Leu Val Asn Gly	
85 90 95	
tgc tgt aat gtc aac gtc cct agc acg aag cag tac tgc tgt gat ggc	336
Cys Cys Asn Val Asn Val Pro Ser Thr Lys Gln Tyr Cys Cys Asp Gly	
100 105 110	
tgc tgg ccc aac ggc tgc tgc agc gcc tat gag tac tgt gtc tcc tgc	384
Cys Trp Pro Asn Gly Cys Cys Ser Ala Tyr Glu Tyr Cys Val Ser Cys	
115 120 125	
tgc ctg cag ccc aac aag caa ctt ctc ctg gag cgc ttc ctc aac cgg	432
Cys Leu Gln Pro Asn Lys Gln Leu Leu Leu Glu Arg Phe Leu Asn Arg	
130 135 140	
gca gcc gtg gca ttc cag aac ctc ttc atg gca gtc gaa gat cac ttt	480
Ala Ala Val Ala Phe Gln Asn Leu Phe Met Ala Val Glu Asp His Phe	
145 150 155 160	
gag ttg tgc ctg gcc aaa tgc agg acc tca tct cag agc gtg cag cat	528
Glu Leu Cys Leu Ala Lys Cys Arg Thr Ser Ser Gln Ser Val Gln His	
165 170 175	
gag aac acc tac cgg gac ccc ata gca aag tat tgc tat gga gaa agc	576
Glu Asn Thr Tyr Arg Asp Pro Ile Ala Lys Tyr Cys Tyr Gly Glu Ser	
180 185 190	
ccg ccc gag ctc ttc ccc gct tga	600

507

Pro Pro Glu Leu Phe Pro Ala *
195

<210> 366

<211> 199

<212> PRT

<213> Homo sapiens

<400> 366

Met Val Trp Arg Arg Leu Leu Arg Lys Arg Trp Val Leu Ala Leu Val
1 5 10 15
Phe Gly Leu Ser Leu Val Tyr Phe Leu Ser Ser Thr Phe Lys Gln Glu
20 25 30
Glu Arg Ala Val Arg Asp Arg Asn Leu Leu Gln Val His Asp His Asn
35 40 45
Gln Pro Ile Pro Trp Lys Val Gln Phe Asn Leu Gly Asn Ser Ser Arg
50 55 60
Pro Ser Asn Gln Cys Arg Asn Ser Ile Gln Gly Lys His Leu Ile Thr
65 70 75 80
Asp Glu Leu Gly Tyr Val Cys Glu Arg Lys Asp Leu Leu Val Asn Gly
85 90 95
Cys Cys Asn Val Asn Val Pro Ser Thr Lys Gln Tyr Cys Cys Asp Gly
100 105 110
Cys Trp Pro Asn Gly Cys Cys Ser Ala Tyr Glu Tyr Cys Val Ser Cys
115 120 125
Cys Leu Gln Pro Asn Lys Gln Leu Leu Leu Glu Arg Phe Leu Asn Arg
130 135 140
Ala Ala Val Ala Phe Gln Asn Leu Phe Met Ala Val Glu Asp His Phe
145 150 155 160
Glu Leu Cys Leu Ala Lys Cys Arg Thr Ser Ser Gln Ser Val Gln His
165 170 175
Glu Asn Thr Tyr Arg Asp Pro Ile Ala Lys Tyr Cys Tyr Gly Glu Ser
180 185 190
Pro Pro Glu Leu Phe Pro Ala
195

<210> 367

<211> 249

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

508

<222> (1)...(249)

<400> 367

atg agc aaa tac aag cac aag agc agc cct tta ttg cct ctt ctt atc	48
Met Ser Lys Tyr Lys His Lys Ser Ser Pro Leu Leu Pro Leu Leu Ile	
1 5 10 15	
ttt cat aat gtt tgc ttc agt cct gca aat aaa ccc aag atc ctg gct	96
Phe His Asn Val Cys Phe Ser Pro Ala Asn Lys Pro Lys Ile Leu Ala	
20 25 30	
aat gaa aaa gtc att act gtg ctt gct gcc tgt ctg gaa agt gag aat	144
Asn Glu Lys Val Ile Thr Val Leu Ala Ala Cys Leu Glu Ser Glu Asn	
35 40 45	
caa aat gct cag agg att gga gca gct gcc ctt ggc tct gat tta caa	192
Gln Asn Ala Gln Arg Ile Gly Ala Ala Ala Leu Gly Ser Asp Leu Gln	
50 55 60	
tta tca gaa ggc aaa aac agc ttt gaa aag ccc atc agt aaa aag aag	240
Leu Ser Glu Gly Lys Asn Ser Phe Glu Lys Pro Ile Ser Lys Lys Lys	
65 70 75 80	
agt gga tga	249
Ser Gly *	

<210> 368

<211> 82

<212> PRT

<213> Homo sapiens

<400> 368

Met Ser Lys Tyr Lys His Lys Ser Ser Pro Leu Leu Pro Leu Leu Ile	
1 5 10 15	
Phe His Asn Val Cys Phe Ser Pro Ala Asn Lys Pro Lys Ile Leu Ala	
20 25 30	
Asn Glu Lys Val Ile Thr Val Leu Ala Ala Cys Leu Glu Ser Glu Asn	
35 40 45	
Gln Asn Ala Gln Arg Ile Gly Ala Ala Ala Leu Gly Ser Asp Leu Gln	
50 55 60	
Leu Ser Glu Gly Lys Asn Ser Phe Glu Lys Pro Ile Ser Lys Lys Lys	
65 70 75 80	

509

Ser Gly

<210> 369
 <211> 285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(285)

<400> 369
 atg gac ggc cgc ggg gct ttc tgg aca gtg gcc att ccc aga gcc agg 48
 Met Asp Gly Arg Gly Ala Phe Trp Thr Val Ala Ile Pro Arg Ala Arg
 1 5 10 15
 cag gaa ggc ctc ggg agg ctg ggg ctc ccg ttc ccg gtg aag cgg acg 96
 Gln Glu Gly Leu Gly Arg Leu Gly Leu Pro Phe Pro Val Lys Arg Thr
 20 25 30
 ccg cca gcg ccc cag aac cca gga gga agc aca cag gcc cca cag aga 144
 Pro Pro Ala Pro Gln Asn Pro Gly Gly Ser Thr Gln Ala Pro Gln Arg
 35 40 45
 gtg gtt ggc aag agt cac tcg ggg att agg atg ccg gcc aaa tcg cgg 192
 Val Val Gly Lys Ser His Ser Gly Ile Arg Met Pro Ala Lys Ser Arg
 50 55 60
 aat ttg agg ctg gaa tcc aag ctc aac agg act gct gtg tgt gaa gca 240
 Asn Leu Arg Leu Glu Ser Lys Leu Asn Arg Thr Ala Val Cys Glu Ala
 65 70 75 80
 ctc aag agg gcc cct aca acc aac ctg cca gga gtc ggc tcc tga 285
 Leu Lys Arg Ala Pro Thr Thr Asn Leu Pro Gly Val Gly Ser *
 85 90

<210> 370
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 370

510

Met Asp Gly Arg Gly Ala Phe Trp Thr Val Ala Ile Pro Arg Ala Arg
 1 5 10 15
 Gln Glu Gly Leu Gly Arg Leu Gly Leu Pro Phe Pro Val Lys Arg Thr
 20 25 30
 Pro Pro Ala Pro Gln Asn Pro Gly Gly Ser Thr Gln Ala Pro Gln Arg
 35 40 45
 Val Val Gly Lys Ser His Ser Gly Ile Arg Met Pro Ala Lys Ser Arg
 50 55 60
 Asn Leu Arg Leu Glu Ser Lys Leu Asn Arg Thr Ala Val Cys Glu Ala
 65 70 75 80
 Leu Lys Arg Ala Pro Thr Thr Asn Leu Pro Gly Val Gly Ser
 85 90

<210> 371

<211> 249

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(249)

<400> 371

atg cgc gac tgc gac atc aac gac gac gaa ttc ctg cac ctg ccg gcg 48
 Met Arg Asp Cys Asp Ile Asn Asp Asp Glu Phe Leu His Leu Pro Ala
 1 5 10 15
 cat ttg cgg gtg gtc ggg ccc cag cag ctg cat tcc gag acc aac gag 96
 His Leu Arg Val Val Gly Pro Gln Gln Leu His Ser Glu Thr Asn Glu
 20 25 30
 cgg ctc ttc gat gag aag tac aag cct gtc gtg ctc acc gac gat cag 144
 Arg Leu Phe Asp Glu Lys Tyr Lys Pro Val Val Leu Thr Asp Asp Gln
 35 40 45
 gtg gac cag gcg ctg tgg gag gag cag gtc ttg cag aag gag aag aag 192
 Val Asp Gln Ala Leu Trp Glu Glu Gln Val Leu Gln Lys Glu Lys Lys
 50 55 60
 gac agg ctc gcc ctg agc cag gcc cac tcg ctg gtg cag gcg gag gcc 240
 Asp Arg Leu Ala Leu Ser Gln Ala His Ser Leu Val Gln Ala Glu Ala
 65 70 75 80
 ccg aga tga 249

511

Pro Arg *

<210> 372
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Arg Asp Cys Asp Ile Asn Asp Asp Glu Phe Leu His Leu Pro Ala
 1 5 10 15
 His Leu Arg Val Val Gly Pro Gln Gln Leu His Ser Glu Thr Asn Glu
 20 25 30
 Arg Leu Phe Asp Glu Lys Tyr Lys Pro Val Val Leu Thr Asp Asp Gln
 35 40 45
 Val Asp Gln Ala Leu Trp Glu Glu Gln Val Leu Gln Lys Glu Lys Lys
 50 55 60
 Asp Arg Leu Ala Leu Ser Gln Ala His Ser Leu Val Gln Ala Glu Ala
 65 70 75 80
 Pro Arg

<210> 373
 <211> 219
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(219)
 <221> misc_feature
 <222> (1)...(219)
 <223> n = A,T,C or G

<400> 373
 atg ggc cga gcg ctg ccc ccc ggg ggt cct cgg cgc cgg gcg can tta 48
 Met Gly Arg Ala Leu Pro Pro Gly Gly Pro Arg Arg Arg Ala Xaa Leu
 1 5 10 15
 nga gcg can gca gca ggc tcc att ccc ggc cgc cgc cgc tca gcc cat 96
 Xaa Ala Xaa Ala Ala Gly Ser Ile Pro Gly Arg Arg Arg Ser Ala His
 20 25 30

512

tac gca aac ctg gcg ggt cca acc aac ccc gct ctg ccg ccg ctg ctg 144
 Tyr Ala Asn Leu Ala Gly Pro Thr Asn Pro Ala Leu Pro Pro Leu Leu
 35 40 45

gaa ccc agg agg cgt gct tgc agg ctt cgg gca cta cgc ggg gct gga 192
 Glu Pro Arg Arg Arg Ala Cys Arg Leu Arg Ala Leu Arg Gly Ala Gly
 50 55 60

aat acc acg cac tgc ccc ttc gcc tag 219
 Asn Thr Thr His Cys Pro Phe Ala *
 65 70

<210> 374

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(72)

<223> Xaa = Any Amino Acid

<400> 374

Met Gly Arg Ala Leu Pro Pro Gly Gly Pro Arg Arg Arg Ala Xaa Leu
 1 5 10 15
 Xaa Ala Xaa Ala Ala Gly Ser Ile Pro Gly Arg Arg Arg Ser Ala His
 20 25 30
 Tyr Ala Asn Leu Ala Gly Pro Thr Asn Pro Ala Leu Pro Pro Leu Leu
 35 40 45
 Glu Pro Arg Arg Arg Ala Cys Arg Leu Arg Ala Leu Arg Gly Ala Gly
 50 55 60
 Asn Thr Thr His Cys Pro Phe Ala
 65 70

<210> 375

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(579)

513

<400> 375

atg gcc ccc aag ccg ggg gcc gag tgg agc aca gcc ctg tcc cat ctg	48
Met Ala Pro Lys Pro Gly Ala Glu Trp Ser Thr Ala Leu Ser His Leu	
1 5 10 15	
gtg ctg gga gtg gtg tct ctg cac gca gcc gtg agc aca gcc gag gca	96
Val Leu Gly Val Val Ser Leu His Ala Ala Val Ser Thr Ala Glu Ala	
20 25 30	
agt cga ggg gct gct gct ggc ttc ctg ctc cag gtc ttg gct gcc acc	144
Ser Arg Gly Ala Ala Ala Gly Phe Leu Leu Gln Val Leu Ala Ala Thr	
35 40 45	
acc acg ctg gcc cca ggg ctg agc aca cat gaa gac tgc ctt gct gga	192
Thr Thr Leu Ala Pro Gly Leu Ser Thr His Glu Asp Cys Leu Ala Gly	
50 55 60	
gcc tgg gtg gcc acc gtc atc ggc ctt ccc ctt ctg gcc ttc gat ttc	240
Ala Trp Val Ala Thr Val Ile Gly Leu Pro Leu Leu Ala Phe Asp Phe	
65 70 75 80	
cac tgg gtg aat ggg gac cgc tcc tct gcc aac ctg ctc ctg gga gga	288
His Trp Val Asn Gly Asp Arg Ser Ser Ala Asn Leu Leu Leu Gly Gly	
85 90 95	
ggc atg gtg ctg gca gtg gct ggc ggc cac ctc ggc cct gag ggc cgc	336
Gly Met Val Leu Ala Val Ala Gly Gly His Leu Gly Pro Glu Gly Arg	
100 105 110	
tct gtg gct ggt cag gca atg ctg ttg gtg gtc gca gtg acc atc ctc	384
Ser Val Ala Gly Gln Ala Met Leu Leu Val Val Ala Val Thr Ile Leu	
115 120 125	
att gta gct gtc ttc acg gcc aac act tat ggg atg tgg ggg ggg gcg	432
Ile Val Ala Val Phe Thr Ala Asn Thr Tyr Gly Met Trp Gly Gly Ala	
130 135 140	
atg ctg ggt gtg gca ggc ctc ctg agc cgg ctg gag gag gac agg ctg	480
Met Leu Gly Val Ala Gly Leu Leu Ser Arg Leu Glu Glu Asp Arg Leu	
145 150 155 160	
ctg ctg cta ccg aag gag gat gtc tgt cgc tgg gcc ttg gct gta ggc	528
Leu Leu Leu Pro Lys Glu Asp Val Cys Arg Trp Ala Leu Ala Val Gly	

514

165

170

175

agc tgg gct tac tgc cgg gcc ctg cat aca cag cgc ctc cag tgg gag 576
 Ser Trp Ala Tyr Cys Arg Ala Leu His Thr Gln Arg Leu Gln Trp Glu
 180 185 190

tga 579
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<210> 376
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 376

Met Ala Pro Lys Pro Gly Ala Glu Trp Ser Thr Ala Leu Ser His Leu
 1 5 10 15
 Val Leu Gly Val Val Ser Leu His Ala Ala Val Ser Thr Ala Glu Ala
 20 25 30
 Ser Arg Gly Ala Ala Ala Gly Phe Leu Leu Gln Val Leu Ala Ala Thr
 35 40 45
 Thr Thr Leu Ala Pro Gly Leu Ser Thr His Glu Asp Cys Leu Ala Gly
 50 55 60
 Ala Trp Val Ala Thr Val Ile Gly Leu Pro Leu Leu Ala Phe Asp Phe
 65 70 75 80
 His Trp Val Asn Gly Asp Arg Ser Ser Ala Asn Leu Leu Leu Gly Gly
 85 90 95
 Gly Met Val Leu Ala Val Ala Gly Gly His Leu Gly Pro Glu Gly Arg
 100 105 110
 Ser Val Ala Gly Gln Ala Met Leu Leu Val Val Ala Val Thr Ile Leu
 115 120 125
 Ile Val Ala Val Phe Thr Ala Asn Thr Tyr Gly Met Trp Gly Gly Ala
 130 135 140
 Met Leu Gly Val Ala Gly Leu Leu Ser Arg Leu Glu Glu Asp Arg Leu
 145 150 155 160
 Leu Leu Leu Pro Lys Glu Asp Val Cys Arg Trp Ala Leu Ala Val Gly
 165 170 175
 Ser Trp Ala Tyr Cys Arg Ala Leu His Thr Gln Arg Leu Gln Trp Glu
 180 185 190

<210> 377
 <211> 606

515

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(606)

<400> 377

atg acc gtg cag aga ctc gtg gcc gcg gcc gtg ctg gtg gcc ctg gtc	48
Met Thr Val Gln Arg Leu Val Ala Ala Ala Val Leu Val Ala Leu Val	
1 5 10 15	
tca ctc atc ctc aac aac gtg gcg gcc ttc acc tcc aac tgg gtg tgc	96
Ser Leu Ile Leu Asn Asn Val Ala Ala Phe Thr Ser Asn Trp Val Cys	
20 25 30	
cag acg ctg gag gat ggg cgc agg cgc agc gtg ggg ctg tgg agg tcc	144
Gln Thr Leu Glu Asp Gly Arg Arg Arg Ser Val Gly Leu Trp Arg Ser	
35 40 45	
tgc tgg ctg gtg gac agg acc cgg gga ggg ccg agc cct ggg gcc aga	192
Cys Trp Leu Val Asp Arg Thr Arg Gly Gly Pro Ser Pro Gly Ala Arg	
50 55 60	
gcc ggc cag gtg gac gca cat gac tgt gag gcg ctg ggc tgg ggc tcc	240
Ala Gly Gln Val Asp Ala His Asp Cys Glu Ala Leu Gly Trp Gly Ser	
65 70 75 80	
gag gca gcc ggc ttc cag gag tcc cga ggc acc gtc aaa ctg cag ttc	288
Glu Ala Ala Gly Phe Gln Glu Ser Arg Gly Thr Val Lys Leu Gln Phe	
85 90 95	
gac atg atg cgc gcc tgc aac ctg gtg gcc acg gcc gcg ctc acc gca	336
Asp Met Met Arg Ala Cys Asn Leu Val Ala Thr Ala Ala Leu Thr Ala	
100 105 110	
ggc cag ctc acc ttc ctc ctg ggg ctg gtg ggc ctg ccc ctg ctg tca	384
Gly Gln Leu Thr Phe Leu Leu Gly Leu Val Gly Leu Pro Leu Leu Ser	
115 120 125	
ccc gac gcc ccg tgc tgg gag gag gcc atg gcc gct gca ttc caa ctg	432
Pro Asp Ala Pro Cys Trp Glu Glu Ala Met Ala Ala Ala Phe Gln Leu	
130 135 140	

516

gcg agt ttt gtc ctg gtc atc ggg ctc gtg act ttc tac aga att ggc 480
 Ala Ser Phe Val Leu Val Ile Gly Leu Val Thr Phe Tyr Arg Ile Gly
 145 150 155 160

cca tac acc aac ctg tcc tgg tcc tgc tac ctg aac att ggc gcc tgc 528
 Pro Tyr Thr Asn Leu Ser Trp Ser Cys Tyr Leu Asn Ile Gly Ala Cys
 165 170 175

ctt ctg gcc acg ctg gcg gca gca tgc tca tct gga aca ttc tcc aca 576
 Leu Leu Ala Thr Leu Ala Ala Ala Cys Ser Ser Gly Thr Phe Ser Thr
 180 185 190

aga ggg agg act gca tgg ccc ccc ggg tga 606
 Arg Gly Arg Thr Ala Trp Pro Pro Gly *
 195 200

<210> 378

<211> 201

<212> PRT

<213> Homo sapiens

<400> 378

Met Thr Val Gln Arg Leu Val Ala Ala Ala Val Leu Val Ala Leu Val
 1 5 10 15
 Ser Leu Ile Leu Asn Asn Val Ala Ala Phe Thr Ser Asn Trp Val Cys
 20 25 30
 Gln Thr Leu Glu Asp Gly Arg Arg Arg Ser Val Gly Leu Trp Arg Ser
 35 40 45
 Cys Trp Leu Val Asp Arg Thr Arg Gly Gly Pro Ser Pro Gly Ala Arg
 50 55 60
 Ala Gly Gln Val Asp Ala His Asp Cys Glu Ala Leu Gly Trp Gly Ser
 65 70 75 80
 Glu Ala Ala Gly Phe Gln Glu Ser Arg Gly Thr Val Lys Leu Gln Phe
 85 90 95
 Asp Met Met Arg Ala Cys Asn Leu Val Ala Thr Ala Ala Leu Thr Ala
 100 105 110
 Gly Gln Leu Thr Phe Leu Leu Gly Leu Val Gly Leu Pro Leu Leu Ser
 115 120 125
 Pro Asp Ala Pro Cys Trp Glu Glu Ala Met Ala Ala Ala Phe Gln Leu
 130 135 140
 Ala Ser Phe Val Leu Val Ile Gly Leu Val Thr Phe Tyr Arg Ile Gly
 145 150 155 160
 Pro Tyr Thr Asn Leu Ser Trp Ser Cys Tyr Leu Asn Ile Gly Ala Cys

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      165      170      175
Leu Leu Ala Thr Leu Ala Ala Ala Cys Ser Ser Gly Thr Phe Ser Thr
      180      185      190
Arg Gly Arg Thr Ala Trp Pro Pro Gly
      195      200

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<220>
<221> CDS
<222> (1)...(297)

<221> misc_feature
<222> (1)...(297)
<223> n = A,T,C or G
```

<400> 379																
atg	gnc	ncg	acg	ctg	gtg	gtc	atc	tgc	aca	gca	gtc	atc	gtg	gtg	gtc	48
Met	Xaa	Xaa	Thr	Leu	Val	Val	Ile	Cys	Thr	Ala	Val	Ile	Val	Val	Val	
1				5					10					15		
<400> 96																
gcg	ttg	act	aga	aag	aaa	gcc	ctc	aga	atc	cat	tct	gtg	gaa	ggc	gac	96
Ala	Leu	Thr	Arg	Lys	Lys	Ala	Leu	Arg	Ile	His	Ser	Val	Glu	Gly	Asp	
			20					25					30			
<400> 144																
ctc	agg	aga	aaa	tca	gct	gga	cag	gag	gaa	tgg	agc	ccc	agt	gct	ccc	144
Leu	Arg	Arg	Lys	Ser	Ala	Gly	Gln	Glu	Glu	Trp	Ser	Pro	Ser	Ala	Pro	
		35					40					45				
<400> 192																
tca	ccc	cca	gga	agc	tgt	gtc	cag	gca	gaa	gct	gca	cct	gct	ggg	ctc	192
Ser	Pro	Pro	Gly	Ser	Cys	Val	Gln	Ala	Glu	Ala	Ala	Pro	Ala	Gly	Leu	
	50					55					60					
<400> 240																
tgt	gga	gag	cag	cgg	gga	gag	gac	tgt	gcc	gag	ctg	cat	gac	tac	ttc	240
Cys	Gly	Glu	Gln	Arg	Gly	Glu	Asp	Cys	Ala	Glu	Leu	His	Asp	Tyr	Phe	
65					70					75					80	
<400> 288																
aat	gtc	ctg	agt	tac	aga	agc	ctg	ggt	aac	tgc	agc	ttc	ttc	aca	gag	288
Asn	Val	Leu	Ser	Tyr	Arg	Ser	Leu	Gly	Asn	Cys	Ser	Phe	Phe	Thr	Glu	
				85					90					95		

518

act ggt tag
 Thr Gly *

297

<210> 380
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(98)
 <223> Xaa = Any Amino Acid

<400> 380
 Met Xaa Xaa Thr Leu Val Val Ile Cys Thr Ala Val Ile Val Val Val
 1 5 10 15
 Ala Leu Thr Arg Lys Lys Ala Leu Arg Ile His Ser Val Glu Gly Asp
 20 25 30
 Leu Arg Arg Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser Ala Pro
 35 40 45
 Ser Pro Pro Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala Gly Leu
 50 55 60
 Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp Tyr Phe
 65 70 75 80
 Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe Thr Glu
 85 90 95
 Thr Gly

<210> 381
 <211> 264
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(264)

<400> 381
 atg gct gtc tta gta ctt cgc ctg aca gtt gtc ctg gga ctg ctt gtc
 Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
 1 5 10 15

48

519

tta ttc ctg acc tgc tat gca gac gac aaa cca gac aag cca gac gac 96
 Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
 20 25 30

aag cca gac gac tcg ggc aaa gac cca aag cca gac ttc ccc aaa ttc 144
 Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
 35 40 45

cta agc ctc ctg ggc aca gag atc att gag aat gca gtc gag ttc atc 192
 Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala Val Glu Phe Ile
 50 55 60

ctc cgc tcc atg tcc agg agc aca gga ttt atg gaa ttt gat gat aat 240
 Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met Glu Phe Asp Asp Asn
 65 70 75 80

gaa gga aaa cat tca tca aag tga 264
 Glu Gly Lys His Ser Ser Lys *
 85

<210> 382

<211> 87

<212> PRT

<213> Homo sapiens

<400> 382

Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
 1 5 10 15
 Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
 20 25 30
 Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
 35 40 45
 Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala Val Glu Phe Ile
 50 55 60
 Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met Glu Phe Asp Asp Asn
 65 70 75 80
 Glu Gly Lys His Ser Ser Lys
 85

<210> 383

<211> 225

<212> DNA

520

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(225)

<400> 383

atg act gcc ctc acc tcc tgg cac ctg gcc tat ctc atc act tgg acc 48
Met Thr Ala Leu Thr Ser Trp His Leu Ala Tyr Leu Ile Thr Trp Thr
1 5 10 15

acc tgc ctg gcc tcc cac ctg ctg cag gct gcc ttt gag cac acg acc 96
Thr Cys Leu Ala Ser His Leu Leu Gln Ala Ala Phe Glu His Thr Thr
20 25 30

cag ctt gcc gag gcc cag gag gtt gaa ccc cag gag gtc tca ggg tct 144
Gln Leu Ala Glu Ala Gln Glu Val Glu Pro Gln Glu Val Ser Gly Ser
35 40 45

tcc ttg ctg ccc tca ctg tct gcg tcc tcg gac tca gag tct gga aca 192
Ser Leu Leu Pro Ser Leu Ser Ala Ser Ser Asp Ser Glu Ser Gly Thr
50 55 60

gtt ttg cca gag caa gaa act ccc aga gaa taa 225
Val Leu Pro Glu Gln Glu Thr Pro Arg Glu *
65 70

<210> 384

<211> 74

<212> PRT

<213> Homo sapiens

<400> 384

Met Thr Ala Leu Thr Ser Trp His Leu Ala Tyr Leu Ile Thr Trp Thr
1 5 10 15

Thr Cys Leu Ala Ser His Leu Leu Gln Ala Ala Phe Glu His Thr Thr
20 25 30

Gln Leu Ala Glu Ala Gln Glu Val Glu Pro Gln Glu Val Ser Gly Ser
35 40 45

Ser Leu Leu Pro Ser Leu Ser Ala Ser Ser Asp Ser Glu Ser Gly Thr
50 55 60

Val Leu Pro Glu Gln Glu Thr Pro Arg Glu
65 70

521

<210> 385
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(288)

<221> misc_feature
 <222> (1)...(288)
 <223> n = A,T,C or G

<400> 385

atg gcc ccc ccg cnc gcg tnc cgg tcc ccg atg tca ccn cng ncg nng	48
Met Ala Pro Pro Xaa Ala Xaa Arg Ser Pro Met Ser Xaa Xaa Xaa Xaa	
1 5 10 15	

ntg ctg ctg ctg ctg ctg ctg agt ctg gcg ctg ctg ggc gcc cgg gcc	96
Xaa Leu Leu Leu Leu Leu Ser Leu Ala Leu Leu Gly Ala Arg Ala	
20 25 30	

cgc gcc gag ccc gcc ggg agt gcc gtc ccc gcg cag agc cgc cca tgc	144
Arg Ala Glu Pro Ala Gly Ser Ala Val Pro Ala Gln Ser Arg Pro Cys	
35 40 45	

gtg gac tgc cac gcc ttc gag ttc atg cag cgc gcc ctg cag gac ctg	192
Val Asp Cys His Ala Phe Glu Phe Met Gln Arg Ala Leu Gln Asp Leu	
50 55 60	

cgg aag aca gcc tgc agc ctg gac gcg cgg acg gag acc cta ctg ctg	240
Arg Lys Thr Ala Cys Ser Leu Asp Ala Arg Thr Glu Thr Leu Leu Leu	
65 70 75 80	

cag gca gag cgc cgt gcc ctg tgt gcc tgc tgg cca gcg ggg cac tga	288
Gln Ala Glu Arg Arg Ala Leu Cys Ala Cys Trp Pro Ala Gly His *	
85 90 95	

<210> 386
 <211> 95
 <212> PRT
 <213> Homo sapiens

522

<220>

<221> VARIANT

<222> (1)...(95)

<223> Xaa = Any Amino Acid

<400> 386

Met	Ala	Pro	Pro	Xaa	Ala	Xaa	Arg	Ser	Pro	Met	Ser	Xaa	Xaa	Xaa	Xaa
1				5				10					15		
Xaa	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Leu	Gly	Ala	Arg	Ala
			20				25					30			
Arg	Ala	Glu	Pro	Ala	Gly	Ser	Ala	Val	Pro	Ala	Gln	Ser	Arg	Pro	Cys
		35				40					45				
Val	Asp	Cys	His	Ala	Phe	Glu	Phe	Met	Gln	Arg	Ala	Leu	Gln	Asp	Leu
	50					55				60					
Arg	Lys	Thr	Ala	Cys	Ser	Leu	Asp	Ala	Arg	Thr	Glu	Thr	Leu	Leu	Leu
65				70				75					80		
Gln	Ala	Glu	Arg	Arg	Ala	Leu	Cys	Ala	Cys	Trp	Pro	Ala	Gly	His	
			85					90					95		

<210> 387

<211> 351

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(351)

<400> 387

atg	aag	gga	ctc	aga	agt	ctg	gca	gca	aca	acc	ttg	gct	ctt	ttc	ctg	48
Met	Lys	Gly	Leu	Arg	Ser	Leu	Ala	Ala	Thr	Thr	Leu	Ala	Leu	Phe	Leu	
1				5					10				15			
gtg	ttt	gtt	ttc	ctg	gga	aac	tcc	agc	tgc	gct	ccg	cag	aga	ctg	ttg	96
Val	Phe	Val	Phe	Leu	Gly	Asn	Ser	Ser	Cys	Ala	Pro	Gln	Arg	Leu	Leu	
			20					25				30				
gag	aga	agg	aac	tgg	act	cct	caa	gct	atg	ctc	tac	ctg	aaa	ggg	gca	144
Glu	Arg	Arg	Asn	Trp	Thr	Pro	Gln	Ala	Met	Leu	Tyr	Leu	Lys	Gly	Ala	
			35					40				45				
cag	ggt	cgc	cgc	ttc	atc	tcc	gac	cag	agc	cgg	aga	aag	gac	ctc	tcc	192
Gln	Gly	Arg	Arg	Phe	Ile	Ser	Asp	Gln	Ser	Arg	Arg	Lys	Asp	Leu	Ser	

523

50	55	60	
gac cgg cca ctg ccg gaa aga cga agc cca aat ccc caa cta cta act			240
Asp Arg Pro Leu Pro Glu Arg Arg Ser Pro Asn Pro Gln Leu Leu Thr			
65	70	75	80
att ccg gag gca gca acc atc tta ctg gcg tcc ctt cag aaa tca cca			288
Ile Pro Glu Ala Ala Thr Ile Leu Leu Ala Ser Leu Gln Lys Ser Pro			
	85	90	95
gaa gat gaa gaa aaa aac ttt gat caa acc aga ttc ctg gaa gac agt			336
Glu Asp Glu Glu Lys Asn Phe Asp Gln Thr Arg Phe Leu Glu Asp Ser			
	100	105	110
ctg ctt aac tgg tga			351
Leu Leu Asn Trp *			
	115		

<210> 388

<211> 116

<212> PRT

<213> Homo sapiens

<400> 388

Met Lys Gly Leu Arg Ser Leu Ala Ala Thr Thr Leu Ala Leu Phe Leu			
1	5	10	15
Val Phe Val Phe Leu Gly Asn Ser Ser Cys Ala Pro Gln Arg Leu Leu			
	20	25	30
Glu Arg Arg Asn Trp Thr Pro Gln Ala Met Leu Tyr Leu Lys Gly Ala			
	35	40	45
Gln Gly Arg Arg Phe Ile Ser Asp Gln Ser Arg Arg Lys Asp Leu Ser			
	50	55	60
Asp Arg Pro Leu Pro Glu Arg Arg Ser Pro Asn Pro Gln Leu Leu Thr			
65	70	75	80
Ile Pro Glu Ala Ala Thr Ile Leu Leu Ala Ser Leu Gln Lys Ser Pro			
	85	90	95
Glu Asp Glu Glu Lys Asn Phe Asp Gln Thr Arg Phe Leu Glu Asp Ser			
	100	105	110
Leu Leu Asn Trp			
	115		

<210> 389

<211> 318

524

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(318)

<400> 389

atg aac ttg ggg gtc agc atg ctg agg atc ctc ttc ctc ctg gat gta	48
Met Asn Leu Gly Val Ser Met Leu Arg Ile Leu Phe Leu Leu Asp Val	
1 5 10 15	

gga gga gct caa gtg ctg gca aca ggc aag acc cct ggg gct gaa att	96
Gly Gly Ala Gln Val Leu Ala Thr Gly Lys Thr Pro Gly Ala Glu Ile	
20 25 30	

gat ttc aag tac gcc ctc atc ggg act gct gtg ggt gtc gcc ata tct	144
Asp Phe Lys Tyr Ala Leu Ile Gly Thr Ala Val Gly Val Ala Ile Ser	
35 40 45	

gct ggc ttc ctg gcc ctg aag atc tgc atg atc agg agg cac tta ttt	192
Ala Gly Phe Leu Ala Leu Lys Ile Cys Met Ile Arg Arg His Leu Phe	
50 55 60	

gac gac gac tct tcc gac ctg aaa agc acg cct ggg ggc ctc agt gac	240
Asp Asp Asp Ser Ser Asp Leu Lys Ser Thr Pro Gly Gly Leu Ser Asp	
65 70 75 80	

acc atc ccg cta aag aag aga gcc cca agg cga aac cac aat ttc tcc	288
Thr Ile Pro Leu Lys Lys Arg Ala Pro Arg Arg Asn His Asn Phe Ser	
85 90 95	

aaa aga gat gca cag gtg att gag ctg tag	318
Lys Arg Asp Ala Gln Val Ile Glu Leu *	
100 105	

<210> 390

<211> 105

<212> PRT

<213> Homo sapiens

<400> 390

Met Asn Leu Gly Val Ser Met Leu Arg Ile Leu Phe Leu Leu Asp Val

525

```

      1             5             10             15
Gly Gly Ala Gln Val Leu Ala Thr Gly Lys Thr Pro Gly Ala Glu Ile
      20             25             30
Asp Phe Lys Tyr Ala Leu Ile Gly Thr Ala Val Gly Val Ala Ile Ser
      35             40             45
Ala Gly Phe Leu Ala Leu Lys Ile Cys Met Ile Arg Arg His Leu Phe
      50             55             60
Asp Asp Asp Ser Ser Asp Leu Lys Ser Thr Pro Gly Gly Leu Ser Asp
      65             70             75             80
Thr Ile Pro Leu Lys Lys Arg Ala Pro Arg Arg Asn His Asn Phe Ser
      85             90             95
Lys Arg Asp Ala Gln Val Ile Glu Leu
      100             105

```

<210> 391
 <211> 150
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(150)

<221> misc_feature
 <222> (1)...(150)
 <223> n = A.T.C or G

```

      <400> 391
atg gcc atc ctc cag gtc act gcg ggc nac ccc ctg gcc atg gcc cag      48
Met Ala Ile Leu Gln Val Thr Ala Gly Xaa Pro Leu Ala Met Ala Gln
      1             5             10             15

ggc ccc cac ccc ctg gtc cac atc act gag gaa gta gaa gaa aac agg      96
Gly Pro His Pro Leu Val His Ile Thr Glu Glu Val Glu Glu Asn Arg
      20             25             30

aca caa gat ggc aag cct gag aga att gcc cag ctg acc tgg aat gag      144
Thr Gln Asp Gly Lys Pro Glu Arg Ile Ala Gln Leu Thr Trp Asn Glu
      35             40             45

gcc taa      150
Ala *

```

526

<210> 392
 <211> 49
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(49)
 <223> Xaa = Any Amino Acid

<400> 392
 Met Ala Ile Leu Gln Val Thr Ala Gly Xaa Pro Leu Ala Met Ala Gln
 1 5 10 15
 Gly Pro His Pro Leu Val His Ile Thr Glu Glu Val Glu Glu Asn Arg
 20 25 30
 Thr Gln Asp Gly Lys Pro Glu Arg Ile Ala Gln Leu Thr Trp Asn Glu
 35 40 45
 Ala

<210> 393
 <211> 294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(294)

<400> 393
 atg gat cct gag gtg acc ttg ctg ctg cag tgc cct ggc ggg ggc ctg 48
 Met Asp Pro Glu Val Thr Leu Leu Leu Gln Cys Pro Gly Gly Gly Leu
 1 5 10 15
 ccc cag gag cag ata cag gcc gag ctg agc ccc gcc cat gac cgt cgc 96
 Pro Gln Glu Gln Ile Gln Ala Glu Leu Ser Pro Ala His Asp Arg Arg
 20 25 30
 cca ctg cca ggt ggg gac gag gcc atc act gcc atc tgg gag acc cgg 144
 Pro Leu Pro Gly Gly Asp Glu Ala Ile Thr Ala Ile Trp Glu Thr Arg
 35 40 45
 cta aag gcc caa ccc tgg ctc ttc gac gcc ccc aag ttc cgc ctg cac 192

527

Leu	Lys	Ala	Gln	Pro	Trp	Leu	Phe	Asp	Ala	Pro	Lys	Phe	Arg	Leu	His	
50					55					60						
tca	gcc	acc	ctg	gcg	cct	att	ggc	tct	cgg	ggg	cca	cag	ctg	ctc	ctg	240
Ser	Ala	Thr	Leu	Ala	Pro	Ile	Gly	Ser	Arg	Gly	Pro	Gln	Leu	Leu	Leu	
65				70				75					80			
cgc	ctg	ggc	ctt	act	tcc	tgc	cga	gtt	cta	tgt	cca	gtg	cag	cct	gac	288
Arg	Leu	Gly	Leu	Thr	Ser	Cys	Arg	Val	Leu	Cys	Pro	Val	Gln	Pro	Asp	
			85					90					95			
ttc	tga															294
Phe	*															

<210> 394
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 394

Met	Asp	Pro	Glu	Val	Thr	Leu	Leu	Leu	Gln	Cys	Pro	Gly	Gly	Gly	Leu	
1			5					10					15			
Pro	Gln	Glu	Gln	Ile	Gln	Ala	Glu	Leu	Ser	Pro	Ala	His	Asp	Arg	Arg	
	20						25					30				
Pro	Leu	Pro	Gly	Gly	Asp	Glu	Ala	Ile	Thr	Ala	Ile	Trp	Glu	Thr	Arg	
	35					40					45					
Leu	Lys	Ala	Gln	Pro	Trp	Leu	Phe	Asp	Ala	Pro	Lys	Phe	Arg	Leu	His	
50					55					60						
Ser	Ala	Thr	Leu	Ala	Pro	Ile	Gly	Ser	Arg	Gly	Pro	Gln	Leu	Leu	Leu	
65				70				75					80			
Arg	Leu	Gly	Leu	Thr	Ser	Cys	Arg	Val	Leu	Cys	Pro	Val	Gln	Pro	Asp	
			85					90					95			

Phe

<210> 395
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

528

<222> (1)...(303)

<400> 395

atg	cga	caa	gtt	ttt	ggt	gat	gag	aag	aag	tac	tgg	ttg	cta	ccc	att	48
Met	Arg	Gln	Val	Phe	Gly	Asp	Glu	Lys	Lys	Tyr	Trp	Leu	Leu	Pro	Ile	
1			5					10					15			

ttt	tca	agt	cta	ggt	gat	ggc	tgc	tcc	ttt	cca	act	tgc	ctt	ggt	aac	96
Phe	Ser	Ser	Leu	Gly	Asp	Gly	Cys	Ser	Phe	Pro	Thr	Cys	Leu	Val	Asn	
			20				25						30			

cag	gat	cct	gaa	caa	gca	tct	act	cct	gca	ggg	ctg	aat	tcc	aca	gct	144
Gln	Asp	Pro	Glu	Gln	Ala	Ser	Thr	Pro	Ala	Gly	Leu	Asn	Ser	Thr	Ala	
			35				40						45			

aaa	aat	ctc	gaa	aac	cat	cag	ttt	cct	gca	aag	cca	ttg	aga	gag	tcc	192
Lys	Asn	Leu	Glu	Asn	His	Gln	Phe	Pro	Ala	Lys	Pro	Leu	Arg	Glu	Ser	
			50				55					60				

cag	agc	cac	ctt	ctt	act	gat	tct	cag	tct	tgg	acg	gag	agc	agc	ata	240
Gln	Ser	His	Leu	Leu	Thr	Asp	Ser	Gln	Ser	Trp	Thr	Glu	Ser	Ser	Ile	
			65				70				75				80	

aac	cca	gga	aaa	tgc	aaa	gct	ggt	atg	agc	aat	cct	gca	tta	acc	atg	288
Asn	Pro	Gly	Lys	Cys	Lys	Ala	Gly	Met	Ser	Asn	Pro	Ala	Leu	Thr	Met	
				85				90						95		

gaa	aat	gag	act	taa												303
Glu	Asn	Glu	Thr	*												
					100											

<210> 396

<211> 100

<212> PRT

<213> Homo sapiens

<400> 396

Met	Arg	Gln	Val	Phe	Gly	Asp	Glu	Lys	Lys	Tyr	Trp	Leu	Leu	Pro	Ile	
1			5					10					15			
Phe	Ser	Ser	Leu	Gly	Asp	Gly	Cys	Ser	Phe	Pro	Thr	Cys	Leu	Val	Asn	
			20				25						30			
Gln	Asp	Pro	Glu	Gln	Ala	Ser	Thr	Pro	Ala	Gly	Leu	Asn	Ser	Thr	Ala	
			35				40						45			

529

Lys Asn Leu Glu Asn His Gln Phe Pro Ala Lys Pro Leu Arg Glu Ser
 50 55 60
 Gln Ser His Leu Leu Thr Asp Ser Gln Ser Trp Thr Glu Ser Ser Ile
 65 70 75 80
 Asn Pro Gly Lys Cys Lys Ala Gly Met Ser Asn Pro Ala Leu Thr Met
 85 90 95
 Glu Asn Glu Thr
 100

<210> 397
 <211> 141
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(141)

<400> 397
 atg ctc tcc ttc ctg ccc ttc ctg gtg ctg ctg gtt ttc atc agg aac 48
 Met Leu Ser Phe Leu Pro Phe Leu Val Leu Leu Val Phe Ile Arg Asn
 1 5 10 15
 ctc cga gcc ctg tcc atc ttc tcc ctg ttg gcc aac atc acc atg ctg 96
 Leu Arg Ala Leu Ser Ile Phe Ser Leu Leu Ala Asn Ile Thr Met Leu
 20 25 30
 gtc agc ttg gtc atg atc tac cag ttc att gtt cag atc ctg tga 141
 Val Ser Leu Val Met Ile Tyr Gln Phe Ile Val Gln Ile Leu *
 35 40 45

<210> 398
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 398
 Met Leu Ser Phe Leu Pro Phe Leu Val Leu Leu Val Phe Ile Arg Asn
 1 5 10 15
 Leu Arg Ala Leu Ser Ile Phe Ser Leu Leu Ala Asn Ile Thr Met Leu
 20 25 30
 Val Ser Leu Val Met Ile Tyr Gln Phe Ile Val Gln Ile Leu
 35 40 45

530

<210> 399
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(360)

<400> 399
 atg cag agc agc cac gcc tac tgc aca cct ctc aat gca gct tta cag 48
 Met Gln Ser Ser His Ala Tyr Cys Thr Pro Leu Asn Ala Ala Leu Gln
 1 5 10 15
 gct tca atg gct gag aat agt ata cct cta tac act acc gct tcc atg 96
 Ala Ser Met Ala Glu Asn Ser Ile Pro Leu Tyr Thr Thr Ala Ser Met
 20 25 30
 gga aat ccc act ctg ggc aac tta gcc agc gca ata cgg gaa gag ctg 144
 Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser Ala Ile Arg Glu Glu Leu
 35 40 45
 aac ggg gca atg gag cat acc aac agc aac gag agt gac agc agt cca 192
 Asn Gly Ala Met Glu His Thr Asn Ser Asn Glu Ser Asp Ser Ser Pro
 50 55 60
 ggc aga tct cct atg caa gcc gtg cat cct gta cac gtc aaa gaa gag 240
 Gly Arg Ser Pro Met Gln Ala Val His Pro Val His Val Lys Glu Glu
 65 70 75 80
 ccc ctc gat cca gag gaa gct gaa ggg ccc ctg tcc tta gtg aca aca 288
 Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro Leu Ser Leu Val Thr Thr
 85 90 95
 gcc aac cac agt cca gat ttt gac cat gac aga gat tac gaa gat gaa 336
 Ala Asn His Ser Pro Asp Phe Asp His Asp Arg Asp Tyr Glu Asp Glu
 100 105 110
 cca gta aac gag gac atg gag tga 360
 Pro Val Asn Glu Asp Met Glu *
 115

531

<210> 400
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 400
 Met Gln Ser Ser His Ala Tyr Cys Thr Pro Leu Asn Ala Ala Leu Gln
 1 5 10 15
 Ala Ser Met Ala Glu Asn Ser Ile Pro Leu Tyr Thr Thr Ala Ser Met
 20 25 30
 Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser Ala Ile Arg Glu Glu Leu
 35 40 45
 Asn Gly Ala Met Glu His Thr Asn Ser Asn Glu Ser Asp Ser Ser Pro
 50 55 60
 Gly Arg Ser Pro Met Gln Ala Val His Pro Val His Val Lys Glu Glu
 65 70 75 80
 Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro Leu Ser Leu Val Thr Thr
 85 90 95
 Ala Asn His Ser Pro Asp Phe Asp His Asp Arg Asp Tyr Glu Asp Glu
 100 105 110
 Pro Val Asn Glu Asp Met Glu
 115

<210> 401
 <211> 474
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(474)

<400> 401
 atg tcg aaa agc tgt gga aat aat tta gcg gcc att tct gta gga att 48
 Met Ser Lys Ser Cys Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile
 1 5 10 15
 tcg ctt ctt tta ctc tta gtg gtt tgt gga att ggg tgt gtt tgg cac 96
 Ser Leu Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His
 20 25 30
 tgg aaa cac cgt gtt gcc aca cga ttt acc tta ccg agg ttt tta caa 144
 Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln
 35 40 45

532

agg aga agc agc agg aga aaa gtc tgt act aaa aca ttc ttg ggc ccc 192
 Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro
 50 55 60

cgc atc att ggc tta agg cat gaa atc tca gtt gaa acc caa gac cac 240
 Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His
 65 70 75 80

aaa tct gct gtc agg gga aat aac aca cac gac aac tat gaa aat gtg 288
 Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val
 85 90 95

gaa gca ggt cct ccc aaa gct aaa gga aaa acc gat aag gaa cta tat 336
 Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr
 100 105 110

gaa aac aca ggg cag tct aat ttc gag gag cat atc tat gga aat gag 384
 Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu
 115 120 125

aca tct tct gac tat tat aac ttc cag aag cct cgt cct tct gaa gtt 432
 Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val
 130 135 140

cct caa gat gaa gat ata tac att ctt cca gat tca tat tag 474
 Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr *
 145 150 155

<210> 402

<211> 157

<212> PRT

<213> Homo sapiens

<400> 402

Met Ser Lys Ser Cys Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile
 1 5 10 15
 Ser Leu Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His
 20 25 30
 Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln
 35 40 45
 Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro
 50 55 60

533

Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His
 65 70 75 80
 Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val
 85 90 95
 Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr
 100 105 110
 Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu
 115 120 125
 Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val
 130 135 140
 Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr
 145 150 155

<210> 403

<211> 279

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(279)

<400> 403

atg tgg cct gtg ttt tgg acc gtg gtt cgt acc tat gct cct tat gtc	48
Met Trp Pro Val Phe Trp Thr Val Val Arg Thr Tyr Ala Pro Tyr Val	
1 5 10 15	
aca ttc cct gtt gcc ttc gtg gtc ggg gct gtg ggt tac cac ctg gaa	96
Thr Phe Pro Val Ala Phe Val Val Gly Ala Val Gly Tyr His Leu Glu	
20 25 30	
tgg ttc atc agg gga aag gac ccc cag ccc gtg gag gag gaa aag agc	144
Trp Phe Ile Arg Gly Lys Asp Pro Gln Pro Val Glu Glu Glu Lys Ser	
35 40 45	
atc tca gag cgc cgg gag gat cgc aag ctg gat gag ctt cta ggc aag	192
Ile Ser Glu Arg Arg Glu Asp Arg Lys Leu Asp Glu Leu Leu Gly Lys	
50 55 60	
gac cac acg cag gtg gtg agc ctt aag gac aag cta gaa ttt gcc ccg	240
Asp His Thr Gln Val Val Ser Leu Lys Asp Lys Leu Glu Phe Ala Pro	
65 70 75 80	
aaa gct gtg ctg aac aga aac cgc cca gag aag aat taa	279

534

Lys Ala Val Leu Asn Arg Asn Arg Pro Glu Lys Asn *
 85 90

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 <211> 92
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 <213> Homo sapiens

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 Trp Phe Ile Arg Gly Lys Asp Pro Gln Pro Val Glu Glu Glu Lys Ser
 35 40 45
 Ile Ser Glu Arg Arg Glu Asp Arg Lys Leu Asp Glu Leu Leu Gly Lys
 50 55 60
 Asp His Thr Gln Val Val Ser Leu Lys Asp Lys Leu Glu Phe Ala Pro
 65 70 75 80
 Lys Ala Val Leu Asn Arg Asn Arg Pro Glu Lys Asn
 85 90

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<220>
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 cag cct aaa agg cga cgg cgg att gac aga agt atg att gga gag ccc 96
 Gln Pro Lys Arg Arg Arg Arg Ile Asp Arg Ser Met Ile Gly Glu Pro
 20 25 30
 aca aac ttt gtg cat aca gct cat gtt gga tca gga gac ctg ttc agt 144
 Thr Asn Phe Val His Thr Ala His Val Gly Ser Gly Asp Leu Phe Ser
 35 40 45

535

gga atg aat tca gtt agc tcc att cag aac caa atg cag tcc aag gga 192
 Gly Met Asn Ser Val Ser Ser Ile Gln Asn Gln Met Gln Ser Lys Gly
 50 55 60

ggt tat gga ggt gga atg cct gcc aat gtc cag atg cag ctc gtg gat 240
 Gly Tyr Gly Gly Gly Met Pro Ala Asn Val Gln Met Gln Leu Val Asp
 65 70 75 80

acg aag gcg gga tag 255
 Thr Lys Ala Gly *

<210> 406
 <211> 84
 <212> PRT
 <213> Homo sapiens

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 35 40 45
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 65 70 75 80
 Thr Lys Ala Gly

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 <212> DNA
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<220>
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536

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 20 25 30

aga att ttg aat act ggc tta gat atg gaa act ctg tct att tgt gta 144
 Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu Ser Ile Cys Val
 35 40 45

cgg ctt tgt gaa caa gga att aac cca gaa gct tta tca tcg gtt att 192
 Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu Ser Ser Val Ile
 50 55 60

aag gag ctt cgc aag gct act gaa gca ctg aag gct gct gaa aat atg 240
 Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala Ala Glu Asn Met
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aca agc tga 249
 Thr Ser *
 249

<210> 408
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 408

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Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu Leu Glu Ile Ser
 20 25 30

Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu Ser Ile Cys Val
 35 40 45

Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu Ser Ser Val Ile
 50 55 60

Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala Ala Glu Asn Met
 65 70 75 80

Thr Ser

<210> 409

537

<211> 156
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 1 5 10 15
 ctc ctg ggt gct gcc aca gag aag aga gag aga gtg aag cgg gca gag 96
 Leu Leu Gly Ala Ala Thr Glu Lys Arg Glu Arg Val Lys Arg Ala Glu
 20 25 30
 act ggc tgt tgc cat cac aca act gag ggc gga cct gga gct cac cgg 144
 Thr Gly Cys Cys His His Thr Thr Glu Gly Gly Pro Gly Ala His Arg
 35 40 45
 ctg agg gtt tga 156
 Leu Arg Val *
 50

<210> 410
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 410
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 Thr Gly Cys Cys His His Thr Thr Glu Gly Gly Pro Gly Ala His Arg
 35 40 45
 Leu Arg Val
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<210> 411
 <211> 420
 <212> DNA

538

<213> Homo sapiens

<220>

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<222> (1)...(420)

<221> misc_feature

<222> (1)...(420)

<223> n = A,T,C or G

<400> 411

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Met	His	Val	Thr	Glu	Ala	Leu	His	Gln	Asn	Met	Gln	Ala	Leu	Phe	Ser	
1				5				10						15		

acc	ctg	gct	cag	gcg	gag	gag	cag	cag	ccc	tac	ctg	gag	ggc	tcc	acc	96
Thr	Leu	Ala	Gln	Ala	Glu	Glu	Gln	Gln	Pro	Tyr	Leu	Glu	Gly	Ser	Thr	
			20				25						30			

gtt	atg	cgc	ggg	act	cgc	tgt	ctg	gca	gag	tac	cac	ctg	ggg	gat	tat	144
Val	Met	Arg	Gly	Thr	Arg	Cys	Leu	Ala	Glu	Tyr	His	Leu	Gly	Asp	Tyr	
		35					40					45				

gga	cac	gcc	tgg	aac	agg	tgt	tgg	gtg	ctg	gac	agg	gtg	gac	acc	tgg	192
Gly	His	Ala	Trp	Asn	Arg	Cys	Trp	Val	Leu	Asp	Arg	Val	Asp	Thr	Trp	
		50				55					60					

gct	gtg	gtc	atg	ttc	att	gat	ttt	gga	cag	ttg	gcc	acc	atc	cct	gtg	240
Ala	Val	Val	Met	Phe	Ile	Asp	Phe	Gly	Gln	Leu	Ala	Thr	Ile	Pro	Val	
65					70					75				80		

cag	tct	ctg	cgc	anc	tna	gac	agc	gac	gac	ttc	tgg	acc	atc	cca	ccc	288
Gln	Ser	Leu	Arg	Xaa	Xaa	Asp	Ser	Asp	Asp	Phe	Trp	Thr	Ile	Pro	Pro	
				85					90					95		

ctg	act	cag	cca	ttc	atg	ctg	gag	aaa	gac	att	ttg	agt	tcg	tat	gag	336
Leu	Thr	Gln	Pro	Phe	Met	Leu	Glu	Lys	Asp	Ile	Leu	Ser	Ser	Tyr	Glu	
			100					105					110			

gtt	gtc	cat	cga	atc	ctc	aaa	ggg	aaa	atc	act	ggt	gct	ttg	aac	tcg	384
Val	Val	His	Arg	Ile	Leu	Lys	Gly	Lys	Ile	Thr	Gly	Ala	Leu	Asn	Ser	
			115				120					125				

gcg	ttg	cac	atc	cta	aag	ttt	gaa	gag	tct	aaa	taa					420
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539

Ala Leu His Ile Leu Lys Phe Glu Glu Ser Lys *
 130 135

<210> 412
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
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 1 5 10 15
 Thr Leu Ala Gln Ala Glu Glu Gln Gln Pro Tyr Leu Glu Gly Ser Thr
 20 25 30
 Val Met Arg Gly Thr Arg Cys Leu Ala Glu Tyr His Leu Gly Asp Tyr
 35 40 45
 Gly His Ala Trp Asn Arg Cys Trp Val Leu Asp Arg Val Asp Thr Trp
 50 55 60
 Ala Val Val Met Phe Ile Asp Phe Gly Gln Leu Ala Thr Ile Pro Val
 65 70 75 80
 Gln Ser Leu Arg Xaa Xaa Asp Ser Asp Asp Phe Trp Thr Ile Pro Pro
 85 90 95
 Leu Thr Gln Pro Phe Met Leu Glu Lys Asp Ile Leu Ser Ser Tyr Glu
 100 105 110
 Val Val His Arg Ile Leu Lys Gly Lys Ile Thr Gly Ala Leu Asn Ser
 115 120 125
 Ala Leu His Ile Leu Lys Phe Glu Glu Ser Lys
 130 135

<210> 413
 <211> 795
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(795)

<400> 413

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1 5 10 15	
ctc cta atg cca gca gta tct gtt gga aat gtt ggc cag ctt gca atg	96
Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala Met	
20 25 30	
gat ctg att att tct aca ctg aat atg tct aag att ggt tac ttc tat	144
Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe Tyr	
35 40 45	
acc gat tgt ctt gtg cca atg gtt gga aac aat cca tat gcg acc aca	192
Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr	
50 55 60	
gaa gga aat tca aca gaa ctt agc ata aat gct gaa gtg tat tca ttg	240
Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu	
65 70 75 80	
cct tca aga aag ctg gtg gct cta cag tta aga tcc att ttt att aag	288
Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys	
85 90 95	
tat aaa tca aag cca ttc tgt gaa aaa ctg ctt tcc tgg gtg aaa agc	336
Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser	
100 105 110	
agt ggc tgt gcc aga gtc att gtt ctt tca agc agt cat tca tat cag	384
Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln	
115 120 125	
cgt aat gat ctg cag ctt cgt agt act ccc ttc cgg tac cta ctt aca	432
Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr	
130 135 140	
cct tcc atg caa aaa agt gtt caa aat aaa ata aag agc ctt aac tgg	480
Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn Trp	
145 150 155 160	
gaa gaa atg gaa aaa agc cgg tgc att cct gaa ata gat gat tcc gag	528
Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser Glu	
165 170 175	

541

ttt tgt atc cgc att ccg gga gga ggt atc aca aaa aca ctc tat gat 576
 Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr Asp
 180 185 190

gaa agc tgt tct aaa gaa atc caa atg gca gtt ctg ctg aaa ttt gtt 624
 Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe Val
 195 200 205

tca gaa ggg gac aac atc cca gat gca tta ggt ctt gtt gag tat ctt 672
 Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr Leu
 210 215 220

aat gag tgg ctt cag ata ctc aaa cca ctt agc gat gac ccc aca gta 720
 Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr Val
 225 230 235 240

tct gcc tca cgg tgg aaa ata cca agt tct tgg aga tta ctc ttt ggc 768
 Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe Gly
 245 250 255

agt ggt ctt ccc cct gca ctt ttc tga 795
 Ser Gly Leu Pro Pro Ala Leu Phe *
 260

<210> 414

<211> 264

<212> PRT

<213> Homo sapiens

<400> 414

Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe Thr
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 Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala Met
 20 25 30
 Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe Tyr
 35 40 45
 Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr
 50 55 60
 Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu
 65 70 75 80
 Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys
 85 90 95
 Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser

542

100 105 110
 Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln
 115 120 125
 Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr
 130 135 140
 Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn Trp
 145 150 155 160
 Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser Glu
 165 170 175
 Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr Asp
 180 185 190
 Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe Val
 195 200 205
 Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr Leu
 210 215 220
 Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr Val
 225 230 235 240
 Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe Gly
 245 250 255
 Ser Gly Leu Pro Pro Ala Leu Phe
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<211> 225

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(225)

<400> 415

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 Met Gly Lys Leu Phe Trp Ile Ile Gln Met Asp Cys Val Gln Ser Gln
 1 5 10 15
 gag ctc tta aaa gca gag acg ctt tcc cag ctt ggg tca gag aga ttc 96
 Glu Leu Leu Lys Ala Glu Thr Leu Ser Gln Leu Gly Ser Glu Arg Phe
 20 25 30
 atc atg aga aga tct cca cta gct gtt gct gga ttt cag gat gga gga 144
 Ile Met Arg Arg Ser Pro Leu Ala Val Ala Gly Phe Gln Asp Gly Gly
 35 40 45

544

aaa gag ttg aat gag aaa caa cca tct tta tct ttt ggt ctt gct ata 144
 Lys Glu Leu Asn Glu Lys Gln Pro Ser Leu Ser Phe Gly Leu Ala Ile
 35 40 45

ctt cat ctg ttc tct gca gac atg aaa aaa gtt ggc att aag cta ctt 192
 Leu His Leu Phe Ser Ala Asp Met Lys Lys Val Gly Ile Lys Leu Leu
 50 55 60

caa gaa atc aat aaa ggt ggg ata gat gca gta gaa agt ctt atg ata 240
 Gln Glu Ile Asn Lys Gly Gly Ile Asp Ala Val Glu Ser Leu Met Ile
 65 70 75 80

aat gat tcc ttt tgc tcc ata gaa aag tgg caa gaa gtg gca aat ata 288
 Asn Asp Ser Phe Cys Ser Ile Glu Lys Trp Gln Glu Val Ala Asn Ile
 85 90 95

tgt tca cag aat ggc ttt gac aaa tta tct aat gac atc acg tct att 336
 Cys Ser Gln Asn Gly Phe Asp Lys Leu Ser Asn Asp Ile Thr Ser Ile
 100 105 110

ctt cga tct cag gct gca gtt aca gaa att tct gaa gag gat gac gca 384
 Leu Arg Ser Gln Ala Ala Val Thr Glu Ile Ser Glu Glu Asp Asp Ala
 115 120 125

gtc aac cta atg gaa cat gtg ttt tgg tag 414
 Val Asn Leu Met Glu His Val Phe Trp *
 130 135

<210> 418

<211> 137

<212> PRT

<213> Homo sapiens

<400> 418

Met Glu Tyr Ile Gln Gln Leu Lys Asp Phe Thr Thr Asp Asp Leu Leu
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Gln Leu Leu Met Ser Cys Pro Gln Val Glu Leu Ile Gln Cys Leu Thr
 20 25 30

Lys Glu Leu Asn Glu Lys Gln Pro Ser Leu Ser Phe Gly Leu Ala Ile
 35 40 45

Leu His Leu Phe Ser Ala Asp Met Lys Lys Val Gly Ile Lys Leu Leu
 50 55 60

Gln Glu Ile Asn Lys Gly Gly Ile Asp Ala Val Glu Ser Leu Met Ile

545

65	70								75						80	
Asn	Asp	Ser	Phe	Cys	Ser	Ile	Glu	Lys	Trp	Gln	Glu	Val	Ala	Asn	Ile	
				85					90					95		
Cys	Ser	Gln	Asn	Gly	Phe	Asp	Lys	Leu	Ser	Asn	Asp	Ile	Thr	Ser	Ile	
			100					105					110			
Leu	Arg	Ser	Gln	Ala	Ala	Val	Thr	Glu	Ile	Ser	Glu	Glu	Asp	Asp	Ala	
		115					120					125				
Val	Asn	Leu	Met	Glu	His	Val	Phe	Trp								
	130					135										

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<210> 419
<211> 285
<212> DNA
<213> Homo sapiens
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<220>
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<222> (1)...(285)

<400> 419

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1 5 10 15

cgt gat gtt cat ttt ggt ttt cta agc gag agg ctc cga gcc ttc caa 96
Arg Asp Val His Phe Gly Phe Leu Ser Glu Arg Leu Arg Ala Phe Gln
20 25 30

cct ctg act ggc tgg tcc tgt gag acc cct cga tca ggg atg ctg ctg 144
Pro Leu Thr Gly Trp Ser Cys Glu Thr Pro Arg Ser Gly Met Leu Leu
35 40 45

caa gtg gtc atg gca gtt gct gac acc tct gcg aag gcc gtg gag acc 192
Gln Val Val Met Ala Val Ala Asp Thr Ser Ala Lys Ala Val Glu Thr
50 55 60

gtg aag aag cag caa ggc gag cag atc tgc tgg ggt ggc agc agc tcc 240
Val Lys Lys Gln Gln Gly Glu Gln Ile Cys Trp Gly Gly Ser Ser Ser
65 70 75 80

gtc atg agt cta gct acc aag atg aat gaa cta atg gag aaa tag 285
Val Met Ser Leu Ala Thr Lys Met Asn Glu Leu Met Glu Lys *
85 90

546

<210> 420
 <211> 94
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Pro Leu Thr Gly Trp Ser Cys Glu Thr Pro Arg Ser Gly Met Leu Leu
 35 40 45
 Gln Val Val Met Ala Val Ala Asp Thr Ser Ala Lys Ala Val Glu Thr
 50 55 60
 Val Lys Lys Gln Gln Gly Glu Gln Ile Cys Trp Gly Gly Ser Ser Ser
 65 70 75 80
 Val Met Ser Leu Ala Thr Lys Met Asn Glu Leu Met Glu Lys
 85 90

<210> 421
 <211> 240
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(240)

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 Met Gln Gly Arg Leu Glu Leu Val Gly Arg Gly Cys Arg Pro Leu Ser
 1 5 10 15
 tgg gtg tgc tgg gag cca ggg atc act ggg tgc cgg cca cag agg aag 96
 Trp Val Cys Trp Glu Pro Gly Ile Thr Gly Cys Arg Pro Gln Arg Lys
 20 25 30
 gtc cct gag gac aca gta ccg aag tct gat ccc aga gga gga agg aag 144
 Val Pro Glu Asp Thr Val Pro Lys Ser Asp Pro Arg Gly Gly Arg Lys
 35 40 45
 gtg ggc cgg gga gaa ggt ctg agt gca ggg atg gtc cag gag gag gac 192
 Val Gly Arg Gly Glu Gly Leu Ser Ala Gly Met Val Gln Glu Glu Asp

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(19) World Intellectual Property Organization
International Bureau



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15/19, C07K 14/47, 14/705, 14/52, C12N 1/21, C07K
16/18, 16/24, 16/28, C12N 5/10

(21) International Application Number: PCT/US00/29052

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(71) Applicant: **ZYMOGENETICS, INC.** [US/US]: 1201
Eastlake Avenue East, Seattle, WA 98102 (US).

(72) Inventors: **CONKLIN, Darrell, C.**: 117 East Louisa
Street, #421, Seattle, WA 98102 (US). **YEE, David, P.**:
116 Henry Street, Cambridge, MA 02139 (US).

(74) Agent: **PARKER, Gary, E.**: ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE,
DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,
ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
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patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,
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Published:
— with international search report

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WO 01/29221 A3

(54) Title: PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract: The present invention provides polynucleotides and secreted proteins encoded by the polynucleotides. The proteins include a variety of fusion proteins, including fusions comprising a signal peptide selected from the group consisting of signal peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide. The invention further provides therapeutic and diagnostic methods utilizing the polynucleotides, polypeptides, and antagonists of the polypeptides.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/29052

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/19 C07K14/47 C07K14/705 C07K14/52
C12N1/21 C07K16/18 C07K16/24 C07K16/28 C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, EMBL, WPI Data, BIOSIS, STRAND

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 31117 A (FLORENCE KIMBERLY ; HUMAN GENOME SCIENCES INC (US); FENG PING (US);) 24 June 1999 (1999-06-24) Sequences ID no.54 and ID no.168 claims	1,3,5,6
X	--- DATABASE EMBL [Online] HSM800805, accession number AL110160, 30 August 1999 (1999-08-30) A. DUESTERHOEF ET AL: "Homo sapiens mRNA; cDNA DKFZp586G1624" XP002165459 100% identity in 1015 nt overlap with sequence ID no.1 (627-1641:1-1014) * * 100% identity in 158 aa overlap with sequence ID no.2 (210-367:1-158) * abstract --- -/--	1,3,5-7, 11,13,15

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
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"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

24 July 2001

Date of mailing of the international search report

26. 10. 01

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel: (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

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LE CORNEC N.D.R.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/29052

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 4 766 075 A (PENNICA DIANE ET AL) 23 August 1988 (1988-08-23) cited in the application the whole document ---	
A	WO 97 29765 A (UNIV CALIFORNIA) 21 August 1997 (1997-08-21) cited in the application ---	
P,X	DATABASE EMBL [Online] AF226048, accession number AF226048, 21 July 2000 (2000-07-21) Y. LI ET AL: "a novel gene expressed in human liver non-tumor-tissue" XP002165460 * 100% identity in 1641 nt overlap with sequence ID no.1 (1-1641:83-1723) * * 100% identity in 546 aa overlap with sequence ID no.2 (1-546:1-546) * abstract & UNPUBLISHED, ---	1,3,5-7, 9,11, 13-15
P,X	DATABASE EMBL [Online] AK000833, accession number AK000833, 22 February 2000 (2000-02-22) S. SUGANO ET AL: "Homo sapiens cDNA FLJ20826 fis, clone ADSE00129. NEDO human cDNA sequencing project" XP002165461 * 99,45% identity in 546 aa overlap with sequence ID no.2 (1-546:1-546) * * 99,81% identity in 1641 bp overlap with seq ID no.1 (1-1641:91-1731) * abstract & UNPUBLISHED, -----	1,3,5-7, 9,11, 13-15

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/29052

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1, 3-7, 9, 11, 13-20, all partially.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Invention 1: Claims (1,3-7,9,11, 13-20) all partially

Polypeptide represented by sequence ID no.M, wherein M is 2 and polynucleotide encoding it represented by sequence ID no.N, wherein N is M-1 (=1). Expression vector. Cultured cell. Antibody.

2. Claims: Invention 2 : Claims (1,3-7,9,11, 13-20) all partially

Polypeptide represented by sequence ID no.M, wherein M is 4 and polynucleotide encoding it represented by sequence ID no.N, wherein N is M-1 (=3). Expression vector. Cultured cell. Antibody.

3. Claims: Inventions 3-211: Claims (1-20) all partially

Polypeptide represented by sequence ID no.M, wherein M is an even integer from 6 to 422 and polynucleotide encoding it represented by sequence ID no.N, wherein N is M-1. Expression vector. Cultured cell. Antibody.

INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/US 00/29052

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Inter. Application No

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